

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 174325

TO: Patricia Duffy

Location: REM-3B05/3C18

Art Unit: 1645

Thursday, December 22, 2005

Case Serial Number: 10/077137

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Duffy,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist REM-1A65 571-272-2527



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From:

Duffy, Patricia

Sent: To: Thursday, December 15, 2005 9:06 AM

STIC-Biotech/ChemLib

Subject:

SEQUENCE SEARCH 10/077,137

IN RE: 10/077,137

PLEASE SEARCH RESIDUES 1-51 OF SEQ ID NO:1. PLEASE SEARCH RESIDUES 8-41 OF SEQ ID NO:1

VECESVE DEC 15 76 STOPPED LE

PLEASE SEARCH BOTH COMMERCIAL AND INTERFERENCE DATABASES. PLEASE PRINT OUT TOP 75 HITS IN EACH CATEGORY.

THANKS MUCHO.

Patricia A. Duffy, Ph.D. Art Unit 1645 Remsen 3B05; Mailbox 3C18 571-272-0855

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#_____ AA#:____

S/L:___ Oligomer:____

Encode/Transl:____

Structure #:____Text:___

Inventor:____ Litigation:___

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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aci BAF B-C BCM

protein

Run on:

Searched:

Database

Result

Sequence:

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Mouse tum
Mouse tum
Vumor nec
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Murine sub
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The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA), APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroms or The scleroms or multiple scleroms or diseases (GVHD) and inflammation. The present sequence represents an extracellular domain of BCMA.
                                                                                                                                                                                                                                                                                          New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.
cytostatic; neoplasm; immunosuppressive; therapeutic; B-cell maturation antigen; BCMA.
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                                                                                                                                                   04-AUG-2004; 2004WO-US025247
                                                                                                                                                                              29-JAN-2004; 2004US-0540271P.
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Best Local Similarity
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                                                                                  WO2005075511-A1
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Gaps

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Length 52; Indels

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BCWA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
 51
                 51
1 MLQMAGQCSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                               /note= "putative transmembrane domain"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                     AAB08843 standard; peptide; 184 AA
                                                                                                                                                           Amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                      24-FEB-2000; 2000WO-US004925
                                                                                                                                                                                                                                                                                                        WO200050633-A1
                                                                                                                                                                                                                                                                                                                               31-AUG-2000
                                                                                                                                                                                                                                                                      Domain
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APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;

Amino acid sequence of an extracellular domain of BCMA.

(first entry)

20-OCT-2005

AECO2032 ID AECC XX AC AECC XX XX DT 20-C XX XX XX XX AMir XW APRI

AEC02032

AEC02032 standard; peptide; 52

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The present sequence represents a BCWA (not defined) polypeptide. BCWA is a necrosis factor (NF)-kB activator. The method of the invention is used to indentify compounds which modulate BCMA activity (and thus NF-kB crivity). The specification describes a method of identifying a retivity). The specification describes a method of identifying a library of with a cell which expresses a recombinant anti-cell death gene expression from a promoter. The method is involves context, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCWA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatory bowel disease or septic shock. BCWA is useful for inflammatory bowel disease or septic shock. BCWA is useful for a contactifying compounds that modulate NF-kB expression and thus for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAMI-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autonommune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; renal neoplasm; multiple myelonephritis; venal neoplasm; multiple myelonephritis; venal neoplasm; multiple myelone; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                    Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 283; DB 3;
100.0%; Pred. No. 1.4e-25;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94001 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                Claim 32; Fig 7A; 53pp; English.
99US-0121485P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-2000; 2000WO-US000396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-2000 (first entry)
                                          (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
                                                                                                                            WPI; 2000-558405/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 184 AA;
                                                                                    Ting A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200040716-A2
24-FEB-1999;
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                                                                                                                                                                                                                                          expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    designing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                    Seed B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor. The receptor. The attendur necrobis factor (TNF) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting zuff activity. Zaff4 is a TMF ligand. They may also be used for inhibiting zuff4 activity. Zaff4 is a TMF ligand. They may also be used for inhibiting staff activity. The antibody production of the activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with an autibody production. The antibody production is associated with an autibody production. The antibody production systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The zinf4 activity asthma, bronchitis, emphysema, end stage renal failure, associated with asthma bronchitis, emphysema, end stage renal failure, associated with an asthma, multiple myelomas, lymphomas, light chain neuropathy, can be used to treat hypertension, graft versus host disease, inflammation, insulin dependent capection, graft versus host disease, inflammation, insulin dependent septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
                                                                                                                                                                               Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 283; DB 3;
100.0%; Pred. No. 1.4e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                   Disclosure; Page 152; 175pp; English.
                                                                                 Yee DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE09241 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-2000; 2000US-0182938P.
22-AUG-2000; 2000US-0226986P.
07-JAN-1999; 99US-00226533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2000; 2000WO-US032378.
                                                                                 Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                        (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                          WPI; 2000-452538/39.
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                                                                                 Χu w,
                                                                                                                                               N-PSDB; AAA58559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200160397-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                 Gross JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE09241;
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Shu HS;

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Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1;
Therapy; autoimmume discorder; rheumatoid arthritis; multiple sclerosis;
systemic lupus erythematosus; SLB; insulin dependent diabetes mellitus;
thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
haemolytic ansemid; Grave's disease; mysathenia gravis; chromosome 16;
post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human BCMA protein
                                                                 Grewal I, Kim KJ, Marsters SA, Pitti RM;
                                                                                                                                                                                                                                                                     Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLITCORYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG
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100.0%; Pred. No. 1.4e-25;
tive 0; Mismatches 0;
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/label= Extracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71979 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2, Fig 2, 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-2000; 2000WO-US012266.
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                                                                    Ashkenazi AJ, Dodge KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
(GETH ) GENENTECH INC.
                                                                                                                                                                          WPI; 2001-541628/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 184 AA;
                                                                                                                                                                                                           N-PSDB; AAD15902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200068378-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1999;
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                                                                                                            Yan M;
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The present invention relates to Tumour necrosis factor (TNF) and Apolcalated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in comparing the interaction between TALL computed and their antibodies. The invention in the comparing the interaction between TALL controllers (ECMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus controllers; machenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, contemponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a human B cell maturation factor (BCMA) protein. The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome contemporation is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome contemporation is absent in the pro-B lymphocyte stage but its expression contemporation in the pro-B lymphocyte stage but its expression contemporation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human BAFF.R; BAFF receptor; TNF family; immunoregulatory agent; immuno-related disorder; B-cell growth inhibitor; BGMA; becall maturation inhibitor; immuno-related disorder; B-cell jarowth inhibitor; autoimmune disorder; B-cell jymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                                                                                  Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphoma; gene therapy; cancer; tumour
                                                                                                                                                                                                             Claim 37; Page 104-105; 112pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human BAFF receptor (BAFF-R).
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                                                           WPI; 2001-016094/02
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Matches 51; Conserv
                                                                                  N-PSDB; AAD02125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 184 AA;
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Length 184; 0; Indels 2

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WO200124811-A1

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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) the acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. Specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders, R-cell lymphoproliferative be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, cumpuressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF-R inhibitis inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases
                                                                                                                                                                                                                                                                                                      Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
                                                                                                                                                               Tschopp J, Schneider P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents human BAFF-R
                                                                                                                                                               Ambrose C,
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Fig 1; 59pp; English.
                   11-FEB-2000; 2000US-0181684P.
99US-0149378P
                                                                                                                   (APOT-) APOTECH R & D SA
                                                                                                                                                                  Browning J,
                                                                                                                                                                                                                                      2001-202866/20
                                                                                          BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                             N-PSDB; AAF59998
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17-AUG-1999;
                                                                                                                                                             Mackay F, B
Thompson J;
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                                   Gaps
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                                                                1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLICORYCNASVTNSVKG
100.0%; Score 283; DB 4; Length 184; 100.0%; Pred. No. 1.4e-25; Live 0; Mismatches 0; Indels (
                                  51; Conservative
                 Local Similarity
 Query Match
                                   Matches
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Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autofimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-call lumpho-profilerative disorder; BCW; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCWA; B cell maturation protein.
1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVINSVKG
                                                                                                                                                                                                                               Human B cell maturation protein (BCMA).
                                                                                                              AAE00506 standard; protein; 184 AA.
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                           31-JUL-2001
                                                                                                                                                    AAE00506;
                                                                        RESULT 7
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Homo sapiens

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The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A referred with undesired cell proliferation comprising A relation by the control (BCM or BCMA) antagonist that antagonises the metucation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, carcinoma, breast carcinoma, colon carcinoma, breast carcinoma, colon carcinoma, breast carcinoma, consistent carcinoma, breast carcinoma, colon carcinoma, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a mammal for a condition associated with undesired cell
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100.0%; Pred. No. 1.4e-25;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 3A; 85pp; English.
                                                                                                                                                          06-OCT-1999; 99US-0157933P.
11-FEB-2000; 2000US-0181807P.
30-JUN-2000; 2000US-0215688P.
                                                                                                           05-OCT-2000; 2000WO-US027579.
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                                                                                                                                                                                                                                                                                                                                                                Schneider P, Thompson J,
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Best Local Similarity 100.
Matches 51, Conservative
                                                                                                                                                                                                                                                                                                         (APOT-) APOTECH R & D SA.
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                                                       12-APR-2001
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Gross JA,

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The present sequence is the protein sequence of a human polypeptide encoded by a gene that exhibits decreased expression in colon cancerderived metastases compared to normal colon tissue. It is an example of claimed polypeptides that are encoded by genes which are differentially expressed in metastatic colorectal cancer cells. Such polypeptides are useful in diagnostic and prognostic assays, for raising antibodies useful e.g. in immunotherapy, and in screening for modulator compounds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes that are up- or down-regulated in colorectal cancer, useful for diagnosing colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; tumour; B-cell maturation antigen; transmembrane activator; calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy; neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease; non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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/note= "Extracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human B-cell maturation antigen (BCMA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE28961 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                          (EOSB-) EOS BIOTECHNOLOGY INC.
(UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 255; 260pp; English.
diagnosis; gene therapy; vaccine.
                                                                                                                                                                                                                              27-FEB-2001; 2001US-0272206P.
02-APR-2001; 2001US-0281149P.
17-APR-2001; 2001US-0284555P.
                                                                                                                                                                                   27-FEB-2002; 2002WO-US006001
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                Markowitz SD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-698677/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapeutic value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABQ81560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 184 AA;
                                                                                           WO200268677-A2
                                                Homo sapiens.
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                                                                                                                                     06-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention describes a numan tumour neclosity factor designated Zinfill (I). (I) has cytostatic, immunosuppressive, dermatological, antinflammatory, neuroprotective, antidiabetic, antianthratic, antianthratic, antidiabetic, antidiathratic, antianthratic, antidiathratic, and can be used in gene therapy. (I) can be used for activities, and can be used in gene therapy. (I) can be used for (e.g. ZTNR4), for treating disorders and diseases associated with B (C) inhibiting the proliferation of tumour cells. (I) is useful for treating inhibiting the proliferation of tumour cells. (I) is useful for treating cutoimmune disorders such as systemic lupus erythematosus, mysathenia cyrhematoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as systemic lupus erythematosus, mysathenia creaming arthritis, and pyelonephritis, and for treating renal cleakemia, nephritis, and pyelonephritis, and for treating renal contents multiple myelomas, lymphomas, light chain neuropathy, or meoplasms, multiple myelomas, lymphomas, light chain neuropathy, or modulating the immune system, for regulating B cell responses and development of other cells, antibody cy production and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a human tumour necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colorectal cancer; metastasis; differential expression; cytostatic;
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  light chain neuropathy, hypertension, large vessel disease, graft-versus host disease; graft rejection, Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 135-136; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Grant FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP54694 standard; protein; 184 AA
                                                                                                                                                                                                                                                           07-NOV-2000; 2000US-0246449P.
20-DEC-2000; 2000US-025131P.
28-JUN-2001; 2001US-0315555P.
29-AUG-2001; 2001US-0315555P.
                                                                                                                                                                                                                05-NOV-2001; 2001WO-US047018.
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                                                                                                                                                                                                                                                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-508212/54.
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                                                                                                                         WO200238766-A2
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                                                                           Homo sapiens
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ABP54694;

ABP54694
ID ABP5
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RESULT 9

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Query Match Best Local S Matches

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The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumnour necrosis factor-like protein (ZYNF)2 or ZYNF4, and an immunoglobulin group comprising a constant region of immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumnour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. apomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is human B-cell maturation receptor (BCMA) protein used in the invention
                                                                                                                                                                                                                                                                          Transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACI receptor group and an immunoglobulin group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; TALL-1; antagonist; immunosuppressive; antirheumatic; antinflammatory; antiarthritic; dermatological; antidiabetic; neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic; vasotine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple solerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 283; DB 6; Length 184; 100.0%; Pred. No. 1.4e-25; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA49361 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 100; 71pp; English
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14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
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20-MAY-2002; 2002WO-US015910.
                                                  24-MAY-2001; 2001US-0293343P.
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                                                                                                     (ZYMO ) ZYMOGENETICS
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Best Local Similarity
                                                                                                                                                                                                          2003-148455/14.
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                                                                                                                                                                                                                                  N-PSDB; AAD53754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 184 AA;
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                                                                                                                                                       Rixon MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the manufacture of a composition for inhibiting the proliferation of tumour cells. The method involves using an antibody component that binds both the B-cell maturation antigen (BCMA) and the transmembrane activator and calcium-modulator and cyclophilin ligand interactor (TACI). BCMA and TACI binding antibody compositions are useful for inhibiting proliferation of tumour cells, particularly inhibiting ZTNF4 activity in a mammal associated with increased endogenous antibody production or a disorder consisting of neoplasm, chronic lymphocytic luckeemia, multiple myeloma, non-Hodgkin's lymphomy or inflammation lymphoproliferative disease or light chain gammopathy or inflammation e.g. asthma. The invention is also useful in gene therapy. The present is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunoglobulin; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; B-cell maturation receptor; BCMA; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-cell maturation antigen and transmembrane activator and calcium-modulator and cyclophilin ligand-interactor, useful for treating disorders e.g. inflammation or lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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100.0%; Pred. No. 1.4e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human B-cell maturation receptor (BCMA) protein.
     /note= "Cysteine rich region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE35216 standard; protein; 184 AA
                                                                                                                                                          06-FEB-2002; 2002WO-US003500
                                                                                                                                                                                                          20-FEB-2001; 2001US-0270274P.
12-APR-2001; 2001US-0283447P.
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                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                          2002-723183/78,
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                                                  WO200266516-A2
                                                                                                                                                                                                                                                                                                                                       Kindsvogel W;
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                                                                                                       29-AUG-2002
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Best Local S
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                                                                                                                                                                                                       The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID No.2, or amino acids 134-285 of SEQ ID NO.2, by at least one modification in the region connecting &bgr; strands D and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antitheumatic, antiinfiammatcry, antiarthritic, dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 a vaccine. A protein of the invention is useful for inhibiting TALL-1 a shead in a mammal. TC is useful for treating autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, chrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, chrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis and cut the present sequence represents human BCMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatological; immunosupecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic; antipsoritatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD; inflammatory disorder; proliferative disorder; single chain antibody; antibody; human; BCMA; tumour necrosis factor.
                                                                                                                 Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 283; DB 6;
100.0%; Pred. No. 1.4e-25;
iive 0; Mismatches 0;
                          (NAJE-) NAT JEWISH MEDICAL & RES CENT.
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                                                                                                                                                                                      Claim 62; Page 613; 618pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour necrosis factor BCMA.
                                                      Xu L;
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 13-AUG-2002; 2002US-0403364P.
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51; Conservative
                                                      Shu H, Liu Y,
                                                                                WPI: 2003-403345/38
                                                                                              N-PSDB; ADA49360
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 184 AA;
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                                                       Zhang G,
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The invention relates to a novel antibody or its fragment, which continuous training the invention relates to a novel antibody of the invention has dermacological, immunosupcressive, antibody of the invention has dermacological, immunosupcressive, antibody of the invention, antibarthritic, cytostatic, antianaemic, antiallergic, antibody or antianted, antialbedic, antipostatic, antiallergic, antianted, antialbedic, antipostatic, anti-HIV, tuberculostatic, antiabedic, antiabedic, antiabedic, antiabedic, antiabedic, antiabedical, immunosubcaterior, and antiabedic, antiabedic, antiabedical, immunosubcaterior, antiather, antiabedic, antiab
                                                                                                                                                                                                                                                                   Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
TALL-1; April; systemic lupus erythematosus; BCMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of human BCMA receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 222; 225pp; English.
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Best Local Similarity 100.0%;
Matches 51; Conservative 0
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30-APR-2002; 2002US-0377171P.
(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome.
                                                                                              Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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                                                                                                                                                                  The present sequence represents a human BCMA polypeptide. The specification also describes TACI and BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April bind to the TACI receptor, while TMF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for preparing a composition for treating systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haematological malignancy; immunoconjugate; cytostatic; immunostimulant; vaccine; immunotherapy; cancer; multiple myeloma cell; chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hematological malignancy-related genes and polypeptides, useful screening anti-cancer agents, and generating antibodies or immunoconjugates for treating e.g. multiple myeloma cell or chronic lymphocytic leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ordonez N;
                                                                                               New nucleic acid encoding a TACIs or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                      1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                        1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                 Length 184;
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                                                                                                                                                                                                                                                                                   100.0%; Score 283; DB 6; 100.0%; Pred. No. 1.4e-25; 100.0%; Mismarches 0;
                             Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 4; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD67527 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mannion J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Ly1732P protein SEQ ID NO:4.
                                                                                                                                         Disclosure; Fig 2; 153pp; English
                           Ridgway J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2003; 2003WO-US002353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                             51; Conservative
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Mcneill PD;
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-598749/56.
N-PSDB; ADD67526.
                           Grewal I,
                                                       2003-256560/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                               Similarity
                                                                      N-PSDB; ABZ68871
                                                                                                                                                                                                                                                                      Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003062401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Carter L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD67527;
                           Dixit V,
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
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The present invention describes an isolated polynucleotide (I), which is overexpressed in haematological malignancies, and which encodes a polypeptide or an immunogenic fragment of the polypeptide. Also

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described: (1) an isolated polypeptide; (2) an expression vector comprising (1) operably linked to an expression control sequence; (3) a host cell comprising an expression vector; (4) an isolated antibody that specifically binds to the polypeptide or its immunogenic fragment; and (5) immunoconjugates comprising the antibody above, or an antibody that specifically binds to a polypeptide or its immunogenic fragment, encoded (5) immunoconjugates comprising the antibody above, or an antibody that specifically binds to a polypeptide, or its immunogenic fragment, encoded (7). (1) has cytostatic and immunostimulant activities, and can be used in vaccines and immunotherapy. The immunoconjugates are useful in composition for treating cancer, e.g. multiple myeloma cell, chronic composition for treating cancer, e.g. multiple myeloma in humans, sheep, primates, goates, bovines, equines, portines, lupines, canines or felines. The polynucleotide (1) or polypeptide can be used for screening anti-cancer agents, and generating antibodies or immunoconjugates for treating cor preventing the above-mentioned isseases. The polynucleotide, or antibody can be used for detecting, diagnosing or prognosticating the haematclogical malignancies described above. The prognosticating the haematclogical malignancies described above. The present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for treating a neurodegenerative immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand (the mammal has or is at risk of developing multiple sclerosis). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating a neurodegenerative immunological disorder, e.g. demyelination or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human, neurodegenerative immunological disorder, demyelination,
Central Nervous System, CNS, inflammation, B-cell maturation antigen,
BCMA; multiple sclerosis, neuroprotective, nootropic, antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 283; DB 7;
100.0%; Pred. No. 1.4e-25;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human B-cell maturation antigen SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG43715 standard; protein; 184 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 184 AA;
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Pred. No. 1.4e-25; Mismatches 0;

51; Conservative

Matches

Best Local Similarity

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method of the invention has neuroprotective, nootropic, and antinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence represents human BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti-TACI receptor monoclonal antibody, useful for diagnosing and treating pathological conditions associated with tumor necrosis factor, e.g. cancer or immune-related disease, such as rheumatoid arthritis or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAML interactor receptor; TACI; Cytostatic; Antiinflammatory; Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic; Antidabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV; Antibacterial; antiparastic; systemic lupus erythematosus; diabetes mellitus; AIDS; BCMA.
                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                       1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                  1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                             Length 184;
                                                                                                                                           100.0%; Score 283; DB 7;
100.0%; Pred. No. 1.4e-25;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 6; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim KJ,
                                                                                                                                                                                                                                                                                                                                             ADK00756 standard; protein; 184 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chuntharapai A, Grewal I,
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                               51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-143841/14.
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Native human BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADK00755
                                                                                                            Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004011611-A2
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                                                                                                                                                                                   Matches
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This sequence represents neutrokine-alpha, BCWA, which may be used in the protein conjugate of the invention. The neutrokine-alpha protein conjugate of the invention. The neutrokine-alpha protein conjugate comprises neutrokine-alpha protein and chelator, where the conjugate comprises neutrokine-alpha protein (also known as B-lymphocyte stimulator (BLyS), TALL-1, THANK and BARF) is capable of binding neutrokine-alpha receptor and is selected from full length or mature neutrokine-alpha protein. The protein conjugate of the invention is useful in a complex with a metal ion associated with the chelator which is useful for administering radiotherapy, which involves administering the complex to the subject, where it is administered as an injectable solution, and the subject has a B-cell mediated disease. The subject has a condition chosen from non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus crythematosus, rheumatodid arthritis, multiple myeloma, systemic lupus creferably non-Hodgkin's lymphoma. The complex is useful for treating cancer, which involves administering it to a subject having cancer, where a cell of the cancer expresses a neutrokine-alpha receptor on its sufface. The cancer is a B cell cancer, which is chosen from non-Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                   neutrokine-alpha; chelator; B-lymphocyte stimulator; BLyS; TALL-1; THANK; BAFF; neutrokine-alpha receptor; complex; metal ion; radiotherapy; BAFF; neutrokine-alpha receptor; complex; metal ion; radiotherapy; chroinic disease; non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; multiple myeloma; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; crohn's disease; diabetes; Wegener's granulomatosis; myasthenia gravis; asthma; cancer; Sjogren's syndrome; diagnostic imaging; lymphocyte; B cell; cancerous cell; metastasis; lymphatic system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neutrokine-alpha conjugate useful for targeting complexed metal ion to cells expressing receptor (predominantly lymphoid) for radiotherapy treatment of, for example, non-Hodgkin's lymphoma comprises neutrokinealpha protein and chelator.
                                                                  1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                            1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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100.0%; Prec. ....
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                                                                                                                                                                                                                             ADQ94442 standard; protein; 184 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2003; 2003US-0467198P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                   Neutrokine-alpha, BCMA.
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infection, fungal infection, protozoal infection and parasitic infection. The present sequence represents native human BCMA.

Sequence 184 AA;

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The complex is also useful for treating an autoimmune disease or disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis and Sjogram's syndrome. The complex may also be used for disquostic imaging. A composition comprising the protein conjugate or the complex is useful for killing a cell chosen from a cell bearing a neutrokine-alpha receptor, and a cell in close proximity to a cell bearing neutrokine-alpha receptor, which involves contacting the cell bearing neutrokine-alpha receptor. The cell is lymphocyte, B cell or cancerous cell that has metastasised into the lymphatic system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antichyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated PRO nucleic acid (I). Also described: (1) a vector comprising (I); (2) a host cell comprising the vector of (I); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO polynucleotides and polypeptides, useful in useful in diagnosing treating an immune related disease, e.g. systemic lupus hematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                               1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                           Length 184;
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                                                                                                                                                                                                                                           100.0%; Score 283; DB 8; 100.0%; Pred. No. 1.4e-25;
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO protein sequence SEQ ID NO:1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP56014 standard; protein; 184 AA
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                                                                                                                                                                                                                                                                                     51; Conservative
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Wu TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004-376182/35.
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                        Sequence 184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP56014;
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cc comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a cmammal; (10) a method for determining the presence of a PRO polypeptide; in a sample suspected of having the polypeptide; (11) a method of disease or an inflammatory immune response continuaming; (12) a method of identifying a compound that inhibits or mammal; (12) a method of similating the immune response in a mammal. The mimics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal. The CC antisathmatic, antidiabetic, antidiflammatory, antipsoriatic, antidiabetic, immunostimulant, immunosuperssive, muscular, comprortopic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and in constant immune response. The present sequence represents a human constant invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive; non-hodgkin lymphoma; hodgkins disease; cytostatic; chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis; antiarthritic; antirheumatic; systemic lupus erythematosus; wegener granulomatosis; antiallergic; antiinflammatory; vasotropic; inflammatory bowel disease; gastrointestinal-gen.; inflammatory bowel disease; gastrointestinal-gen.; asthatic thrombocytopenic purpura; hemostatic; multiple sclerosis; asthma; antiasthmatic; psoriasis; antipsoriatic; muscular-gen.; neuroprocective; vasculitis; diabetes; antidiabetic; glomerulonephritis; nephrotropic; BCMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLQMAGQCSQNEYFDSLLHACIPCQRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 283; DB 8; Length 1
100.0%; Pred. No. 1.4e-25;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADW03432 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2003; 2003US-0476414P.
05-JUN-2003; 2003US-0476481P.
06-JUN-2003; 2003US-0476531P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-2004; 2004WO-US017693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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N-PSDB; ADW03431.
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Matches 51; Conserv
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population of cells, the method involves contacting the mixed population of cells with BLyS antagonist (e.g. an immunoadhesin) and a CD20 binding antibody (e.g. hu2H7.v16). The method of the invention is useful for treating B cell malignancies and autoimmune disorders, such as: non-Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas, lymphocytic leukemia, Hairy cell leukemia, rheumatoid arthritis, systemic lupus erythematoous, Wegener's disease, inflammantory bowel disease, idiopathic thrombocytopenic purpura, multiple sclerosis, asthma, psoriasis, IgA nephropathy, myasthenia gravis, vasculitis, diabetes and glomerulonephritis. The present amino acid sequence represents a human
                                                          The invention comprises a method of depleting B cells from a mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 283; DB 9;
100.0%; Pred. No. 1.4e-25;
ive 0; Mismatches 0;
                   Disclosure; Fig 2; 114pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                           BCMA protein.
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Gaps

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Length 184; Indels 5

necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis; Human tumor necrosis factor receptor BCMA. Location/Qualifiers Ą ADZ67760 standard; protein; 184 (first entry) Homo sapiens 14-JUL-2005 cytostatic ADZ67760; Domain Tumor ADZ67760

IID ADZ6

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I4-J

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I4-J

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I4-J

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I4-D

III

I4-J

6. .45 /note= "Cys-rich domain" WO2005037865-A2

28-APR-2005

18-OCT-2004; 2004WO-US034375

16-OCT-2003; 2003US-0511698P.

(ZYMO) ZYMOGENETICS INC

Holloway JL, Sheppard PO, WPI; 2005-315682/32 Fox BA,

Dillon SR

New tumor necrosis factor receptor (TNFR) polypeptides, useful as detecting ligands, and for modulating tumor growth, metastasis and immunity, such as separating resting from stimulated immune cells.

Disclosure; SEQ ID NO 8; 132pp; English.

In Invalidation provides and polypeptides ADZ67754, expression vectors polynucleocides ADZ67753 and polypeptides ADZ67754, expression vectors and antibodies. Ztnfr14 polynucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer are partient. Recombinant Ztnfr14 polypeptide, optionally conjugated to toxin, is used in a claimed method of killing cancer cells. Ztnfr14 The invention provides novel tumor necrosis factor receptor ztnfr14

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The invention describes a method of inhibiting the growth of a cell that expresses a protein comprising contacting the cell with an antibody, cligopeptide or organic molecule that binds to the protein, the binding of free antibody, oligopeptide or organic molecule to the protein and causing an inhibition of growth of the cell. Also described is a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of a protein having at least 80 % amino cid sequence identity to: a polypeptide having any of SEQ ID NO: 2, 8, 10, 12, 16, 20, 22, 49 and 51; a polypeptide having the amino acid sequence of (a), lacking its associated signal peptide; an extracellular sequence of (a), lacking the amino acid sequence of (a), with or without its associated signal peptide; a polypeptide encoded by any of SEQ ID NO: 1, 7, 9, 11, 15, 19, 21, 48 and 50; or a polypeptide encoded by the full-length coding region of the nucleotide sequence of (d), comprising administering to a subject in need of such treatment an antagonist of the protein, and effectively treating or preventing the
                                                                                                                                                                                                                       ö
polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modilate tumor growth, metastasis, and immunity such as separating resting from stimulated immune cells. The present sequence is that of human TNFR BCMA. This sequence was compared with that of ztnfr14 in the identification of ztnfr14 as a member of the TNFR Family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting the growth of a cell that expresses a protein by contacting the cell with anti-tumor antigens of hematopoietic origin (TAMO) polypeptide, antibody or organic molecule, useful for treating hematopoietic and malignant tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein purification;
                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                           1 MLOMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                    1 MLQWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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                                                                                                                                                                                100.0%; Score 283; DB 9; Length 1
100.0%; Pred. No. 1.4e-25;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; therapy; cell growth; DNA purification; hyperproliferation; neoplasm; tumor antigen of hematopoietic origin; TAHO23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor antigen of hematopoietic origin TAH023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FJ, Eaton DL,
                                                                                                                                                                                                                                                                                                                                                                                                          AEA23348 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2003; 2003US-0520842P.
24-DEC-2003; 2003US-0532426P.
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                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                       Similarity
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                                                                                                                                               Sequence 184 AA;
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                                                                                                                                                                                        Local Sim
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                                                                                                                                                                                      Query Match
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Matches
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cell proliferative disorder. Also disclosed are anti-tumor antigens of hematopoietic origin (TAHO) polypeptides, encoding nucleic acids, oligopeptides, vectors, host cells and antibodies used in the methods of the invention. The methods and compositions of the present invention are useful for treating hematopoietic and malignant tumors in mammals. This is the amino acid sequence of tumor antigen of hematopoietic origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;
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                                                                                                                                                                                                                                                                                                                                                                  Length 184;
                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 283; DB 9;
100.0%; Pred. No. 1.4e-25;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amin acid sequence of a BCMA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEC02031 standard; protein; 184 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-cell maturation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents a BCMA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                               Sequence 184 AA;
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AECO2031
ID AECO2
XX
AC AECO2
XX
DT 20-OC
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DE Amin
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DE ABCO2
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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TMF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and reached disorders. BAFF-R, fusion proteins containing it, and BAFF-R-C related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-C related disorders and be used for inhibiting B-cell growth, dendritic and in the treatment of autoimmune disorders. B-cell lymphoproliferative and in the treatment of autoimmune disorders. B-cell lymphoproliferative cell-induced B-cell growth and maturation, and immunoglobulin production, be used in the treatment of immunosuppressive disorders and HIV concerns or BAFF-R specific antibodies may be used for treating.

C suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R such as systemic lupus erythematosus, autoimmune haemolytic anaemia, cancer as disease, multiple myeloma, B-cell carcinomas, leuksemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
                                                                                                                                                                                                                                                                                                                Human BAFF.R; BAFF receptor; TNP family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; diminibitor; manunoglobulin production inhibitor; autoimmuned disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; autoimmune haemolytic anaemia; grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
                                                                                                                                                                                                                                                                               Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
1 MLQWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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                                                                                                                                 Z
                                                                                                                            AAB60699 standard; protein; 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1999; 99US-0149378P.
11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
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                                                                                                                                                                                                                 (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                 11-SEP-2003
22-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mackay F,
                                                                                                                                                                         AAB60699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric.
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Query Match 100.0%; Score 283; DB 9; Best Local Similarity 100.0%; Pred. No. 1.4e-25; Matches 51; Conservative 0; Mismatches 0;

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Gaps

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0; Indels

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human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents the BAFF-R fusion protein BAFF-R-FC, comprising a mouse IgG-kappa signal sequence, residues 1-153 of human BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Mature_human_BCMA_IgG_Fc_fusion_protein
23. 75
                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                          24 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 74
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/label= Signal peptide
/note= "Derived from murine Ig kappa sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rennert P;
                                                                                                                                                                                                                                                                                                                                                                            1 MLOMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                         100.0%; Score 283; DB 4; Length 302; 100.0%; Pred. No. 2.4e-25; ive 0; Mismatches 0; Indels
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/note= "Derived from human IgG Fc region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Derived from human BCMA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BCMA-Immunoglobulin G Fc region fusion construct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24. .302
/label= Cysteine rich domain
/note= "Derived from human BCMA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE00507 standard; protein; 302 AA.
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11-FEB-2000; 2000US-0181807P.
30-JUN-2000; 2000US-0215688P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                       51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
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                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD03847.
                                                                                                                                                                                                      Sequence 302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200124811-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric.
                                                                                                                                                                                                                                                                  Query Match
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11D AAE00507
11D AAE00507
XX AAE0
XX 11.-S
DT 11.-S
DT 31.-J
DE Huma
XX Huma
XX Huma
XX Garc
XW Garc
XW Organ
XX CALM
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The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A B relation comprising A B relation comprising A B relation protein Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(8). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, carcinoma, breast carcinoma, and other carcinomas whose proliferation B modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLB); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, cimmunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering on immuno construct containing human APRIL-R also referred as BCMA or BCM protein, Pc region of human immunoglobulin G (IgG) and a signal construct containing human APRIL-R also referred as BCMA or protein, profession of human immunoglobulin G (IgG) and a signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
         Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; neurodegenerative immunological disorder; demyelination;
Central Nervous System; CNS; inflammation; B-cell maturation antigen;
BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
gene therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 283; DB 4; Length 3
100.0%; Pred. No. 2.4e-25;
ive 0; Mismatches 0; Indels
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1. .23
/note= "Murine IgGkappa signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24. .74
/note= "Human BCMA extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75. .302
/note= "Human Ig heavy chain Fc region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human B-cell maturation antigen-Fc SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG43717 standard; protein; 302 AA
                                                                                                         Example 1; Fig 3B; 85pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 302 AA;
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                                                                         antagonist.
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06-AUG-2001; 2001US-0310754P.
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                                                                                                                                                                                                                                                                                                                                                        50; Conservative
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N-PSDB; ABS73235.
                                                                   WPI; 2003-268160/26.
                                              Dialynas
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                      (GEST ) GENSET SA
                                                                                N-PSDB; ACC00340.
                                                                                                                                                                                                                                                                                                              Sequence 184 AA;
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                                               Lucas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG95060;
                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                    The invention relates to a novel method for treating a neurodegenerative immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand (the mammal has or is at risk of developing multiple sclerosis). The method of the invention has neuroprotective, nootropic, and antiinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant; antidiaberic; hypotensive; ophthalmological; neuroprotective; nephrotropic; obseity; Tumour Necrosis Factor Receptor Super Family; Type III transmembrane protein; insulin resistance; atherosclerosis; atheromatous disease; heart disease; hypertenaion; stroke; syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia.
                                                                                                     Treating a neurodegenerative immunological disorder, e.g. demyelination
                                                                                                                 or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
                                                                                                                                                                                                                                                                                                                                                           Gape
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                                                                                                                                                                                                                                                                                                                                                                                1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                 Length 302;
                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 283; DB 7;
100.0%; Pred. No. 2.4e-25;
Live 0; Mismatches 0;

    .54
    /label= Extracellular domain

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/label= Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Transmembrane_domain
                                                                                                                                                 Claim 12; Page 70-71; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR40082 standard; protein; 184 AA
21-FEB-2002; 2002US-0358427P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                         51; Conservative
                                                                   WPI; 2003-721758/68
                      (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                              N-PSDB; ADG43718.
                                                                                                                                                                                                                                                                                                             Sequence 302 AA;
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                                             SI,
                                                                                                                                                                                                                                                                                       invention
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                                          Kalled
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The present invention relates to the use of an agonist or antagonist of Genoxit activity for preventing or treating obesity. Genoxit is a member of the Tumour Necrosis Factor Receptor Super Family and is a Type III transmembrane protein. The agonists or antagonists of the invention are useful for treating or preventing obesity-related diseases or disorders, e.g. obesity, insulin resistance, atherosels, atheromatous disease, heart disease (e.g. cardiac insufficiency, coronary insufficiency, high blood pressure), hypertension, stroke, syndrome X, diabetes mellitus (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic complications, e.g. microangiopathic lesions, ocular lesions, retinopathy, neuropathy and renal lesions
New use of agonist or antagonist of Genoxit activity for preventing or treating obesity-related diseases or disorders, e.g. hyperlipidemia and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosome aberration, oncogenic fusion protein, cancer, protein 90; proliferative disease, cellular protein isoform, heat shock protein 90; HSP-90; rheumatoid arthritis, cancer, hematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; APL; NL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
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98.0%; Pred. No. 7.3e-25;
ive 0; Mismatches 1.
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                                                                                                                                                                                 Disclosure, Page 32; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG95060 standard; protein; 288 AA
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Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCWA; tumour necrosis factor; TNF; Pymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; coln; a disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
     Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90.
                                                                                                                                                                                                                                                                              This represents a protein encoded by the DNA sequence of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human B-cell maturation (BCMA) protein extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                            2 LOMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                96.8%; Score 274; DB 5; Length 288; 98.0%; Pred. No. 2.7e-24;
                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                  Disclosure; Page 189-190; 389pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE15485 standard; peptide; 51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0214591P.
2001US-00214591.
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Best Local Similarity 98.vv.
Best Local Similarity
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                                                                                                                                                                                                                                                                                                              Sequence 288 AA;
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14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                nfections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5. .38 hote= "Cysteine-rich consensus region; This is region is specifically claimed as SEQ ID NO: 7 in claim 1 of the specification"
                                                                           Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic demaritis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colltis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein extracellular domain
                                                                                                                                                                                                                          The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering specific binding partner for ARRIL (GTO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI BCMA extracellular consensus sequence, but not the extracellular region of TACI and/or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell symphoproliferative disporders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. ARRIL, BCMA, and TACI entagonists are useful for treating inflammation and immune function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 1.7e-24; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE15484 standard; protein; 181 AA
                                                                                                                                                                                           Claim 1; Fig 10A; 94pp; English.
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                                          WPI; 2002-066686/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 51 AA;
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rheill LE,
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Region
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding patter for APRIL (G70, a tumour necrosis factor-TNF Eamly ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI and/or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative discorders, one or more solid tumours such as lung, gastrointeetinal, pancreatic or proseate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dereases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dematitis, respiratory allergic disease (asthma, hypersensitivity lung dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, collitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atheroscise, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.1%; Score 269; DB 5; 100.0%; Pred. No. 1e-23; iive 0; Mismatches (
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                                                                                                               14-MAY-2001; 2001WO-US015567.
                                                                                                                                                                                             27-JUN-2000; 2000US-0214591P.
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nes 48; Conservative
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WO200187979-A2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
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100.0%; Pred. No. 6.5e-24;
ive 0; Mismatches 0; Indels
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                                                                                                            12-MAY-2000; 2000US-0204039P
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                                                         14-MAY-2001; 2001WO-US015567
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22-NOV-2001
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WO2005075511-A1

Homo sapiens

Human;

RESULT 31 AAE15488

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                                                                                                                                                                                                                    The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TMF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroward or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a BCMA-Fc fusion protein, where I22 of BCMA is changed to Lys.
                                                                                                                                      New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                 90.8%; Score 257; DB 9; Length 296; 97.9%; Pred, No. 2.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               5 AGOCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                 Example 6; SEQ ID NO 31; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis; atherosclerosis
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2001US-00214591.
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                       04-AUG-2004; 2004WO-US025247.
                                              29-JAN-2004; 2004US-0540271P.
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                                                                                                                                                                                                                                                                                                                                                                                          46; Conservative
                                                                    (GETH ) GENENTECH INC.
                                                                                          Kelley RF, Patel D;
                                                                                                                 WPI; 2005-555932/56.
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                                                                                                                                                                                                                                                                                                                                            Sequence 296 AA;
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14-MAY-2001;
                                                                                                                                                                            inflammation.
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 18-AUG-2005
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a pecific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI or TACI or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI cantagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivtic) ung disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region
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                                                                                                                    Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tumor necrosis factor receptor (TNFR) polypeptides, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.7e-22;
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADZ67761 standard; protein; 40 AA.
                                                                                                                                                                                                                                                                                                Disclosure, Fig 13; 94pp; English.
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18-OCT-2004; 2004US-0619552P.
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Best Local Similarity
                                                                  WPI; 2002-066686/09
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Theill LE,
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                                                                             The invention provides novel tumor necrosis factor receptor zinfild polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors and antibodies. Zinfil4 polynucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant zinfil4 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Zinfil4 polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastasis, and immunity such as separating resting from stimulated immune cells. The present sequence is that of the Cys-rich domain of human TNFR BCMA ADZ67760. This sequence was compared with that of zinfil4 in the identification of zinfil4 as a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APRIL; BAFP; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic; B-cell maturation antigen; BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
detecting ligands, and for modulating tumor growth, metastasis and immunity, such as separating resting from stimulated immune cells.
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100.0%; Pred. No. 5.9e-20;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of an extracellular domain of BCMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GQCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                Disclosure; SEQ ID NO 9; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEC02033 standard; peptide; 38 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-2004; 2004WO-US025247
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Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                 Sequence 40 AA;
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The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple

Disclosure; SEQ ID NO 22; 140pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; lenkaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
                                                                                                                                                   Gaps
scleroma; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents an extracellular domain of BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
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                                                                                                                 Length 38;
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                                                                                                                                                 0; Indels
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                                                                                                                                                                                                            1 SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVT 38
                                                                                                                                  Pred. No. 3.4e-18;
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                                                                                                                 DB 9;
                                                                                                  76.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                   38; Conservative
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                                                                                                                                    Local Similarity
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                                                                             Sequence 38 AA;
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                                                                                                                 Query Match
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for AFRIL (G70, a tumour necrosis factor-INF
proteins or BAFF-R specific antibodies may be used for treating, between BAFF-R specific antibodies may be used for treating, between BAFF-R and altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, grave's disease, multiple myelom, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; crown's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                            present sequence represents a human BAFF-R protein sequence as encoded by plasmid PUST535. However, this BAFF-R protein sequence is 27 amino acids shorter than that given in AAB60698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
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                                                                                                                                                                                                                                                                                                                             72.8%; Score 206; DB 4; Length 157; 87.2%; Pred. No. 1.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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27-JUN-2000; 2000US-021459IP.
14-MAY-2001; 2001US-00214591.
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                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
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                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                          Sequence 157 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE15486;
                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                       Matches
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ID AAE1
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family ligand), having the consensus region of TACI, BCWA, or the TACI/
BCWA extracellular consensus sequence, but not the extracellular region
of TACI or BCWA. The method is useful for inhibiting activity of TACI
and/or BCWA in a mammal which is useful for treating B-cell or T-cell
indicates and an ammal which is useful for treating B-cell or T-cell
Imphoproliferative disorders, one or more solid tumours such as lung,
gastrointestinal, pancreatic or prostert tumour. ARXIL, BCWA and TACI
antagonists are useful for treating inflammation and immune function
diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
dermatitis, respiratory allergic disease (asthma, hypersensitivty lung
disease), drug and insect sting allergy, inflammatory bowel disease
(Crohn's disease, colltis), scleroderma, autoimmune disease (multiple
sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
with leucocyte infiltration of the skin or organs. The present sequence
is human BCWA protein cysteine-rich consensus region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TALL-1; antagonist; immunosuppressive; antirheumatic; antinflammatory; antiarthritic; dermatological; antidiabetic; neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thromboytopenic purpurs; Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCWA; CRD;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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                                                                                                                                                                                                                                                                                                                                                                                Length 34;
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100.0%; Pred. No. 1.4e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA49366 standard; peptide; 34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human BCMA cysteine rich domain.
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14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
13-AUG-2002; 2002US-0403364P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 34, Conservative
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                                                                                                                                                                                                                                                                                                                                            Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEO ID NO:2, or amino acids 134-285 of SEO ID NO:2, by at least one modification in the region connecting &bgr; strands or and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antitheumatic, antifilammatory, antithyroid, antidiabetic, neuroprotective, antithyroid, antidyretic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for treating TALL-1 biological activity in a mammal. TC is useful for treating autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus multiple sclerosis, myasthaenia gravis, Grave's disease, autoimmune hemolytic anaemia, autoimmune thromatic fever, post-streptococcal glomerulonephritis and cute rheumatic fever, post-streptococcal glomerulonephritis and collabora. The present sequence represents a cysteine rich domain (CRD) module of human BCMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                71.0%; Score 201; DB 6; Length 34; 100.0%; Pred. No. 1.4e-16; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Formula II derived polypeptide E that binds BAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; SEQ ID NO 15; 140pp; English.
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Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-555932/56.
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                            APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see AEC02021), that that bind BAFF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
                                                                                                                              Gape
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                                                                                                Score 197; DB 9; L
Pred. No. 4.2e-16;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                Formula II derived polypeptide F that binds BAFF
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                                                                                                                                                              8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; SEQ ID NO 16; 140pp; English.
                                                                                                                                                                                                                                                                       AEC02027 standard; peptide; 34 AA
                                                                                                 69.6%;
97.1%;
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                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                Local Similarity 97.1
nes 33; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Matches
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The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCWA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple sclerosis or content as leukemia, prymphoma, or multiple sclerosis of diseases (GWHD) and inflammation. The present sequence represents polypeptide of the invention that binds APRIL, derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
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                                                                                                                                                                                                                                     New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.6%; Score 194; DB 9; Best Local Similarity 97.1%; Pred. No. 9.7e-16; Matches 33; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYC 41
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                                                                                                                                                                                                                                                                                                                                 Claim 7; SEQ ID NO 6; 140pp; English
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                                                                  04-AUG-2004; 2004WO-US025247.
                                                                                                    29-JAN-2004; 2004US-0540271P.
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                                                                                                                                      (GETH ) GENENTECH INC
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WO2005075511-A1.
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                                 18-AUG-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthitis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleromi; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see AEC02021), that that bind BAFF.
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                                                                                                                                                                          APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
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                                                                                                                                       Formula II derived polypeptide G that binds BAFF.
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                                      AEC02028 standard; peptide; 34 AA
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33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patel D;
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Gaps

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Length 34; Indela AEC02021), that that bind BAFF

Sequence 34 AA;

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                                                                                                                    The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple solerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple soleromi, or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see AEC02021), that that bind BAFF.
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for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                          Score 192; DB 9;
Pred. No. 1.7e-15;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSQNESFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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                                                                                    Claim 13; SEQ ID NO 14; 140pp; English.
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1 Similarity 97.1%;
33; Conservative
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Best Local Similarity
Matches 33; Conserv
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Score 192; DB 9;
Pred. No. 1.7e-15;
0; Mismatches 1
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                                                                                         CSONEAFDSLLHACIPCOLRCSSNTPPLTCORYC 34
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                                                              8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC
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 67.8%;
97.1%;
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Matches 32; Conservative
                               33; Conservative
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   Query Match
Best Local Similarity
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RESULT 46

AEC02018

AEC02018

Synthetic

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The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCWA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleromi, or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see ABC02021), that that bind BAFF.
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94.1%; Pred. No. 3.8e-15;
ive 0; Mismatches 2;
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Best Local Similarity
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                                                                                                                    Formula I derived polypeptide G that binds APRIL.
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Pred. No. 3.8e-15;
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    AEC02018 standard; peptide; 34 AA.
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94.1%;
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les 32; Conserv
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cytostatic; r
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AEC02012.

Query Match

Matches

AEC02029;

RESULT 47

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Gaps

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Gape

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8; Indels

Length 185;

DB 3;

64.0%; Score 181; DB 3; 70.8%; Pred. No. 2e-13; ive 4; Mismatches

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recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contect with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatory arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
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34; Conservative
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                                                                                                                               The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen BCMA). ARRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroms, or to select a scleroms or the present sequence of disease (GYHD) and inflammation. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCMA, necrosis factor-kB activator, NF-kB, gene expression, cancer, anti-cell death gene, apoptosis, viral infection, inflammatory response, rheumatoid arthritis, inflammatory bowel disease, septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.3%; Score 182; DB 9; Length 34; 91.2%; Pred. No. 2.6e-14;
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/note= "putative transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of murine BCMA polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                Claim 7; SEQ ID NO 8; 140pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08844 standard; peptide; 185 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34 AA;
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related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte
                                                                                                                             Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1;
Therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
hemolytic anaemia; Grave's disease; mysathenia gravis; BCMA;
B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;
post-streptococcal glomerulonephritis; polyarteritis nodosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to Tumour necrosis factor (TNF) and Apol-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
                                                                                              Murine B cell maturation factor (BCMA) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NAJE-) NAT JEWISH MEDICAL & RES CENT.
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                                                         (first entry)
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N-PSDB; AAD02130.
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lymphoproliferative disorders, one or more solid tumours such as lung

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associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLB), insulin dependent diabetes mellitus, multiple socierosis, myasthenia gravis, Gravé's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a murine B cell maturation factor (BCWA). BCMA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; Pymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; corbn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                    DB 4; Length 185;
                                                                                                                                                                                                                                                                                       1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG
                                                                                                                                                                                                                                                                  4 MAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG
                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                   Score 181; DB 4;
Pred. No. 2e-13;
                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse B cell maturation (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                        AAE15490 standard; protein; 185 AA
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                                                                                                                                      receptor for TALL-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
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                                                                                                                                                                                                      64.0%;
70.8%;
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Best Local Similarity 70.89
Matches 34; Conservative
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                                                                                                                                                                       Sequence 185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-2002
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA. The method is useful for treating B-cell or I-cell and/or BCMA in a mammal which is useful for treating B-cell or I-cell

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The invention provides novel tumor necrosis factor receptor ztnfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors and antibodies. Human zuffr14 polynucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastasts, and immunity such as separating resting from stimulated immune cells. The present sequence is that of murine TNRR BOWA. This sequence was compared with that of murine ztnfr14 ADZ67756 in the identification of ztnfr14 as a member of
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     gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psortasis, allergies pneumonia, atopic diseases such as diarrhoea, psortasis, allergies pneumonia, atopic disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New tumor necrosis factor receptor (TNFR) polypeptides, useful as detecting ligands, and for modulating tumor growth, metastasis and immunity, such as separating resting from stimulated immune cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                           64.0%; Score 181; DB 5; Length 185; 70.8%; Pred. No. 2e-13;
                                                                                                                                                                                                                                                                                                                                    4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse tumor necrosis factor receptor BCMA.
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18-OCT-2004; 2004US-0619552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                  34; Conservative
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                                                                                                                                                                                      is mouse BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-315682/32.
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                         Sequence 185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic.
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Gaps

5 21

Length 281;

64.0%; Score 181; DB 5; Length 28 70.8%; Pred. No. 3.2e-13; ive 4; Mismatches 8; Indels

34; Conservative

4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG

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sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leuroscyte infiltration of the skin or organs. The present sequence is mouse BCMA protein-human immunoglobulin Fc region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                               Sequence 281 AA;
                                                                                                                                                                                            Best Loc
Matches
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(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; crohn's disease; scleroderma, autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                         Gaps
                                                                                         5
                                                                                                                                                        1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46
                                                                                                                                 51
                                                Score 181; DB 9; Length 185; Pred. No. 2e-13;
                                                                                                                               4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse BCMA-human immunoglobulin Fc region fusion protein.
                                                                                       8; Indels
                                                                                         4; Mismatches
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                                                64.0%;
70.8%;
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27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
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                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                        Ouery Match
Best Local Similarity 70.8
Matches 34; Conservative
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            Sequence 185 AA;
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12-MAR-2002
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The invention relates to a novel TALL-1-binding polypeptide comprising a defined sequence in the specification. The composition is useful in medulating the activity of TALL-1, and in treating, preventing, ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or lymphoma. The composition may also be used in treating inflammations (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease, asthma, atherosclerosis, cachexia, cirrhosis, diabetes glomerulomephritis, Hashimoto's thyroiditis, ischemic injury, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriaeis and vasculitis. Disorders may be treated with the novel composition using gene therapy. This sequence represents a TALL-1 related protein of the
                                                                                                                                           TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease; systemic lupus erythematosus; B-cell-mediated cancer; lymphoma; inflammation; rheumatoid arthritis; acute pancreatitis, atherosclerosis; Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis; glomerulonephitis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New TALL-1-binding polypeptide, useful for modulating the activity of TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune diseases, cancers or lymphomas.
                                                                                                             TALL-1 related protein SEQ ID No 197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 26; 236pp; English.
ABJ38417 standard; protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2001; 2001US-0290196P.
                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAY-2002; 2002WO-US015273
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-156719/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                            WO200292620-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hen H;
                                                                                                                                                                                                                                                                       gene therapy.
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                       12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42
                                                                                                                                                                                                                                                                                                                                                                                21-NOV-2002.
                                   ABJ38417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Min H,
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Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; collitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; mouse.

Human-murine B cell maturation protein (BCMA) consensus sequence.

(first entry)

(revised)

29-AUG-2003 12-MAR-2002

AAE15491;

AAE15491 standard; protein; 117 AA

AAE15491

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The invention relates to a neutrokine-alpha protein in crystalline form. The crystalline neutrokine-alpha protein is useful for designing molecules that have biological erivity or compounds that bind, inhibit or mind a neutrokine-alpha protein and/or enhance the activity of a neutrokine-alpha protein. The three-dimensional structure of a neutrokine-alpha protein. The three-dimensional structure of a neutrokine-neutrokine-alpha protein in determining the three-dimensional of other neutrokine-alpha proteins and their homologs. The compounds that minic, prevent or inhibit the activity of the protein are useful for treating ancest allergic disorders, or autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus erythematosus or asthma. This sequence represents the residues in the
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New crystalline Neutrokine-alpha protein, useful for designing compounds that bind, inhibit or mimic a Neutrokine-alpha protein or enhance the activity of a Neutrokine-alpha protein for treating e.g. cancer or allergic disorders.
                                                                                                                                                                                                                                                                                                                                             protein co-ordinate data, cytostatic; antiallergic; immunosuppressive; antirheumatic; antiarthritic; neuroprotective; antiniflammatory; antidabetic; dermatological; antiasthmatic; neutrokine-alpha; crystallography; cancer; allergic disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
                                         Gaps
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.8%; Score 158; DB 6; Length 42; Best Local Similarity 100.0%; Pred. No. 2.4e-11; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic lupus erythematosus; asthma; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.4%; Score 100.0%; Pred. No. 9.7%
                                                                            28
                                                                                                     15 MLQMAGQCSQNEYFDSLLHACIPCQLRC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor for binding a cytokine ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Volovik Y;
                                                                          1 MLQMAGQCSQNEYFDSLLHACIPCQLRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 4; 362pp; English.
                                                                                                                                                                                                      Ę
                                                                                                                                                                                                                                                                                                           Human BCMA receptor binding site.
                                                                                                                                                                                                      ADI53060 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2002; 2002WO-US035661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2001; 2001US-0331049P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li Y, Oren DE, Arnold E,
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-532895/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003050134-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 AA;
                                                                                                                                                                                                                                                                            22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2003
                                                                                                                                                                                                                                          ADI53060;
                                                                                                                                                                 RESULT 55
                                                                                                                                                                                     AD153060
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12-MAY-2000; 2000US-0204039P. 27-JUN-2000; 2000US-0214591P. 14-MAY-2001; 2001US-00214591.

(AMGE-) AMGEN INC.

WPI; 2002-066686/09.

Yu G;

Theill LE,

14-MAY-2001; 2001WO-US015567

WO200187979-A2.

Chimeric.

22-NOV-2001.

sapiens

Homo

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BrOAM) activity in a mammal. The method comprises administering a specific binding partner for APRLI (GTO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA extracellular region of TACI and/or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in amammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRLI, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (lathma, hypersenaitivity) ung disease, colitis), scleroderma, autoimmune disease (mutiple cleronis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, equence with leucocyte infiltration of the Stin or organs. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is human-murine B cell maturation protein (BCMA) consensus sequence. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 11; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
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9

Gape

2; Indels 10; Length 117;

Score 104; DB 5; Pred. No. 0.00019; 1; Mismatches 2,

36.7%;

Query Match 36.7 Best Local Similarity 69.8 Matches 30; Conservative

Gaps

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EYFDSLLHACIPCQLRCSSNTPPLTC 37

12

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Query Match 53.4 Best Local Similarity 100. Matches 26; Conservative

Sequence 24 AA;

X S

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a pecific binding partner for APRIL (G70, a tumour necrosis factor-INF family ligand), having the consenus region of TACI, BCMA, or the TACI BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (athma, hypersensitivity lung disease), drug and insect seting allergy, inflammation, disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bactezoal and viral infections (HIV), atheroselerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human-murine B cell maturation protein (BCMA) consensus sequence cysteine rich region. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; pytpoprofoliferative disorder; tumour; lung; gastroinestinal; pacteatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; colon's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                            transmembrane activator and intracellular CAML interactor; TACI;
                                                                                                                                                                                                                                                                                                      Human-murine BCMA consensus sequence cysteine rich region.
                      2 AQCEYFDSLLHAC-PC-LRCS----PPTCQ-YC--SVT-SVKG 34
SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 11; 94pp; English
                                                                                                                                                  AAE15492 standard; peptide; 24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-2000; 2000US-0204039P
27-JUN-2000; 2000US-0214591P
14-MAY-2001; 2001US-00214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-2001; 2001WO-US015567
                                                                                                                                                                                                                                       (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200187979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
                                                                                                                                                                                                                                     29-AUG-2003
12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric.
                                                                                                                                                                                            AAE15492;
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                                                                                                         RESULT 57
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The present sequence represents murine zinf4, a tumour necrosis factor ligand. The extracellular domains of BR43x2 (an isoform of the transmembrane activator and CAML-interactor (TACI) receptor). TACI or transmembrane activator and CAML-interactor (TACI) receptor). TACI or ECHA activity. They may also be used for inhibiting that activity. They may also be used for inhibiting SR43x2. TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The zinf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, ceptor-ligand engagement incoplasms, multiple myelomas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response. Immunosuppression, graft rejection, graft versus host disease, joint inflammation, insulin dependent diabetes mellitus, Crohn's disease,
                                               4
                                                                                                                                                                                                                                                                                                                                                                                                              Human, BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; striff activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclarosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
                                               Gaps
                                             7;
32.0%; Score 90.5; DB 5; Length 24; 73.3%; Pred. No. 0.0015; 17.0% 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                            A murine ztnf4, a tumour necrosis factor ligand.
                                                                                           41
                                                                                                                                 24
                                                                                                                        FYFDSLLHAC-PC-LRCS----PPTCO-YC
                                                                                           12 EYFDSLLHACIPCQLRCSSNTPPLTCQRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 163; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP;
                                                                                                                                                                                                                                               AAY94006 standard; protein; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-2000; 2000WO-US000396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JAN-1999; 99US-00226533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gross JA, Xu W, Madden K,
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                               22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-452538/39.
                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                     20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-2000.
                                                                                                                                                                                                                                                                                            AAY94006;
         Query Match
                                                  Matches
                                                                                                                                                                                                   RESULT 58
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RESULT 60
ADZ67773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid useful for diagnosis and treatment of carcinoma
pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                 Gaps
                                                                                                                                                                 1;
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25.3%; Score 71.5; DB 7; Length 249;
Best Local Similarity 35.3%; Pred. No. 3.1;
Matches 12; Conservative 8; Mismatches 13; Indels 1
                                                                                                                               DB 3; Length 249;
                                                                                                                                                                 Indels
                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; carcinoma; lymphoma; cancer; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 41
                                                                                                                                                                                                                           | :::|:|| : | | | | : | :| :| :| CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                                                                                                                                                                     8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                             Score 71.5; DE
Pred. No. 3.1;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; SEQ ID NO 1647; Opp; English.
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                                                                                                                                                                                                                                                                                                                                 ABM85744 standard, protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid useful comprises a nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse protein sequence mCP1369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003; 2003WO-US006235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002; 2002US-00087192.
                                                                                                                            / Match 25.3%;
Local Similarity 35.3%;
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 249 AA;
                                                                                             Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003073826-A2
                                                          or renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morris DW;
                                                                                                                                                                                                                                                                                                                                                                     ABM85744;
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                             RESULT 59
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The invention provides novel tumor necrosis factor receptor (TNFR) ztnfr14 polynucleotides ADZ67754, expression vectors and antibodies. Human ztnfr14 polynucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Ztnfr14 polypeptides can be used to detect ligands, adonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastagis, and immunity such as separating resting from stimulated immunity such as esparating resting from stimulated immune cells. The present sequence is that of murine TNFR TARLIA in the identification of ztnfr14 as a member of the TNFR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor necrosis factor receptor superfamily member 13b protein, SEQ: 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tumor necrosis factor receptor (TNPR) polypeptides, useful as detecting ligands, and for modulating tumor growth, metastasis and immunity, such as separating resting from stimulated immune cells.
                                                                                                                          Tumor necrosis factor receptor; TACI; cancer; neoplasm; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.3%; Score 71.5; DB 9; Length 249; 35.3%; Pred. No. 3.1; ive 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Dillon SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  necrosis factor receptor TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 21; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEA55078 standard; protein; 249 AA.
ADZ67773 standard; protein; 249 AA
                                                                                                                                                                                                                                                                                                        16-OCT-2003; 2003US-0511698P.
18-OCT-2004; 2004US-0619552P.
                                                                                                                                                                                                                                                                          18-OCT-2004; 2004WO-US034375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-2005 (first entry)
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 35.3 hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                         Fox BA, Holloway JL,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-315682/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 249 AA;
                                                                                                                                                                                                            WO2005037865-A2.
                                                                                                                                                                              Mus musculus.
                                                                                               Mouse tumor
                                                               14-JUL-2005
                                                                                                                                                                                                                                            28-APR-2005
                                                                                                                                                 cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEA55078;
                                 ADZ67773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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6 CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38

disruption in

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Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney; renal cell; head; neck; heart; multiple sclerosis; lesion; cervix; pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach; proprotein convertase subtilish; furin-like repeat; Alzheimer's disease; Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia; gastritis; ulcers; urinary incontinence; lupus nephritis; renal transplant rejection; myocardial infarction; erectile dysfunction; ovary; lung; thyroid; carcinoma; lymphoma; Raposi's sarcoma; congestive heart failure; ischaemia; hypertensive vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New subtilase-encoding polynucleotide and its encoded protein, useful for
                                                                                                                                                                  The invention describes a transgenic mouse (I) comprising a disruption in an subtilisin-like protein convertase (SPC6) gene, where there is no native expression of an endogenous SPC6 gene. The therapeutic agent is administered by inhalation or insufflation or oral, buccal, parenteral, topical, subcutaneous, intraperitoneal, intravenous, intrapleural, intraocular, intraarerial, or rectal route. The transgenic mouse and associated methods are useful for identifying potential therapeutic agents (e.g. SPC6 agonists and antagonists) for treating conditions associated with SPC6. The identified agents are potentially useful for treating diseases such as schizophrenia. The mouse is useful for investigating the biological roles of SPC6. This is the amino acid sequence of mouse SPC6.
                                                          New transgenic mouse useful in methods for identifying potential therapeutic agents for treating a variety of diseases, including schizophrenia, comprises a disruption in a subtilisin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 QCSONEYFDSLLHACIPCOLRCSSNTPP----LITCORYCNASVINSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Score 70.5; DB 7;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                      24.9%; Sco...
34.7%; Pred. No. 20, ...
5; Mismatches
                                                                                                                                           Disclosure; SEQ ID NO 2; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80243 standard; protein; 1877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2002; 2002US-0347876P.
29-JUL-2002; 2002US-0398734P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2003; 2003WO-EP000253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 34.7
Matches 17; Conservative
                                                                                                           convertase 6 (SPC6) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-608065/57.
             WPI; 2003-777261/73.
N-PSDB; ADC71567.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine subtilase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80243
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                                                                                                                                                                                                                                                                                                                      Characterizing proteins present in a plasma membrane of a cell, useful in identifying diagnostic markers and potential drugs, comprises subjecting
                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method of characterizing proteins present in the plasma membrane (PM) of live calls. The proteins of the invention are useful in identifying diagnostic markers and potential drugs. The invention is useful for identifying drugs for diagnosing and treating disorders unto as cancer which are associated with abnormal representation of cell surface proteins. The present sequence is mouse tumor necrosis factor receptor superfamily member 13b protein.
Plasma membrane; diagnosis; therapeutic; cancer; cytostatic; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroleptic; subtilisin-like protein convertase 6 agonist; subtilisin-like protein convertase 6 antagonist; transgenic; subtilisin-like protein convertase 6; SPC6; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse subtilisin-like protein convertase 6 (SPC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71.5; DB 9;
Pred. No. 3.1;
8; Mismatches 13;
                                                                                                                                                                                                          UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPKDOYWDSSRKSCVSCALTCSORS-ORICIDEC 38
                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 54; 196pp; English.
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                                                                                                                                                                                                         (YISS ) YISSUM RES DEV CO HEBREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC71568 standard; protein; 1548
                                                                                                                                                                                                                                                                                                                                                       cell to a protease treatment.
                tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.3%;
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                                                                                                                                            25-NOV-2004; 2004WO-IL001085
                                                                                                                                                                            26-NOV-2003; 2003US-0524885P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-2002; 2002US-00180903
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Les 12, Conservative
                                                                                                                                                                                                                                         Inberg A,
                                                                                                                                                                                                                                                                         WPI; 2005-418017/42.
                                                                                                                                                                                                                                                                                         REFSEQ; NP 067324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 249 AA;
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                                                                              WO2005052182-A2
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                                              Mus musculus
                                                                                                              09-JUN-2005
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Gaps

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This sequence shows a murine subtilase. The homologous human subtilase coding sequence is located on chromosome 9q21.13. Related EST's are expressed in Kidney (renal cell adenocarcinoma), head and neck tissue, heart, multiple sclerosis lesions, cervix, pooled garm cell tumours, uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin of protein is a long membrane bound protein which shows 96% identity to chuman proprotein convertase subtilisin. There are two blocks of 11 furinise repeats in the C-terminal portion. Sew suggesting that the cransmembrane domain, also in the C-terminal portion. Suggesting that the protein is localised on the outside of the membrane. The subtilase cransmembrane domain, also in the C-terminal portion, suggesting that the polymucleotide and polypeptide are useful for identifying test compounds, which may act a sagonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. Vectors comprising the objuncleotide are useful for modulating the activity of subtilase in a disorder, cancer, a cardiovascular disorder, a gastrointessinal calsorder, cancer, a cardiovascular disorder, a gastrointessinal calsorder, cancer, a cardiovascular disorder, a gastrointessinal compassions of disease, pain, colon tumour, pre-oscophageal dysphagia, cansplant rejection, pelvic pain, reconstruction, ovary tumour, cardinar diseases, etc. These are also useful for preventing or congestive heart failure, myocardial infarction, ischaemia, hypertensive cameliorating the diseases cited above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; antimiflammatory; immunosuppressive; glomerulonephritis; acthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; mouse; FCS protein; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TACI-Fc5 fusion protein comprising murine 26-10 VH signal peptide.
identifying modulators of subtilase activity, and in gene therapy for treating e.g. Alzheimer's disease, cancers, congestive heart failure or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 OCSONEYFDSLLHACIPCOLRCSSNTPP----LICORYCNASVINSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches 22; Indels
                                                                                     Disclosure; Page 122-26; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE35228 standard; protein; 332 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.9%;
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Best Local Similarity (
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24-MAY-2001; 2001US-0293343P

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The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or ZTNF9; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammallan subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple solerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft crejection, anaemia and septic shock. The fusion proteins are also used in comprising murine 26-10 VH signal peptide. This sequence is used in the invention. (Updated on 23-OCT-2003 to standardise OS field)
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                                                                                                                    Transmembrane activator and calcium modulator and cyclophilin ligand-
interactor (TACI)-immunoglobulin fusion protein, for treating cancer o
diabetes, comprises a TACI receptor group and an immunoglobulin group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
24.2%; Score 68.5; DB 6; Length 332;
Best Local Similarity 27.9%; Pred. No. 9.7;
Matches 12; Conservative 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLQMAGQCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                     Disclosure; Col 137-138; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR18921 standard; protein; 1569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mucin glycoprotein, MUC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2004; 2004WO-EP050082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2003; 2003US-0445217P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
               (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-604324/58
                                                                                        WPI; 2003-148455/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 332 AA;
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                                                     ξ,
                                                       Rixon
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The present invention relates to novel mucin-like proteins (I) and their coding sequences. The mucin-like proteins and coding sequences are useful in the therapy or in the prevention of a disease when the increase in the mucin-like activity of a polypeptide is needed e.g. bacterial infections, allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced disease, allergic conjunctivitis, otitis, tissue injury, epithelial adenocarcinoma of the lung, lung cancer, Crohn's disease, small adenocarcinoma of the lung, lung cancer. The present sequence is a mucin glycoprotein which was used in a sequence alignment with the mucin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated mucin-like polypeptides, useful for diagnosing or treating, eg. bactecrial infections, allergic asthma, inflammation, allergic conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung cancer, or skin cancer.
                               New isolated mucin-like polypeptides, useful for diagnosing or treating, e.g. bacterial infections, allergic asthma, inflammation, allergic conjunctivitie, ottiis, inflammatory bowel disease, Crohn's disease, lung cancer, or skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory; Ophthalmological; Auditory; Vulnerary; Gastrointestinal; Cytostatic; Gene Therapy; Mucin-like protein; human; mucin; bacterial infection; allergic asthma; inflammation; viral infection; allergic conjunctivitis; officis; tissue injury; epithelial wounding; inflammatory bowel disease; Crohn's disease; small adenocariome of the lung; lung cancer; gastric intestinal metaplasia; cholecystitis; skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1179 CSQDEYFDHEEGVCVPCM-----PPTTPQ 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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                                                                                                                              Example 2; Fig 1; 170pp; English.
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                                                                                                                                                                                                                                                                                                                                                              proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 45.2.
Best Local 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-604324/58.
GENBANK; AAQ82434.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004069136-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ното варіепв
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Gaps

7;

Indels

9 . 6

Length 1569;

DB DB

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The present invention relates to novel mucin-like proteins (I) and their coding sequences. The present sequence is one such human mucin-like proteins and coding sequences are useful in the therapy or in the prevention of a disease when the increase in the mucin-like activity of a polypeptide is needed e.g. bacterial infections, allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced wounding, inflammatory bowel disease, tissue injury, epithelial wounding, inflammatory bowel disease, Crohn's disease, small adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia, chronic cholecystitis, or skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated mucin-like polypeptides, useful for diagnosing or treating, e.g. bacterial infections, allergic asthma, inflammation, allergic conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung cancer, or skin cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory; Ophthalmological; Auditory; Vulnerary; Gastrointestinal; Cytodetatic; Gene Therapy; Mucin-like protein; human; mucin; bacterial infection; allergic asthma; inflammation; viral infection; allergic conjunctivitis; otitis; tissue injury; epithelial wounding; inflammatory; bowel disease; Crohn's disease; small adenocarchone of the lung; lung cancer; gastric intestinal metaplasia; chronic cholecystitis; skin cancer.
                                                                                                                                                                                                                                                                                      Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human mucin-like protein, SCS0004, variant SEQ ID 3.
                                                                                                                                                                                                                                                                                                                                                            1161 CSODEYPDHEEGVCVPCM-----PPTTPQ 1184
                                                                                                                                                                                                                                                                                                                         8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ 38
                                                                                                                                                                                                                                               24.2%; Score 68.5; D
45.2%; Pred. No. 73;
ive 2; Mismatches
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/label= Signal_peptide
19. .2258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                              Sequence 2240 AA;
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New isolated mucin-like polypeptides, useful for diagnosing or treating, e.g. bacterial infections, allergic asthma, inflammation, allergic conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung cancer, or skin cancer.
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like activity of a polypeptide is needed e.g. bacterial infections, allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced disease, allergic conjunctivitis, otitis, tissue injury, epithelial wounding, inflammatory bowel disease, Crohn's disease, small adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia, chronic cholecystitis, or skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory; Ophthalmological; Auditory; Vulnerary; Gastrointestinal; Cytostatic; Gene Therapy; Mucin-like protein; human; mucin; becterial infection; allergic asthma; inflammation; viral infection, allergic conjunctivitis; otitis; tissue injury; epithelial wounding; inflammatory bowel disease; Crohn's disease; small adenocarcinoma of the lung; lung cancer; gastric intestinal metaplasia; chronic cholecystitis; skin cancer.
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                                                                                                                                                                             Length 2258;
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                                                                                                                                                                                                 Pred. No. 73;
2; Mismatches
                                                                                                                                                                           24.2%; Score 68.5; 45.2%; Pred. No. 73
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                                                                                                                                                                                                                                                                                                                                                                                             ADR18915 standard; protein; 2264 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                 Best Local Similarity 45.2
Matches 14; Conservative
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                                                                                                                                         Sequence 2258 AA;
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Length 2264;

8;

ВВ

Score 68.5;

24.2%;

Query Match

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The invention relates to a composition (I) comprising AGP-3 receptor (tumour necrosis factor ligand family member) related protein (II) at attached to a vehicle protein. (I) is useful for modulating AGP-3-related attached to a vehicle protein. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins casays to identify cells and tissues that express AGP-3R or proteins or attagonists) that interact with AGP-3R proteins and goon service or antagonists) that interact with AGP-3R proteins. (II) is also useful or identifying intracellular proteins that interact with the respective cycoplasmic domains by yeast two-hybrid screening process. (II) is cytoplasmic domains by yeast two-hybrid screening process. (II) is completed in B cell growth, survival and activation particularly in lymph conde, spleen, and Peyer's patches. AGP-3R agonists and antagonists of identified using (II) are used for modulating B cell response and are used to rreat diseases characterised by inflammatory processes or cycoplated immune response such as rheumatoid arthritis, graft-versus-cycoplated immune response such as rheumatoid arthritis, graft-versus-cycoplated immune response such as rheumatoid arthritis, graft-versus-cycoplated immune response such as rheumatoid arthritis, which conditions of joints, e.g., rheumatoid creatment of inflammatory conditions of joints, e.g., rheumatoid consecuence of arthritis, osteoarthritis, amyotrophic lateral sclerosis cuseful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, disbates, geven glomerulonephritis, inflammatory bowel disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive; dermatological; meuroprotective; nootropic; immunomodulator; metabolic; antidiabetic; analgealc; nephrotropic; osteopathic; cytostatic; fever; antiparkinsonian; antiparcialc; vasotropic; antibacterial; asthma; AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor; mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn; disease; panotrophic lateral sclerosis; ALS; Alzhaimer's disease; diabetes; glomerulonophicis; inflammatory bowel disease; ischaemia; multiple sclerosis; Parkinson's disease; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor ligand family member) receptor and encoding nucleic acids.
                        Gapa
                        7;
                          IndelB
                                                                                                                                                                                                                                                                                                                                                                               Human AGP-3 receptor cysteine rich repeat region #1.
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1179 CSQDEYFDHEEGVCVPCM-----PPTTPQ 1202
                                                                      8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQ 38
  45.2%; Pred. No. 73; ive 2; Mismatches
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                                                                                                                                                                                                                                        AAU10951 standard; protein; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-2001; 2001WO-US004568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-2000; 2000US-0181800P
                                                                                                                                                                                                                                                                                                                                     (first entry)
                          14; Conservative
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                         AAU10951;
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Gaps

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Indels

15;

9; Mismatches

11; Conservative

Matches

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metastasis, and immunity such as separating resting from stimulated fimmune cells. The present sequence is that of the Cys-rich domain of human TNFR TACI ADZ67771. This sequence was compared with that of ztnfr14 in the identification of ztnfr14 as a member of the TNFR family.
   ischaemic injury including cerebral ischaemia, multiple myeloma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides novel tumor necrosis factor receptor (TNFR) ztnfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors and antibodies. Ztnfr14 polynucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Ztnfr14 polypeptides and be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth,
                              sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGP-3 cysteine-rich repeat region #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         necrosis factor receptor; TACI; cancer; neoplasm; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                  23.9%; Score 67.5; DB 5; Length 37; 30.6%; Pred. No. 1.3; ive 9; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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18-OCT-2004; 2004US-0619552P
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                                                                                                                                                                                                                                                                                              Sequence 37 AA;
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ADZ67772
ADZ7772
ADZ7 ADZ67
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Length 48;

DB 9;

Score 67.5; DI Pred. No. 1.7;

23.9%; 30.6%;

Query Match Best Local Similarity

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crivator and intracellular CAMI, interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for ARRIL (GTO), a tumour necrosis factor-INF specific binding partner for ARRIL (GTO), a tumour necrosis factor-INF amily ligand), having the consensus requence, but not the extracellular region of TACI BCMA, or the TACI BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA in a mammal which is useful for inhibiting activity of TACI conformance of TACI or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. ARRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (acthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with laucocyte infiltration of the skin or organs. The present sequence is human TACI cysteine-rich extracellular region
                                                                                                                                                                                                                                                                                                                                                Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCWA; tumour necrosis factor; TNF; Pymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; coron; a disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for inhibiting TACI (transmembrane
8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
                                          13 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 47
                                                                                                                                                                                                                                                                                                           Human TACI cysteine rich extracellular region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 13; 94pp; English
                                                                                                                                                                AAE15500 standard; peptide; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-2001; 2001WO-US015567.
                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                               12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theill LE,
                                                                                                                                                                                                                  AAE15500;
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This is the amino acid sequence of the N-terminal, i.e. the extracellular, domain of novel human transmembrane activator and CAML-cinteractor (TACI) protein (see AAW75783). TACI is a lymphocyte receptor protein that is involved in the calcium activation pathway. It is normally present in B-lymphocytes, and to a much lesser extent in impact of the capture T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. The extracellular domain of TACI functions as a binding site for a ligand that atimulates the activation of the cell by inducing the binding of the cterminal portion (see AAW75784) of TACI to the N-terminal domain of CAMI. A recombinant form of the extracellular portion of TACI acts as a dominant-negative or blocking agent and acts to suppress the immune system. It can be used to treat or prevent autoimmune disease, graft rejection or graft versus host disease. The extracellular region is also used in a claimed method for identifying a ligand for TACI, in which binding of a candidate molecule is determined by detecting cellular cut activation of the AP-1, CAMP or NF-XB pathway, of NF-AT transcription contraction, or of NF-AT dependent transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACI; transmembrane activator and CAML-interactor; calcium signal-modulating cyclophilin ligand; human; lymphocyte surface receptor; human; B-cell; B lymphocyte; infection; cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis; immunosuppressive; graft versus host disease; transplant rejection; therapy; signal transduction.
                                                                        Gaps
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   Length 59;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphocyte surface receptor extracellular domain.
                                                                    15;
                                                                                                                                                                                 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
   DB 5;
Score 67.5; DE Pred. No. 2.1; 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         AAW75785 standard; protein; 166 AA.
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23.9%;
Local Similarity 30.6%;
hes 11; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-506346/43.
N-PSDB; AAV57330.
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          Query Match
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Claim 1; Fig 12A; 94pp; English.

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Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psortasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
43
                   68
8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA
            34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS
                                                                               AAE15494 standard; protein; 166 AA
                                                                                                                                                  Human TACI extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                           12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu G;
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA extracellular consensus sequence, but not the extracellular region of TACI of TACI or BCMA, in a mammal which is useful for inhibiting activity of TACI and/or BCMA, in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointesthal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatities, respiratory allergi, disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, theumatorid arthrities, systemic lupus erythematosus), tungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is a human TACI protein extracellular domain 23.9%; Score 67.5; DB 5; Length 166; Sequence 166 AA; Query Match

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Gaps

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23.9%; Score 67.5; DB 2; Length 166; 30.6%; Pred. No. 6.1; ive 9; Mismatches 15; Indels 1

Query Match 23.9 Best Local Similarity 30.6 Matches 11; Conservative

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Indels

15;

9; Mismatches

11; Conservative

8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43

Length 171;

Score 67.5; DB 8;

23.9%; 30.68;

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Query Match
Best Local Similarity
    Sequence 171 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complex. The polypeptide has antiinflammatory, antiarthritic, activities, immunosuppressive, antiarteriosclerotic and cytostatic activities, and can be used in gene therapy. The polypeptides are useful for treating and controlling inflammatory diseases, e.g. rheumatoid arthritis or inflammatory bowel disease, autoimmune disease, attherosclerosis, osteoporosis, allograft rejection and cancer. The present sequence represents a human TACI and heat shock binding protein (HSBP) fusion protein fragment, which is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                             transmembrane activator and CAML interactor; TACI; extracellular domain; trimerising polypeptide; homotrimeric protein complex; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; antiarteriosclerotic; cytostatic; gene therapy; inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; autoimmune disease; atherosclerosis; osteoporosis; allograft rejection; cancer; human; heat shock binding protein; HSBP; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising an extracellular domain of the transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activator and calcium-signal modulating cyclophilin ligand (CAML) interactor (TACI), and a trimerizing polypeptide, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated polypeptide comprising an
                         Gaps
                         1,
                         Indels
                         15;
                                                                                           34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
                                                               8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNA 43
      Pred. No. 6.1;
                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 18; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                      Human TACI-HSBP fragment SEQ ID NO:18.
                                                                                                                                                                                                                        ADN03188 standard; protein, 171 AA
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30.6%;
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                         11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-364855/34.
    Best Local Similarity
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                                                                                                                                                                                                                                                                  ADN03188;
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                                                                                                                                                                                                                                                                                                                                                                                                      Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pitti RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 40
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                                                                                                                                                                                                                                                                                                                                                     Human TACI splice variant protein.
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                                                                                                                                                                          AAE09244 standard; protein; 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2000; 2000WO-US032378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0182938P.
2000US-0226986P.
                                                                                                                                                                                                                                                                                        (first entry)
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nes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-541628/60.
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22-AUG-2000;
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                                                                                    December 21, 2005, 15:57:04 ; Search time 28.2 Seconds (without alignments) 174.009 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1: pirl:*
2: pir2:*
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ò	S-locus-specific g	•	431	16.8	47.5	299
20170111	s-rocus-specific q S-locus-specific q	2 T07811		16.8	47.5	297
Best Loca	hypothetical prote			16.8	47.5	296
Query Mat	hypothetical prote			16.8	47.5	295
	protein R09B5.5 (i	E82369 A88949	370 2	16.8 16.8	7.7.5	293 294
A;Cross-ret	gamma-1-microglobu			16.8	47.5	292
A; Residues:	ribonucleoside-dip	_		16.8	47.5	291
A, Molecule	hypothetical prote	_		16.8	47.5	290
A;Status: p	ADP-heptose-LPS he			16.8	47.5	289
A, Accession		-		0.01	47.7	200
A:Reference	hypotherical prote	D/1190		16.8	7.5	286
7.550 Decc.	eoginophil-derived			16.8	47.5	285
R; Nakagawa,	Norrie disease pro				47.5	284
C;Accession	alpha-2-macroglobu		_		4.8	283
C,Date: 02-	nyponetical proce surface protein ty	S50820			8 4 8 8	281
serine proc	LR11 protein - mou	-			48	280
S34583	vitellogenin II pr				4.0	279
RESULT 2	Motch B protein -	T42/26			4, 4 20 a	277
	gag-Rmil-env polyp				48	276
qq	subtilisin-like pr		975 2	17.0	. 4. 0 80	275
Š	subtilisin-like pr	JC5571			48	273
	cell differentiati	•	888 2		48	272
Matches	P95 orf83 - Bombyx	•			4 4 0 6	271
Rest Loca	ovotransierrin pre	TECHE		17.0	4.	269
	hypothetical prote			0.	48	268
C; Superfami	brefeldin A-sensit			. 0.	4 4	267
A, Introns:	hypothetical prote	E/142/ T30098		17.0	4, 4 80 0	265
A;Cross-rer	adenosylhomocystei	•		0.	48	264
A; Gene: GDB	hypothetical prote	•		0.	48	263
C;Genetics:	CTP synthase (EC 6	•		. 0.	4 8	262
A:Cross-ref	nypotnetical prote	T02623	479	17.0	4, 4	260
A; Molecule	protein kinase (EC	•		٥.	48	259
A;Status: p	hypothetical prote	_		. 0	4 4	258
A, Cross ter	pendme polyprocein hypothetical prote	722652		17.0	4, 4 80 00	256
A; KeBidues:	env polyprotein -	•.		0.	48	255
A; Molecule	hypothetical prote	•			48	254
A; Accession	NF-kappaB inhibito				4.	253
A;Reference	morybachtm bros	•		17.0	4. 4 2) C	251
A.Title. A	hypothetical prote	T46314			4 ,	250
R;Laabi, Y.	hypothetical prote				48	249

ALIGNMENTS

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NyAlternate mass: sperm-specific membrane protein C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42215
S;Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot A;Accession: T42215
A;Accession: T42215
A;Accession: T42215
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: canalated from GB/EMBL/DDBJ
A;Residues: 1-5376 cGAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:g3327420; PII
C;Genetics:
A;Gene: Zan
T42215
zonadhesin - mouse
                                                                   Action factor - human

N.Alternation factor - human

N.Alternate names: BCM protein; BCMA protein; BEL protein

C; Accession: 83466; 331208; 335661

C; Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C; Accession: 843466; 331208; 335661

N; Cabbi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.

Nucleic Acids Res. 22, 1147-1154, 1994

A; Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire

A; Accession: 843466

A; Accession: 843466

A; Accession: BAA

A; Residues: DNA

A; Residues: 1-184 < LAA>

A; Residues: UNIPROT: Q02223; UNIPARC: UPI0000034D1B; EMBL: Z29574; NID: 9471244; PID
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8: 1-1548 <NBK>
eferences: UNIPROT:004592; UNIPARC:UPI000016CF9E; GB:D17583; NID:g407344; PIDN:E
.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, 7, 3897-3904, 1992
new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16
                                      inew gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16 to number: S31208; MUID:93010984; PMID:1396583 nr. S31208
                                                                                                                        Lype: mRNA
: 1-184 <LA2>
ferences: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a, T.; Murakami, K.; Nakayama, K.
. 327, 165-171, 1993
Identification of an isoform with an extremely large Cys-rich region of PC6, cen number: S34583; MUID:93327934; PMID:8335106
on: S34583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              teinase (EC 3.4.21.-) PC6B - mouse
Mus musculus (house mouse)
-Dec_1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 24.9%; Score 70.5; DB 2; Length 1548; Similarity 34.7%; Pred. No. 4.2; 17; Conservative 5; Mismatches 22; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                ferences: UNIPARC:UPI000046868; EMBL:Z14955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 283; DB 2; 100.0%; Pred. No. 8.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                          ily: human B-cell maturation factor
                                                                                                                                                                                                                                                                                                                                     iferences: GDB:135977; OMIM:109545
tion: 16p13.1-16p13.1
44/1; 93/1
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                                                                                                                                                                                                                                                               4-184 <LA3>
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                                                                                                                                                                                                                    preliminary
                                                                                                                                                                                                                                              type: mRNA
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Map position: 5

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A;Cross-references: UNIPARC:UPI0000079A41; EMBL:Z34799; PIDN:CAA84320.1; GSPDB:GN00021; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 3
A;Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q17969; UNIPARC:UPI0000079A41; EMBL:Z37139; PIDN:CAA85494.1;
A;Experimental source: clone C14B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:018118; UNIPARC:UP100006118C; EMBL:Z81129; PIDN:CAB03405.1;
                                                                       Cispedies: Caenorhabditis elegans
Cispedies: Caenorhabditis
Cispedies: Cae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62; DB 2; Length 330;
Pred. No. 10;
7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CSONEYFDSLLHACIP----COLRCSSNTPPL---TCORYCNASVTN
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    Caenorhabditis elegans

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, June 1994
A;Reference number: Z19464
A;Accession: T21723
A;Accession: T21723
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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ilarity 29.2%;
Conservative '
                                                   hypothetical protein F34D10.2
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nes 14; Conserv
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Matches 17; Conserv
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C;Superfamily: gliadin
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N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
S;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T43251

R;Cieplik, M.; Klenk, H.

Submitted to the EMBL Data Library, January 1996

A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiper A;Reference number: Z22368

A;Accession: T43251
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 1-1299 <CIE>
A;Esidues: 1-1299 <CIE>
A;Cross-references: UNIPROT:Q26489; UNIPARC:UPI0000083055; EMBL:Z68888; NID:g1167859; PI
A;Experimental source: clone Sfurin 6; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: responsible for the endoproteolytic processing of proproteins with specifi C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: CBSP:T10E10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reaidues: 1-1101 <GEI>
A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339;
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                           3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T10E10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16840
R;Geisel, C.
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels 13;
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2
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                                                                                                                                                               DB 2; Length 5376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: functions in multiple cell adhesion processes A; Note: found exclusively on the apical region of the sperm head C; Keywords: cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCSQNEYFDSLLHACIPCOLR--CSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                           3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rigeisel, C. submitted to the EMBL Data Library, October 1995 A; Description: The sequence of C. elegans cosmid T10E10. A; Reference number: Z18588
                                                                                                                                                                                                                                                                                                               7 QCSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 41
                                                                                                                                                       Query Match 24.6%; Score 69.5; DB 2;
Best Local Similarity 36.8%; Pred. No. 16;
Matches 14; Conservative 5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65.5; DB Fred. No. 13; B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
24.2%; Score 68.5; DE
Best Local Similarity 36.2%; Pred. No. 5.2;
Matches 17; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.1%;
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A; Status: preliminar
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Matches
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DB 2; Length 520

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs h
A;Reference number: Z14126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T13954
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1.1574 <NAK>
A;Crose-references: UNIPROT:OB8281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293; i
A;Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R. submitted to the EMBL Data Library, October 1997
A; Description: The Celsr family of novel evolutionarily conserved seven-pass transmembrar A; Reference number: Z17881
A; Accession: <u>T14119</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3034 <HAD>
A;Cross-references: UNIPROT:035161; UNIPARC:UPI000002931C; EMBL:AF031572; NID:g3800735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001 QCKENYYKPPAQDACLPCDCFPHGSHSRACDMDTGQCACKPGVIGRQCNRCDNPFAEVTS 2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 OCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQ-----RYCN-----ASVTN 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eeven-pass transmembrane receptor protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AGQCSQNEYFDSLLHACIPCQL----RCSSNTPPLT----CQRYC---NASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.4%; Score 60.5; DB 2; Length 3034; Best Local Similarity 28.3%; Pred. No. 99; Matches 17; Conservative 5; Mismatches 19; Indels 19
                                                                                                                                                                                                                                                                               145 CMNDGYFNHTLGRCV-----CTSNWVGEHCIFRCNSGVVNKTSG 183
                                                                                                                    Query Match 21.7%; Score 61.5; DB 2; Length 5
Best Local Similarity 31.8%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                                                         8 CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.4%; Score 60.5; D
32.2%; Pred. No. 56;
tive 8; Mismatches
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C, Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 19; Conserva
                                  A,Gene: T12A7.2
A,Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: MEGF6
      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
T13954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G88846
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Feference number: A75000; MUID:99065613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                        A;Residues: 1-99 «HER»
A;Cross-references: UNIPROT:P46687; UNIPARC:UP1000000066; EMBL:U11764; NID:g887934; PIC
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q22423; UNIPARC:UPI000008213D; EMBL:Z73911; PIDN:CAA98142.2; A;Experimental source: clone T12A7
                                                                                                                                                             S
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A,Molecule type: DNA
Residues: 1-520 <STO>
A,Cross-references: UNIPROT:Q22423; UNIPARC:UPI000017A62A; GB:chr_IV; PIDN:CAA98142.1;
            C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60231
R;Herzog, M.; Dorne, A.M.; Grellet, F.
Plant Mol. Biol. 27, 743-752, 1995
A;Title: GASA, a gibberellin-regulated gene family from Arabidopsis thaliana related 'A;Reference number: S60229; MUID: 95244835; PMID: 7727751
A;Acteus: nucleic acid sequence not shown
A;Molegule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: GASA3
C,Superfamily: gibberellin-regulated protein GASA2
C,Superfamily: gibberellin-regulated predicted <SIG>
F,11-18/Domain: gibberellin-regulated protein GASA3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T12A7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Acceasion: T24856
R;Lennard, N.
submitted to the EMBL Data Library, June 1996
Species: Arabidopsis thaliana (mouse-ear cress)
:Date: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
:Accession: S60231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Introns: 36/3; 71/1; 146/1; 255/2; 287/2; 340/3; 387/1; 449/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 GRCSKSSRPNLCLRACNSCCYRCNC-VPPGTAGNHHLCPCYASIT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 CMNDGYFNHTLGRCV----CTSNWVGEHCIFRCNSGVVNKTSG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRY----CNASVT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61.5; DB 2;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-483 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61.5; DB; Pred. No. 16; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 21.7%; Score 61.5; DE Local Similarity 35.6%; Pred. No. 4.1; es 16; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.7%;
Best Local Similarity 31.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z19943
A;Accession: T24856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP:T12A7.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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21

Gape

13;

19; Indels

DB 2; Length 1574;

19; Gaps

9

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A;Wolecule type: DNA
A;Residues: 1-438 <GRE>
A;Cross-references: UNIPROT:016502; UNIPARC:UPI000007AF62; EMBL:AF016451; PIDN:AAB65995.3
A;Experimental source: strain Bristol N2; clone C03A7
A;Genetics:
A;Gene: CESP:C03A7.8
A;Map position: 5
A;Introns: 75/3
C;Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:016511; UNIPARC:UPI000007B691; EMBL:AF016451; PIDN:AAB66007.1
A;Experimental source: strain Bristol N2; clone C03A7
C;Genetics:
A;Gene: CESP:C03A7.14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31898
K;Greco, T.; Bradshaw, H.; Elliott, G.
submitted to the EMBL Data Library, July 1997
A;Reference number: Z21096
A;Reference number: Z21096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C23G10.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caep-1999 #text_change 31-Dec-2004 C;Accession: T15577 R;Latreille, P. Submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid C23G10. A;Reference number: Z18372 A;Accession: T15577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 QCAPQCEQS------CQQCVQQQPAAQCQTACQSSCSNS 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 QCAPQCEQS-------CQQQCVQQQQPAAQCQTACQSSCSNS 407
                                                                                                                                                                                                                                                                                                              Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.8%; Score 59; DB 2; Length 758; Best Local Similarity 42.9%; Pred. No. 44; Matches 9; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.0%; Score 59.5; DB 2; Length 46 Best Local Similarity 31.9%; Pred. No. 25; Matches 15; Indels Matches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 OMAGOCSONEYFDSLLHACIPCOLRC-SSNTPPLTCORYCNASVTNS
                                                                                                                                                                                                                                                                                                                                                                                                                         3 OMAGOCSONEYFDSLLHACIPCOLRC-SSNTPPLTCORYCNASVTNS
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A;Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C03A7.14 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-445 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-758 <LAT>
                                                                                                                                                                                                                                                                                                          / Match 21.0%; Score 59.5; D Local Similarity 31.9%; Pred. No. 24; Pred. S. Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Map position: 5
A Introns: 18/3; 75/3
C Superfamily: gliadin
                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 15
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A;Molecule type: DNA
A;Mosidues: 1-388 cGRE>
A;Kosidues: 1-388 cGRE>
A;Cross-references: UNIPROT:O16501; UNIPARC:UPI0000077D46; EMBL:AF016451; PIDN:AAB65996.
A;Experimental source: strain Bristol N2; clone C03A7
                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: MIPROT:O16500; UNIPARC;UPI000007BC52; EMBL:AF016451; PIDN:AAB66001.
A;Experimental source: strain Bristol N2; clone C03A7
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accesion: T18189
R;Greco, T.; Bradahaw, H.; Elliott, G.
Submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C03A7.
A;Reference number: Z21096
A;Reference number: Z21096
A;Reference; preliminary; translated from GB/EMBL/DDBJ
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C; Date: 29-Oct.1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C; Accession: T31888
R; Greco, T.; Bradshaw, H.; Elliott, G.
Submitted to the EMBL Data Library, July 1997
A; Reference number: 221096
A; Reference number: 221096
                                    hypothetical protein C03A7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.0%; Score 59.5; DB 2; Length 388; Best Local Similarity 31.9%; Pred. No. 22; Matches 15; Conservative 4; Mismatches 15; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 QCAPQCEQS------CQQQCVQQQQPAAQCQTACQSSCSNS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 QCAPQCEQS------CQQQCVQQQPAAQCQTACQSSCSNS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 OMAGOCSONEYFDSLLHACIPCOLRC-SSNTPPLTCORYCNASVTNS 48
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                                                                                                                     C,Accession: T31887
R;Greco, T.; Bradshaw, H.; Elliott, G.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C03A7.
A;Reference number: Z21096
A;Accession: T31887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein CO3A7.7 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 75/3
C;Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: C03A7.4
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A; Introns: 75/3
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alpha-51D-immobilization antigen - Paramecium tetraurelia alpha-51D-immobilization antigen - Paramecium tetraurelia (;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T28674 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T28674 #sequence_revision 1995 A;Accession: T28674 A;Reference number: Z20505 A;Accession: T28674 A;Reference number: Z20505 A;Accession: T28674 A;Accession: T28674 A;Accession: Dreliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-2533 acCH>A;Coss-references: UNIPROT:Q27183; UNIPARC:UPI000007E3B2; EMBL:X85135; NID:g728634; PID: C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ciymotrypsin/elastase inhibitor - common roundworm
CiSpecies: Ascaris lumbricoides (common roundworm)
CiSpecies: Ascaris lumbricoides (common roundworm)
CiDate: 19-Var-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
CiAccession: S07127
Ribabin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem Bioghys. 23, 143-141, 159.
Airtle: The isoinhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the priman A; Ritle: The isoinhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the priman A; Reference number: S07127; MUID:84255715; PMID:6564898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:017970; UNIPARC:UPI000007686D; EMBL:281573; PIDN:CAB04625.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21681
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CSQNEYFDSLLHACIPCQLRC--SSNTP-PLTCQR-YCNAS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 58.5; DB 2;
Pred. No. 1.4e+02;
7; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, November 1996 A; Reference number: 219781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI000012D146 C;Superfamily: roundworm trypsin inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone M02G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.5%;
Best Local Similarity 36.6%;
Matches 15; Conservative :
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Best Local Similarity 20.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Superfamily: G surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1-63 <BAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Genetic code: SGC5
A; Note: alpha-51D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T23681
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                                                                                                                                                                      A45558
epideral growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Schistosoma mansoni
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A5558; S27836
R;Shocemker, C.B.; Ramachandran, H; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep. A;Cecession: A45558
A;Accession: A45558
A;Accession: A45558
A;Molecule type: mRWA
A;Molecule type: mRWA
A;Mesidues: 1-1717 < SHO>
A;Cross reference sulphyror:Q26566; UNIPARC:UPI000007DCD7; EMBL:M86396; NID:g160957; PIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-51D immobilization antigen - Paramecium tetraurelia
C;Species: Paramecium tetraurelia
C;Species: Paramecium tetraurelia
C;Species: Date: 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28675
R;Schwegmann, K.J.
R;Schwegmann, K.J.
R;Schwegmann, K.J.
R;Schwegmann, K.J.
R;Schwegmann, T28675
R;Schw
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A,Gene: SER
C,Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C,Superfamily: fluke epidermal growth factor receptor homolog 1; protein; phosphoprotein
C,Superfamily: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
E,1-19/Domain: signal sequence #status predicted <SIG>
F,20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F,1018-1323/Domain: protein kinase homology <KIN>
F,1026-1034/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: M86396; NID: 9160957; PII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.8%; Score 59; DB 1; Length 1717; 39.1%; Pred. No. 89; ive 3; Mismatches 11; Indels
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                                          :|: | | | ::|||:: |||
260 ESVFHPLYPAEIRCSADGPPL 280
DSLLHACIPCOLRCSSNTPPL 35
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A,Introns: 280/3; 538/2; 1248/2
C,Superfamily: G surface protein
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Matches 9; Conserva
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Matches 17; Conserv
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F;1488-1636/Domain: laminin G repeat homology ciG4>
F;1665-1816/Domain: laminin G repeat homology ciG5
F;104,215,308,458,524,550,571,574,631,639,735,751,754,780,803,1086,1281,1359,1411/Binding
F;266,269/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CiSpecies: Drosophila melanogaster
CiSpecies: Drosophila melanogaster
CiSpecies: Orosophila melanogaster
CiSpecies: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
CiAccession: A43434
RiRoebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.J.
J. Blol. Cham. 267, 17208-17215, 1992
A;Fitle: Cloning and functional expression of Dfurinz, a subtilisin-like proprotein proce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A43434
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rostatus: 1-1680 cROE>
A;Cross-references: UNIPROT:P30432; UNIPARC:UPI000016BC03; GB:M94375; NID:g157461; PID:g3
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20130
C;Accession: T20130
A;Accession: Caenorial Source: Clone C50H2
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                                                                                                                                                                                                                                                                                                                                                                                                   64 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDGSGYCVHCQRNTTGEHCEKCLDGYIGDSI
                                                                                                                                                                                                                                                                                                                                                       5 AGQCSQNEYFDSLLHACIPCQ------LRCSSNTPPLTCQRYCNASVTNSV
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A;Introns: 72/1; 122/1; 152/3; 188/1; 209/1; 255/1; 301/1; 339/1;
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A;Gene: FlyBase:Fur2
A;Cross: FlyBase:FBgn0004598
C;Keywords: hydrolase; serine proteinase; transmembrane protein F;409-652/Domain: subtilisin homology <SBT>
F;418,457,618/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                         20; Indels
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                                                                                                                                                                                               Score 58; DB 1; Pred. No. 1.2e+02;
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20.1%; Score 57; DB
Best Local Similarity 34.7%; Pred. No. 52;
Matches 17; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                               20.5%;
                                                                                                                                                                                               Query Match
Best Local Similarity 21.04
Matches 13; Conservative
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123 RG 124
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C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin C;Function:
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote C;Superfamily: laminin G repeat homology; laminin-type EGF-like homology
C;Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycoprof; P;12-4/Domain: signal sequence #status predicted coil; extracellular matrix; glycoprof; F;25-1816/Product: laminin alpha-4 chain #status predicted cMAT>
F;32-184/Domain: laminin-type EGF-like homology cLE2>
F;341-265/Domain: laminin-type EGF-like homology cLE2>
F;341-265/Domain: laminin-type EGF-like homology cLE3>
F;341-265/Domain: l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1816 <RIC>
A; Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; UNIPARC:UPI0000161B53; EMBL:X91171;
A; Experimental source: tissue type heart
R; Itivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
R; Itivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
A; Title: Primary structure and expression of a novel human laminin alpha-4 chain.
A; Reference number: I53516; MUID:95300971; PMID:7781776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-142, 'P. 143-177, 'F', 179-490, 'Y', 492-1056, 'P', 1058-1816 <1IV>
A; Residues: 1-142, 'P. 14-177, 'F', 179-490, 'Y', 492-1056, 'P', 1058-1816 <1IV>
A; Cross-references: UNIPARC: UP1000003498C; EMBL: S78569; NID: 91042081; PIDN: AAB34635.1;
R; Richards, A.J.; Al-Imara, L.; Carter, N.; Leversha, M.; Lloyd, J.C.; Pope, F.M.
eubmitred to the EMBL Data Library, December 1993
A; Description: Localisation of the gene (LAMA4) to chromosome 6q21 and isolation of a F.A; Reference number: S49149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: S49149
A,Molecule type: mRNA
A,Residues: 236-1816 <RI2>
A,Cross-references: UNIPARC:UPIO00016ABEA, EMBL:X76939, NID:g509805, PIDN:CAA54258.1; I
R,Richards, AJ.; Al.I-mara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
Submitted to the EMBL Data Library, February 1993
A,Degcription: Isolation of a partial cDNA encoding a protein homologous to laminin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1403-1541,'S',1543-1816 <RI3>
A;Crosetics:
A;Gene: GDB:LAMA4; LAMA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NiAlternate names: laminin Ah
C;Species: Homo sapiens (man)
C;Daccession: S68960; S65926; S49149; S40150; I53516
R;Richards, A.; Al-Imara, L.; Pope, F.M.
Bur. J. Biochem. 238, 813-821, 1996
A;Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the characteric number: S68960; MUID:96300249; PMID:8706685
                                                                                                                                                                                                                                                                                 5
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                                A;Gene: CESP:M02G9.1
A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
                                                                                                                                                                                           Length 1513;
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                                                                                                                                                                                           Score 58; DB 2;
Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                       15 DSLLHAC-IPCQLRC-SSNTPPLTCQRYCNAS 44
                                                                                                                                                                                                                                                                             3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laminin alpha-4 chain precursor - human
                                                                                                                                                                                       cn 20.5%;
il Similarity 43.8%;
14; Conservative
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Best Local Similarity
Matches 14; Conserv
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        C;Genetics:
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A;Reference number: Z21745
A;Recession: T38571
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Resius: 1-701 <BA2>
A;Resius: 1-701 <BA2>
A;Cross-references: UNIPROT:Q09807; UNIPARC:UP1000013A007; EMBL:Z54354; NID:g1019398; PII
A;Experimental source: strain 972h-; cosmid c2G11
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A;Cross-references: UNIPROT:Q28983; UNIPARC:UP1000013C373; EMBL:U40024; NID:g1066465; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residuss: 1-2824 <WIL>
A;Cross-references: UNIPROT:P90891; UNIPARC:UPI000017BA22; EMBL:Z81091; PIDN:CAB03143.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A.Title: A sperm membrane protein that binds in a species-specific manner to the egg
A.Reference number: 221464; MUID:96064658; PMID:7592795
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C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T22759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zonadhesin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T34022
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: T38571; S62460
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 701;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 Match 20.0%; Score 56.5; Local Similarity 28.6%; Pred. No. 79; les 14; Conservative 12; Mismatches
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A;Map position: 1L
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Best Local S:
Matches 14
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                                                                                                                                                                                                                                                                                                                                            hypothetical protein T23K8.9 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear crees)
C; Species: Arabidopsis thaliana (mouse-ear crees)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: 636675
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Aneen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Recession: G96675
A; Status: preliminary
A; Rocession: G96675
A; Status: preliminary
A; Rocession: G96675
A; Rocession: G9675
A; Rocession: G96675
A; Rocession: G9675
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A;Introns: 31/1; 98/1; 162/1; 199/1; 244/1; 279/1; 323/1; 354/2; 391/1; 408/1; 458/1; 48
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S62460
hypothetical protein SPAC2G11.05c - fission yeast (Schizosaccharomyces pombe)
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                                                                                                              4 MAGQCSQNEYFDSLLHACIPCOL----RCSSNT-----PPLTCQRYCNA 43
                                                                --PPLTCQRYCNA 43
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1 Similarity 38.9%; Pred. No. 66;
14; Conservative 3; Mismatches 13: Indele
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                                                                     MAGQCSQNEYFDSLLHACIPCQL----RCSSNT
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A,Gene: T23K8.9
A,Map position: 1
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Matches
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A; Accession: B89588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WHENE Cathepsin B (EC 3.4.22.1) precursor - rat
Cathepsin B (EC 3.4.22.1) precursor - rat
NyAlternate names: cathepsin B1; RSG-2 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Apr-1984 #Bequence revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: 551041; A00977; T59019
R;Guenette, R.S.; Mooibroek, M.; Wong, K.; Wong, P.; Tenniswood, M.
R;Guenette, R.S.; Mooibroek, M.; Wong, K.; Wong, P.; Tenniswood, M.
Eur. J. Biochem: 226, 311-321, 1994
A;Title: Cathepsin B, a cysteine protease implicated in metastatic progression, is also
A;Reference number: S51041; MUID:95094788; PMID:8001549
A;Residues: 1-339 -GUES
A;Residues: 1-330 -GUES
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A; Residues: 69-339 <-RES.
A; Crose-references: UNIPARC:UPI00001708P9; GB:M11305; NID:g203647; PIDN:AAA40993.1; PID:
C; Function:
A; Description: broad specificity endopeptidase and peptidyl dipeptidase
C; Function:
A; Pestramily: papain: a signal sequence signal estaction degradation
C; Superfamily: papain: a signal sequence sequence specificed <-RG>
F; 1.17 (Domain: signal sequence sequence described <-RG>
F; 1.87 (Domain: propeptide sequence sequence apperimental <-RL>
F; 180-126, 100main: light chain sequence experimental <-RL>
F; 180-126, 129-333/Product: carbepsin B status experimental <-RH>
F; 129-333/Domain: heavy chain status experimental <-RH>
F; 129-333/Domain: heavy chain status experimental <-RH>
F; 129-333/Domain: carbohydrate (Asn) (covalent) status experimental
A,Introne: 87/1; 98/1; 126/2; 201/3; 343/3; 406/1; 576/3; 656/1; 825/3; 869/1; 909/1; 96/1; 1755/2; 1800/1; 1850/3; 1896/1; 2003/3; 2035/3; 2082/3; 2119/1; 2144/1; 2200/2; 227 F;243-279/Domain: LDL receptor ligand-binding repeat homology <LDL>
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A; Residues: 80-126,129-158, 'G', 160-333 < TAK>
A; Cross-references: UNIPARC: UP10000172C7A
B; San Segundo, B.; Chan, S.J.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 82, 2320-2324, 1985
A; Title: Identification of cDNA clones encoding a precursor of rat liver cathepsin B.
A; Reference number: IS9019; MUID: 85190489; PMID: 2986112
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                                                                                                                                                                                                       Query Match 19.8%; Score 56; DB 2; Length 2824; Best Local Similarity 32.5%; Pred. No. 3e+02; Matches 13; Conservative 10; Mismatches 15; Indels
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ilarity 25.5%; Pred. No. 55;
Conservative 7; Mismatches
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Matches 12; Conser
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C)Accession: B89588; C89588
C)Accession: B89589; C89588
C)Accession: B89589; C89588
C)Accession: Calegans Sequencing Consortium.
R;anonymous The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nemarode C. elegans: a platform for investigating biology
A;Reference number: A79600; MUID:9960596113; PMID:9981916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www. sanger.ac.uk/Projects/C_elegans/ appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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R, Bewan, M., Relchert, B.J.; Barel, E.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuell
submitted to the Protein Sequence Database, June 1998
A, Reference number: 215450
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A,Note: glutamine-rich protein
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 31-Dec-2004
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A;Experimental source: cultivar Columbia; BAC clone M4122
C;Genetics:
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29.8%; Pred. No. 61;
tive 6; Mismatches
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A;Introns: 471/1; 516/3; 587/1; 666/2; 716/3
A;Note: M4122.110
C;Function:
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A;Map position: X
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Best Local Similarity
Matches 14; Conservi
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A;Molecule type: DNA
A;Residues: 1-378 <STO>
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A; Molecule type: mRNA
A; Residues: 1-339 <Q12-
A; Cross-references: UNIPARC: UPI0000018A4; GB:S69034; NID:g239906; PIDN:AAB20536.1; PID:
A; Experimental source: B16a melanoma
A; Experimental source: B16a melanoma closs were found to have identical coding sec A; Note: three mRNA forms from B16a melanoma closs were found to have identical coding sec R; Chan, S.J.; San Segundo, B.; McCormick, M.B.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 83, 7721-7725, 1986
A; Title: Nucleotide and predicted amino acid sequences of cloned human and mouse preproce A; Reference number: A26498; MUID:87017021; PMID:3463996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-159, N',161-173, D',175-176, 'I',178-283, 'V',285-339 <CHA>
A,Cross-references: UNIPARC:UD1000016CCE0; GB:M14222; NID:g192841; PIDN:AAA37494.1; PID:
F,Ferrara, M.; Wojcik, F.; Rhaissi, H.; Mordier, S.; Roux, M.P.; Bechet, D.
FEBS Lett. 273, 195-199, 1990
A,Title: Gene structure of mouse cathepsin B.
A,Reference number: S12901; MUID:91032179; PMID:2226854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 314-339 <FRI>
A;Cross-references: UNIPARC:UP1000016CCE1; EMBL:X54966; NID:950596; PIDN:CAA38713.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Description: broad specificity endopeptidase and peptidyl dipeptidase
A) Description: broad specificity endopeptidase and peptidyl dipeptidase
A) Pathway: intracellular protein degradation
C) Superfamily: papain
C) Superfamily: papain
C) Reywords: cysteine proteinase; glycoprotein; hydrolase; lysosome; protein degradation
E) 1-17/Domain: signal sequence #status predicted <NBT>
E) 80-339/Product: cathepsin B #status predicted <NBT>
E) 819.192/Binding site: carbohydrate (Asn) (covalent) #status predicted
E) 93-122,105-150,141-207,422-146,179-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-2111,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-211,187-
                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-399 <QIA.
A; Cross-references: UNIPROT: P10605; UNIPARC: UPI00000018A4; GB: M63999
A; Cross-references: UNIPROT: P10605; UNIPARC: UPI00000018A4; GB: M63999
R; Qian, F.; Frankfater, A.; Steiner, D.F.; Bajkowski, A.S.; Chan, S.J.
Anticancer Res. 11, 1445-1451, 1991
A; Title: Characterization of multiple cathepsin B mRNAs in murine B16s melanoma.
A; Reference number: A49826; MUID:92082172; PMID:1746902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiFriemert, C.; Closs, E.I.; Silbermann, M.; Erfle, V.; Strauss, P.G. Gene 103, 259-261, 1991
A;Title: Isolation of a cathepsin B-encoding cDNA from murine osteogenic cells. A;Reference number: PS0360; MUD:91365255; PMID:1889751
A;Accession: PS0360
A, Reference number: A38458; MUID:91190267; PMID:2012677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-159,'N',161-173,'D',175-176,'I',178-283,'V',285-339 <FER>
A;Cross-references: UNIPARC:UPI000016CCE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 finger protein YJL206c - yeast (Saccharomyces cerevisiae)
N;Alternate names: probable membrane protein YJL206c; protein J0316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 339;
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19.4%; Score 55; DB 1; Length 339
Best Local Similarity 25.0%; Pred. No. 63;
Matches 16; Conservative 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Note: single copy gene C,Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSVK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 NSVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: B26498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: S12901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
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                                                                                                                                                                                                                                                                                                          hypothetical protein T10M13.17.1 - Arabidopsis thaliana ($Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
S;Jacession: T01519
Martienssen, R.; McCombie, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott Martienssen, R.; McCombie, W.
A.Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A.Reference number: Z14346
A.Accession: T01519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-294 <MIL>
A;Cross-references: UNIPROT: Q9XUSO; UNIPARC: UPI0000076A8F; EMBL: Z81573; PIDN: CAB04626.1;
A;Experimental source: clone M02G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
A;Aclecule type: DNA
A;Residues: 1-989 <JOH>
A;Cross-references: UNIPROT:Q9ZU00; UNIPARC:UPI00000A0E3D; EMBL:AF001308; NID:g2104523;
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein M02G9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: D=Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23682
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHMSB cathopsin B (EC 3.4.22.1) precursor - mouse cathopsin B (EC 3.4.22.1) precursor - mouse Cithopsin B (S. 2.4.22.1) precursor - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 31-Mar-1992 #sequence revision 26-Apr-1996 #text_change 09-Jul-2004 C; Accession: A38458; A49826; E36498; S12901; PS0350 R; Qian, F:; Frankfater, A.; Chan, S.J.; Steiner, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 QMAGQCSQ--NEYFDSLLHACIPCQLRCSS--NTPPL--TCQR----YCNA---SVTN
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Pred. No. 56;
3; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 CARN-IDDRLFYHCSPCNFTLDLRCVLNPPP 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                   | ::: | | | | : | | | | CKIKCSSN---CSCTAYANTDIREGGKG 402
                                               51
                                               COLRCSSNTPPLTCORYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 20/3; 76/2; 182/3; 223/3
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Best Local Similarity 37.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.9%;
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Best Local Similarity 41.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z19781
A;Accession: T23682
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A;Gene: CESP:M02G9.3
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Genetics:
A,Map position: 4S
A,Introns: 31/3
A,Note: T10M13.17.1
                                                        24
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Matches
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24; Gaps

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A, Molecule type: DNA
A, Residues: 1-392 <WIL>
A, Festidues: 1-392 <WIL>
A, Festidues: 1-392 <WIL>
A, Festidues: 1-302 content of the type: UNIPROT: 09XXP6; UNIPARC: UPI000007EED1; EMBL: AL021503; PIDN: CAA16424.1
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vascular endothelial growth factor C precursor - human
NyAlternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Apte: 27-Apt-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S69207; S61795; S71443; S69208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, C
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for A;Reference number: S69207; MUID:96203094; PMID:8612600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Residues: 1-419 <00D.
A;Residues: 1-419 <00D.
A;Cross-references: UNIPROT: P49767; UNIPARC: UPI0000001C2A; EMBL: X94216; NID: g1177488; PII
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, C
EMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: mRNA;
;Residues: 1-419 <LEE>
;Cross-references: UNIPARC:UPI000001C2A; EMBL:U43142; NID:91150988; PIDN:AAA85214.1; PJ
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A;Reidudes: 'Y', 104-120 cJ0U2>
A;Reidudes: 'Y', 104-120 cJ0U2>
A;Cross-references: UNIPARC:UP1000014E2AF
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
Bubmitred to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and A;Reference number: 869208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 392;
                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 45/2; 74/3; 139/3; 175/2; 190/3; 241/3; 305/3; 356/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 70-419 <JOUI>
A;Cross-references: UNIPARC:UP10000150795
A;Note: this sequence has been revised in reference 869207
A;Accession: S71443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-12/Domain: signal sequence #status predicted <SIG>F;13-102/Domain: propeptide #status predicted <PRO>
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                                                                                                                                                                                                                                                                                                                                                                                    19.3%; Score 54.5; I
40.0%; Pred. No. 81;
tive 7; Mismatches
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submitted to the EMBL Data Library, May 1996
A,Reference number: H01557
A,Racession: G02659
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189 SCLPCQ-TCASFIDPMSEKATCTAT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 ACIPCQLRCSSNTPPLTCQRYCNAS 44
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 40.0 Matches 10; Conservative
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                                                                                                                                                                                                               C, Genetics:
A, Gene: CESP: Y68A4A.10
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                      C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: S6625; S6593
R;Purnelle, B: Costerr F: Goffeau, A.
Yeast 10, 1235-1249, 1994
A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifie ase gene ACO1 and two homologues to chromosome III genes.
A;Reference number: S46621; MUID:95274326; PMID:7754713
A;Accession: S46625
A;Accession: S46625
A;Accession: S46625
A;Residues: 1-758 <PUR>
A;Accession: Costerr BNA
A;Residues: 1-758 <PUR>
A;Crose-references: UNIPROT:P39529; UNIPARC:UPI000013B60A; EMBL:X77688; NID:g1183992; PI
A;Crose-references: Uniproc: F: Goffeau, A.
Submitted to the Protein Sequence Database, September 1995
A;Reference number: S56977
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A;Accession: T27283
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DMP
A;Residues: 1-1620 <WILb
A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 10L
C;Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc
F;42-78/Domain: GAL4 zinc binuclear cluster homology <GAL4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPARC: UPI000013B60A; EMBL: Z49481; NID: g1015584; PIDN: CAA89502.1; C; Genetics:
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C;Genetics:
A;Gene: CESP:Y64G10A, £
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accesion: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T27303
hypothetical protein Y68A4A.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 12-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27303
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Local Similarity 25.6%; Pred. No. 2.4e+02;
les 11; Conservative 7; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 2; 1
Pred. No. 1.3e+02;
2; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 ACIPC---QLRCSSNTPPLTCQRYCNASVTNS 48
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A;Reference number: Z20340
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11 Similarity 43.8%;
14; Conservative
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A;Molecule type: DNA
A;Residues: 1-758 <PUW>
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Matches
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Matches
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membrane protein ydbH - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Datesion: H64888
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A;Title: The Complete genome sequence of Escherichia coli K-12.
A;Title: The Complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-879 < BLAT>
A;Residues: 1-879 < BLAT>
A;Residues: 1-879 < Coloneric Strain K-12, substrain MG1655
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A;Experimental source: strain 0157:H7, substrain EDL933
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Cipate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
Cipate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
CiAccession: T130197
RiLegan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.
Biol. Chem. 272, 8791-8801, 1997
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com A;Reference number: Z20771; MUID:97236843; PMID:9079715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Escherichia coli (strain 0157:H7, substrain EDL932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cjaccession: G85739 Ciburland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, P.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grocbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: G85739
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: ydbH
C;Superfamily: Escherichia coli membrane protein ydbH
F;8-24/Domain: transmembrane #status predicted <TWOl>
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Pred. No. 1.6e+02;
6; Mismatches 12;
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A;Molecule type: mRNA
A;Residues: 1-2155 <LEG>
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Best Local Similarity 40.09
Matches 14; Conservative
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Best Local Similarity 40.01
Matches 14; Conservative
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A Molecule type: DNA
A;Residues: 1-879 <STO>
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C90879
hypothetical protein EC82003 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Bacherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90879
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
A;Aritle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Retus: preliminary
A;Molecule type: DNA
A;Retus: preliminary
A;Retus: preliminary
A;Retus: Preliminary
A;Retus: Dreliminary
A;Retus: Drelimi
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F;19-493/Product: membrane glycoprotein CD30 homolog #status predicted <MAT>
F;278-304/Domain: transmembrane #status predicted <TMM>
F;305-493/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane glycoprotein CD30 homolog precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Uul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Azdesion: U55486
R;Azdwa, S.; Satoh, H.; Horie, R.; Ito, K.; Choi, S.H.; Takeuchi, H.; Watanabe, T.
Gene 182, 155-162, 1996
A;Fitle: Cloning and characterization of a cDNA for rat CD30 homolog and chromosomal ase
A;Feference number: U55486; MUID:97136705; PMID:8982082
A;Contents: T cell
A;Accession: U55486.
                                              F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 19.3%; Score 54.5; DB 2; Length 493; I Similarity 32.7%; Pred. No. 99; 16; Conservative 6; Mismatches 16; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 19.3%; Score 54.5; DB 2; Length 879; I Similarity 40.0%; Pred. No. 1.6e+02; 14; Conservative 6; Mismatches 12; Indels ...
                                                                                                                              Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 SQNEYFDSLLHACIPC-----QLRCSSNTPPL-TCQ--RYCNASVTNS
                                                                                                                                                                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                          327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                               7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 44
                                                                                                                          Query Match
19.3%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 86;
Matches 14; Conservative 2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|:||||||330 LQLTGEAKQ---ADLILYARLPAQLSGSLSDPTLT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LOMAGQCSONEYFDSLLHACIPCOLRCSSNTPPLT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-493 <AIZ>
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A;Residues: 1-474 <WIL>
A;Cross-references: UNIPROT:Q9XXQ2; UNIPARC:UPI00000783D7; EMBL:AL021503; PIDN:CAA16417.1
A;Experimental source: clone Y68A4A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rileimbac, D.
submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid T07D1,
A; Reference number: Z18584
A; Accession: T16822
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residue: type: DNA
A; Residues: 1-1099 < LEI>A; Residues: UNIPARC: UPI000017BB77; EMBL: U41531; NID: g1109802; PID: g1109803; PIDN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-497 <WIL>
A;Cross-references: UNIPROT:Q23460; UNIPARC:UPI000007F2F3; EMBL:Z70757; PIDN:CAA94805.1;
A;Experimental source: clone ZK287
                                                                                                                                                                                                                                                                                                                                   A;Gene: CESP:Y68A4A.5
A;Map position: 5
A;Introns: 47/2; 80/3; 145/3; 181/2; 196/3; 238/2; 269/2; 306/3; 342/2; 357/3; 418/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27827
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MASEMSRAINY----CCECVASQGRCSADTCPCVAARKTCDEHCEST 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.1%; Score 54; DB 2; Length 1099;
Best Local Similarity 35.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.8%; Pred. No. 1.18+02;
Matches 13; Conservative 4; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ZK287.1 - Caenorhabditis elegans
                                              A;Accession: T27297
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 CIPCQLRCSSNTPPLTCQRYCNASV-TNS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, April 1996 A;Reference number: 220425 A;Accession: T27827
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A;Introns: 20/1; 44/2; 99/3; 339/3; 443/2
            A; Reference number: Z20340
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A;Gene: CESP:ZK287.1
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A;Cross-references: UNIPROT:008523; UNIPARC:UPI000002793C; EMBL:X99805; NID:g1915908; PI
A;Experimental source: strain CD1; whole cochleae
A;Note: non-collagenous protein only expressed in the inner ear, by cells both in and su
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A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:P61092; UNIPARC:UP100000B9B3; EMBL:Z19579; NID:g297034; PID
C;Superfamily: Drosophila developmental protein sina; RING finger homology
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signal and the mouse signal and the mouse
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S35754
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C;Bocies: Mus musculus (house mouse)
C;Bocies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: I48764; S35754
R;Della, N.G.; Senior, P.V.; Bowtell, D.D.
Development 117, 1333-1343, 1993
A;Title: Isolation and characterisation of murine homologues of the Drosophila seven in A;Reference number: I48763; MUID:94008336; PMID:8404535
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*Residues: 1-282 <RES.
A;Cross-references: UNIPROT:Q06985; UNIPARC:UPI000002451E; EMBL:219580; NID:g297801; PIC
C;Superfamily: Drosophila developmental protein sina; RING finger homology
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T27297
T27297
T27297
Phypothetical protein Y68A4A.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accesard, C.
R;Steward, C.
submitted to the EMBL Data Library, January 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 FDSLLHACIPCQ---LRCSSNTPPLTCQRYCNA-----SVTNSV 49
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19.1%; Score 54; DB 2; Length 282;
Best Local Similarity 34.0%; Pred. No. 70;
Matches 17; Conservative 3; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.1%; Score 54; DB 2; Length 282; Best Local Similarity 34.0%; Pred. No. 70; Matches 17; Conservative 3; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                           1372 CPPNSHYESCVSVCQP---RCAAIRLKSDCNHYC 1402
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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hypothetical protein At2g16770 [imported] - Arabidopsis thaliana C. Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84544
M; Kaul, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. R.Lin, X.; Kaul, S. Kaul, W.C.; White, O.; Sleen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9SLE1; UNIPARC:UPI00000A1869; GB:AE002093; NID:94581120; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-332 <WIL>
A;Cross-references: UNIPROT:Q09553; UNIPARC:UPI000008359F; EMBL:Z48582; PIDN:CAA88466.1;
A;Experimental source: clone F27E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cispecies: Caenorhabditis elegans
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cibacession: T21458
A;Reference number: Z19425
A;Reference number: Z19425
A;Accession: T21458
A;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F32H5.1 - Caenorhabditis elegans
hypothes: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.5; DB 2; I Pred. No. 73; 3; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lucry match
Best Local Similarity 28.6%; Pred. No. 91;
Matches 14; Conservative 6; Mismarchea
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A; Introns: 87/3; 101/2; 152/2; 236/1; 284/3
1852 PCLLRCPDNSDPLTSMK 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.2%;
Matches 16; Conservative
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A;Accession: T21681
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A;Molecule type: DNA
A;Residues: 1-255 <STO>
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A;Map position: 2
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A84544
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A;Molecule type: mRNA
A;Residues: 1-2022 *MIR>
A;Residues: 1-2022 *MIR>
A;Crosa-references: UNIPROT: Q14788; UNIPARC: UPI0000161189; GB:U42391; NID:g1147782; PIDN
A;Crosa-references: UNIPROT. Q14788; UNIPARC: UPI0000161189; GB:U42391; NID:g1147782; PIDN
B;Denct, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overlapping expression of multiple unconventional myosin gen
A;Accession: 161700
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: myosin motor domain homology; protein kinase C zinc-binding repeat homolo
C;Keywords: nucleotide binding; P-loop
F;149-941/Pomain: myosin motor domain homology #status atypical <MMO>
F;239-246/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1980 <REL:
A; Cross-tences: UNIPROT:Q63358; UNIPARC:UPI000012FAD6; EMBL:X77609; NID:g639998; PID
C; Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zi
C; Keywords: nucleotide binding; P-loop
F; 149-942/Domain: myosin motor domain homology <MMOT>
F; 139-246/Region: nucleotide-binding motif A (P-loop)
F; 1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>
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Myosin-IXD [similarity] - human

myosin-IXD [minilarity] - human

myosin-IXD [minilarity] - human

myosin-IXD [minilarity] - human

C;Species: Homo sapiens (man)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 31-Dec-2004

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 31-Dec-2004

C;Date: 19-May-2000 #sequence_revision 15-May-2000 #text_change 31-Dec-2004

R;Mirch, J.,; Jensen, K., Post, P.L.; Bement, W.M.; Mooseker, M.S.

J. Cell Sci. 109, 653-661, 1996

J. Title: Human myosin-IXD, an unconventional myosin with a chimerin-like rho/rac GTPase-A;Accession: A59256; MUID:97063843; PMID:8907710
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A,Cross-references: UNIPARC:UP10000073918; GB:L29149; NID:g457257; PIDN:AAA20912.1; PID.
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                                                                                                                                                                                                                                                                                                      myosin heavy chain - rat
C;Specias: Rattus norregicus (Norway rat)
C;Date: 15-Uul-1995 #text_change 09-Jul-2004
C;Accession: S54307
R;Reinhard, J: Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A;Title: A novel type of myosin implicated in signalling by rho family GTPases.
A;Reference number: S54307; MUID:95188874; PMID:7882973
A;Accession: S54307
A;Status; preliminary; nucleic acid sequence not shown
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                                                                 n similarity 52.9%; Pred. No. 3.7e+02; 9; Conservative 2; Mismatches 6; Indels
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Pred. No. 3.7e+02;
2; Mismatches 6; Indels
                 LOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSV
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Matches 9; Conserve
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A; Reference number: 219870
A; Accession: 124296
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-927 < WI2>
A; Molecule type: DNA
A; Residues: 1-927 < WI2>
A; Molecule type: DNA
A; Residues: 1-927 < WI2>
A; Rossereferences: UNIPARC: UPI0000086677; EMBL: Z81110; PIDN: CAB03262.1; GSPDB: GN00023; C; Genetics: CESP: T01D3
C; Genetics: CESP: T01D3.6
A; Map position: 5
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C; Species: Schizosaccharomyces pombe
C; Species: O3-bec-1999 #sequence_revision O3-bec-1999 #text_change O9-Jul-2004
C; Accession: T39411
R; Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, April 1998
A; Accession: T39411
A; Accession: T39411
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1935 cLYN>
A; Coss-references: UNIPROT: O60072; UNIPARC: UPI000013A2C9; EMBL: AL022600; PIDN: CAA18663.1
A; Experimental source: strain 972h-; cosmid c13G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-1895 < PAU>
A; Cross-references: UNIPARC: UPI000004 CAEB; EMBL: U00065; NID: 9495681; PID: 9495684; PIDN: A) Experimental source: Brrain Bristol N2
C; Genetics:
A; Gene: CESP: D1044.3
A; Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apporterical protein D1044.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15881
R;Pauley, A.
Bubmitted to the EMBL Data Library, June 1994
A;Description: The sequence of C. elegans cosmid D1044.
A;Reference number: Z18423
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
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                                                                                                                                                                                                                                                                                                                                                                A;Introns: 38/2; 87/3; 128/2; 242/2; 374/3; 416/3; 734/3; 842/3; 857/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1465 GQCNSNQVYYNNQCYNTVPIGSQCQITQQCLGNSQCMNSFCQCPSGTTN 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.9%; Score 53.5; DB 2; Length 1935; Best Local Similarity 37.2%; Pred. No. 4.1e+02; Matches 16; Conservative 7; Mismatches 9; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 AFKCTEPTYFLQYCQLALPQVAMNQNWRAQINCPLACPLNAHPSTCTSSC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
18.9%; Score 53.5; DB 2; Length 927;
Best Local Similarity 26.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 4; Mismatches 20; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 GOCSONE-YFDSLLHACIP----CQL--RCSSNTPPLTCQRYCNASVTN
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18.9%; Score 53.5; DB 2; Length 10
Best Local Similarity 26.5%; Pred. No. 4e+02;
Matches 13; Conservative 12; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-915 <WIL>
A;Cross-references: UNIPROT:002364; UNIPARC:UPI000002A1C9; EMBL:281527; PIDN:CAB04280.1;
A;Experimental source: clone F35E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Caenorhabditis elegans
Cispecies: Lacor-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T21772; T24296
Risteward, C.
Risterence number: 219470
Risterence number: 219470
Risteward, C.
Risteward, C.
Risteward, C.
Risteward, C.
Risteward, C.
      A,Molecule type: DNA
A,Residues: 1-356 <MILD.
A,Cross-references: UNIPROT: P91991; UNIPARC:UPI000007EF35; EMBL:281524; PIDN:CAB04249.1;
A,Experimental source: clone F32H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Residues: 1-915 <WI2>
;Cross-references: UNIPARC:UPI000002A1C9; EMBL:Z81110; PIDN:CAB03263.1; GSPDB:GN00023;
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accesion: T21772; T24296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T01D3.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T21773; T24297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 5
A;Introns: 38/2; 87/3; 128/2; 242/2; 374/3; 404/3; 722/3; 830/3; 845/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                      Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
18.9%; Score 53.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 4; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QMAGQC---SQNEYFDSLLHACIPCQLRCSSNTPPL---
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A,Accession: T24297
A;Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Steward, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19470
A;Acession: T21773
                                                                                                                                                                                                                                                                                                                               Query Match
18.9%; Score 53.5; Di
Best Local Similarity 21.8%; Pred. No. 97;
Matches 12; Conservative 13; Mismatches
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                                                                                                                                                                                             A,Map position: 5
A,Introns: 64/3; 118/1; 166/2; 328/1
C,Superfamily: papain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Experimental source: clone T01D3
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A,Gene: CESP:T01D3.6b
                                                                                                                                     C, Genetics:
A, Gene: CESP: F32H5.1
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A387; R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
Genomics 13, 219-224, 1992
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRFI) and localization to ch)
A;Reference number: A38208; MUID:92250049; PMID:1315717
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A;Accession: A38208
A;Molecule type: DNA
A;Rocession: A38208
A;Molecule type: DNA
A;Rocession: A38208
A;Cross-references: UNIPROT: P19438; UNIPARC: UPI000002CE11; GB:M75864; GB:M75865; GB:M7586
A;Cross-references: UNIPROT: P19438; UNIPARC: UPI000002CE11; GB:M75864; GB:M75865; GB:M7586
B;Loctscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslaue
Cell 61, 351-359; 1990
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recept
A;Reference number: A34899; MUID: 90235284; PMID: 2158862
A;Reference number: A34899
A;Molecular type: mRNA
A;Residues: 1-455 < LOB>
A;Residues: 1-455 < LOB>
A;Residues: 1-455 < LOB>
A;Residues: 1-455 < LOB>
A;Residues: 1-450 < LOB>
A;Re
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A;Title: Molecular Cloning and expression of human and rat tumor necrosis factor recepton A;Reference number: A36555; MUID:91090841; PMID:1702293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor necrosis factor receptor 1 precursor (validated) - human
N;Alternate names: PS5 tumor necrosis factor receptor; TNF receptor type 1
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aloce: part of this sequence, including the amino end of the mature protein, confirmed Rischall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T. Cell 61, 361-370, 1990
A,Title: Molecular cloning and expression of a receptor for human tumor necrosis factor. A;Reference number: A34900; MUID:90235285; PMID:2158863
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C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 53; DB 2; 28.3%; Pred. No. 1.3e+02; Live 10; Mismatches 22
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A; Residues: 1-455 <SCH>
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A,Molecule type: mRNA
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C; Species: Arabidopsis thaliana (mouseau cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: F86276
C; Arabidopsis A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Nature 408, 4016-820, 2000
A; Huter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Roney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Retr. M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Rizzo, M.; Roberg, S.L.; Schwartz, J.C.; Davis, R.W.
A; Rizzo, M.; Roberg, R.S.; Schwartz, J.C.; Davis, R.W.
A; Rizzo, M.; Roberg, R.S.; Schwartz, J.C.; Davis, R.W.
A; Rizzo, M.; Roberg, R.S.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                  protein CloG8.4 (imported) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89046
C;Accession: C89046
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Fitle: Genome sequence of the nematode C. elegans; a platform sequence 282, A;Reference number: A75000; MUID:99065613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCPSNEEFRSCGTACEPTCQ----NPNPQVCTLQCILNVCQCSQG 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 2; Length 98;
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                                                                                                                         6 GOCSONEYFDSLLHA -- CIPCOLRCSSNT--PPLTC-
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3; Mismatches
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ilarity 30.2%;
Conservative
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Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: C10G8.4
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A;Accession: JC2404

A;Accession: JC2404

A;Molecule type: protein
A;Accession: JC2404

A;Molecule type: protein
A;Accession: JC2404

A;Molecule type: protein
A;Cross-references: UNIPARC: UP100001736E4
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNP-alpha (cachectin) and C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type of transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2245/Froduct: tumor necrosis factor receptor; transmembrane protein
F;1-21/Domain: extracellular #status predicted <SIG>
F;245/Froduct: TNF binding protein | (tumor necrosis factor repeat homology <NG1>
F;41-201/Product: TNF binding protein | (tumor necrosis factor alpha inhibitor) #status F;127-167/Domain: NGF receptor repeat homology <NG2>
F;41-201/Product: TNF binding protein | (tumor necrosis factor alpha inhibitor) #status predicted <AMN>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: Transmembrane #status predicted <AMN>
F;127-167/Domain: Irransmembrane #status predicted <AMN>
F;212-234/Domain: intracellular #status predicted <AMN>
F;212-234/Domain: intracellular #status predicted <AMN>
F;215-2145/Domain: intracellular #status predicted <AMN>
F;24,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
A; Reference number: JC2404; MUID:95128033; PMID:7765720
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Best Local Similarity 34.9%;
Matches 15; Conservative
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Best Local Similarity
Matches 14; Conserva
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A,Mocession: A60594
A,Mocession: A60594
A,Mocession: A60594
A,Cross-references: UNIPARC:UPI0000736E2
A,Experimental source: renal failure patient urine
R,Emgelmann, H,; Novick, D,; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A,Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A,Recession: A35010; MuID:90110215; PMID:2153136
A,Accession: A35010
A,Mocession: A35010
A,Mocession: A35010
A,Residues: 41-45 - ENGS
A,Cross-references: UNIPARC:UPI00001736E3
A,Essidues: 41-45 - ENGS
A,Essidues: 41-44, A, Kirihara, S.; Kato, K.
Biosci Biotechnol: Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-455 cGRA>
A; Residues: 1-455 cGRA>
A; Cross-references: UNIPARC:UPI00002CE11; GB:M37764
A; Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
A; Noplar, Y:, Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A; Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ
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R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Bur. J. Immunol. 20, 1167-1174, 1990
Bur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc A;Reference number: A60231; MUID:90292116; PMID:2113477
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A;Residues: 41-43, X',45-53, X',55-57 <SEC>
A;Cross-references: UNIPARC:UPI000072FDB
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ne
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A;Residues: 30-38;41-53,7x',55-79,7x',82-94,7NK';7xx',100-104;107-128;162-167,7x',169-2
A;Residues: 30-38;41-53,7x',55-79,7xx',82-94,7NK';7xx',100-104;107-128;162-167,7x',169-2
A;Cross-references: UNIPARC:UPI00002D398; UNIPARC:UPI00001736DE;
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Arc., Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human necrosis factor (INF) receptor cDNA and expression of re
A;Reference number: A38281; MUID:91017509; PMID:2170974
    A;Reaidues: 1-455 <HIM>
A;Cross-references: UNIPARC:UPI00002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:
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A; Residues: 41-60 < GAT>
A; Residues: 41-60 < GAT>
A; Residues: 41-60 < GAT>
A; Cross-references: UNIPARC:UPI00001736E1
A; Experimental source: cancer patient serum
R; Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Bur. J. Haematol. 42, 270-275, 1989
A; Title: Isolation and characterization of a tumor necrosis factor binding protein from A; Reference number: A60594; MUID:89171156; PMID:2924890
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A,Title: Cloning and partial characterization of the promoter for the human p55 tumor n A,Reference number: J10758; MUID:94085779; PMID:8262379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               le form of the receptor.
A;Reference number: S12057; MUID:91006021; PMID:1698610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S12057
A; Molecule type: mRNA
A; Residues: 1-455 <NOP>
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A; Residues: 1-13 < KEM>
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Directan kinase C (EC 2.7.1.-) zeta - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 05-Way-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
C;Accession: JC1480
B;Goodnight, J.; Kazanietz, M.G.; Blumberg, P.M.; Mushinski, J.F.; Mischak, H.
Gene 122, 305-311, 1992
A;Title: The cDNA sequence, expression pattern and protein characteristics of mouse prote
A;Reference number: JC1480; MUID:93138400; PMID:1487145
A;Accession: JC1480
A;Accession: JC180
A;Accession: JC180
A;Residues: 1-592 <GOOA
A;Cross-references: UNIPROT:Q02956; UNIPARC:UPI0000029ADD; GB:M94632; NID:g200498; PIDN:)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Experimental source: brain

C. Superfamily: procein Nanase C, zeta/iota types; protein kinase C zinc-binding repeat ht C. Superfamily: protein Nanase C zinc-binding repeat pt C; Keywords: AffP; phorbol ester binding; phosphotransferase; serine/threonine-specific prore; P; 131-180/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F; 250-518/Domain: protein kinase homology <KNN>
F; 256-526/Region: protein kinase ATP-binding motif
F; 228-266/Region: protein kinase ATP-binding motif
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F8B188
R;anonymous, The C. elegans Sequencing Consortium.
                                                                              Gaps
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Length 455;
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                                                                              19; Indels
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                                                                                                                                                                                                                                    127 CRKNOYRHYWSENLFOCFNCSL-CLNGTVHLSCOEKONTVCT 167
                                                                                                                                                         8 CSQNE---YFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVT 46
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Score 53; DB 1; I
Pred. No. 1.4e+02;
                                                                              5; Mismatches
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C; Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
P;1-19/Domain: signal sequence #status predicted <SIG>
P;20-712/Product: env polyprotein #status predicted <ENV>
P;20-501/Product: surface glycoprotein gp120 #status predicted <SGG>
P;20-501/Product: transmembrane glycoprotein gp41 #status predicted <TPG>
P;507-523/Region: hydrophobic
P;675-694/Domain: transmembrane #status predicted <TWN>
P;675-694/Domain: transmembrane #status predicted <TWN>
P;675-694/Domain: transmembrane #status predicted <TWN>
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F;36,69,78,113,119,131,137,145,160,173,186,200,232,235,242,266,272,283,294,304,359,392,40
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C;Species: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5S98
R;Inatomi, T.; Tisdale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.
B;Inatomi, T.; Tisdale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.
A;Title: Cloning of rat MucBAC mucin gene: Comparison of its structure and tissue distrib
A;Reference number: JCS598; MUID:97396181; PMID:9245735
A;Accession: JC5598

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.M.; J. Virol. 64, 890-901, 1990
A;Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A;Reference number: A33943; MUID:90112662; PMID:2296086
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NiAlternate names: coat polyprotein
NiContains: surface glycoprotein gpl20; transmembrane glycoprotein gp41
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo appiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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29.3%; Pred. No. 2.3e+02;
tive 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 53; DB 1; Length 712; ilarity 29.3%; Pred. No. 2e+02; Conservative 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 HACIPCOLRCSSNT------PPLTCORYCNASVTNSV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PPLTCQRYCNASVTNSV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPARC:UPI0000174A3A; EMBL:M86924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 507-523/Region: hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 HACIPCQLRCSSNT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
ses 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1034 <INA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: H33943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: H33943
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S:
Matches 12
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NyAlternate names: coat polyprotein
NyAlternate names: coat polyprotein
NyContains: surface glycoprotein gpl20; transmembrane glycoprotein gp41
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Date: 30-Jun-3975, 1992
R;Mulligan, M.J; Yamshchikov, G.V.; Ritter Jr., G.D.; Gao, F.; Jin, M.J.; Nail, C.D.; S.J., Virol. 66, 3971-3975, 1992
A;Title: Cytoplasmic domain truncation enhances fusion activity by the exterior glycopro A;Reference number: A45355; MUD:92266681; PMID:1583738
                                                A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000, MUID:99069613; PMID:9851916 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: F88188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Residues: 1-654 <DUZ>
A,Cross-references: UNIPROT:Q17982; UNIPARC:UPI000017B77E; EMBL:U53141; PIDN:AAA96110.1;
A,Experimental source: strain Bristol N2; clone C14C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P32536; UNIPARC:UPI000012A033; GB:M86924; NID:g325760; PIDN:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: Q09485; UNIPARC: UPI0000816F3; GB: chr_II; PID: 9722386; GSPDB
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A;Map position: 5
A;Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C14C11.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 596;
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R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Bescription: The sequence of C. elegans cosmid C14C11.
A;Reference number: Z20742
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 DSLLHACIP-COLRCSSNTPPLT-CORYCNASVTN 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 CDÓGEYEGMLSYALSOMOLATDONDSAMKCEAFLN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCN 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 2;
Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.4%;
Matches 11; Conservative
                                            Science 282, 2012-2018, 1998
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   A:Status: preliminary
A:Molecule type: DNA
A;Residues: 1-596 <STO>
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Gene: C18H9.7
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Matches

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RESULT 66 T30136

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A; Internets: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12(493/1; 2555/1; 2720/1; 2739/3; 2819/1
493/1; 2555/1; 2720/1; 2739/3; 2819/1
493/1; 2555/1; 2720/1; 2739/3; 2819/1
493/1; 2555/1; 2720/1; 2739/3; 2819/1
493/1; 2555/1; 2720/1; 2739/3; 2819/1
6; 242-249/Domain: animal Kunitz-type proteinase inhibitor homology <BP13>
6; 424-492/Domain: animal Kunitz-type proteinase inhibitor homology <BP15>
6; 645-706/Domain: animal Kunitz-type proteinase inhibitor homology <BP15>
6; 647-706/Domain: animal Kunitz-type proteinase inhibitor homology <BP15>
6; 1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BP17>
6; 1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BP18>
6; 1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BP19>
6; 1952-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BP19>
6; 1952-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BP19>
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A;Reference number: 867708
A;Accession: S67714
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A,Rosidubes: 1-118 «POW»
A,Grose-references: UNIPARC:UPI00006A6BC; EMBL:Z742l0; NID:g1431255; PIDN:CAA98735.1; PJ
A,Experimental source: strain S288C
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N;Alternate names: hypothetical protein D1510
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S61051; S67714
R;Pohl, T.M.
Submitted to the EMBL Data Library, November 1995
A;Reference number: S61010
A;Reference number: S61010
                                                                                                             C.Species: Caenorhabditis elegans
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Accession: S28291
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                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCE9; EMBL:Z19157 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2844;
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18.7%; Score 53; DB 2; Length 284
Best Local Similarity 35.9%; Pred. No. 6.5e+02;
Matches 14; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1924 ROSSSCPANFECYFDGNMHGCCPTKAFTCSLSPSPGKTC 1962
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C;Superfamily: Saccharomyces hypothetical protein YDL162c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QMAGQCSQNE--YFDSLLHACIPCQ-LRCS-SNTPPLTC
                                                                                      hypothetical protein ZC84.1 - Caenorhabditis elegans
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                                                                                                                                                                                                          R;Thomas, K.
submitted to the EMBL Data Library, December 1992
submitted number: $28285
A;Recession: $28291
A;Accession: $28291
A;Scatus: prel!minary
A;Molecule type: DMA
A;Residues: 1-2844 <THO>
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Best Local Similarity
Matches 11; Conserv
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A; Residues: 1-118 < POH>
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Accession: p88550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces pomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
RyResidues: 1-1077 <HLL>
A;Residues: 1-1077 <HLL>
A;Cross-references: UNIPROT: 074853; UNIPARC: UPI00006A9D7; EMBL: AL031907; PIDN: CAA21417.
A;Experimental source: strain 972h-; cosmid c18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:062504; UNIPARC:UPI00000781E7; GB:chr_III; PIDN:CAA79570.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          procein ZCB4.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cidate: 03-Dec-1999 #sequence_revice.
CiAccession: T41146
RiHilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21973
A;Accession: T41146
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                                                                                                                                                                                                                                                 Gaps
                      C;Genetics:
A;Gene: Muc5A
F;45-149/Domain: cysteine-rich <CYS>
F;762-830/Domain: von Willebrand factor type C repeat homology <VWC>
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                                                                                                                                                                                Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1077;
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                                                                                                                                                                             Query Match
18.7%; Score 53; DB 2; Length 103
Best Local Similarity 40.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 5; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                           1 MLQMAGQCSQNEYFDSLLHA---CIPCQLRCSSNTPPLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.7%; Score 53; DB 2; I
29.5%; Pred. No. 2.8e+02;
Live 7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 3
F;193-252/Domain: RING finger homology <RRN>
ntestinal tract and reproductive tract
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35.9%;
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Matches 13; Conservative
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A;Molecule type: DNA
A;Residues: 1-1474 <STO>
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Best Local Similarity
Matches 14; Conserv
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myb-related transcription factor MYB33 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51647
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; Jac-Ares, J.; Weisshaar, B.
Par-Ares, J.; Weisshaar, B.
Par-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Fitle: Towards functional characterisation of the members of the R2R3-MYB gene from Ar, Reference number: Z14349; MUID:9839469; PMID:9839469
A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51647
A;Accession: T51647
A;Accession: T51647
A;Accession: L378 «KRA»
A;Accession: L378 «KRA»
A;Gene: WRB3
A;Map position: III
C;Keywords: transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein M01H9.2 - Caenorhabditis elegans
CiSpecies. Caenorhabditis elegans
CiSpecies. Caenorhabditis elegans
CiSpecies. Caenorhabditis elegans
CiAccession: T29488
R; Pauley, A.; Gattung, S.
Submitted to the EMBL Data Library, September 1996
A; Description: The sequence of C. elegans cosmid M01H9.
A; Reference number: Z20626
A; Description: T39488
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-399
A; Molecule type: DNA
A; Residues: 1-389
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A; Experimental source: strain Bristol N2; clone M01H9
C; Genetics:
A; Gane: CESP: M01H9.2
A; Map position: 4
A; Map position: 4
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18.6%; Score 52.5; DB 2; Length 389;
Best Local Similarity 34.1%; Pred. No. 1.4e+02;
Matches 14; Conservative 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.6%; Score 52.5; DB 2; Length 378; Best Local Similarity 23.5%; Pred. No. 1.3e+02; Matches 16; Conservative 9; Mismatches 20; Indels 2
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Search completed: December 21, 2005, 16:11:34 Job time : 38.2 secs

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QBnav8 homo saplen Q501y7 entamoeba h Q50y51 entamoeba h Q50y53 homo saplen	Qenaus nomo sapien Qelv24 caenorhabdi Qe6uz9 homo sapien	Q8ix30 homo sapien Q7ggv0 anopheles g Q4n9us theileria p G729f0 demilfovibr	0410y5 gibberella 054kf9 dictyoerell 09g48 giardia lam 068f99 mus musculu	Q66py1 mus musculu Q4ue95 theileria a O9d8do mus musculu	Q8r4w8 mus musculu Q678b7 lymphocysti	Qecfa7 mus musculu Q9d351 mus musculu	Q6p233 mus musculu Q5jsg7 homo sapien Q4uhw4 theileria a	Q8iz06 homo sapien Q7z5t8 homo sapien Q5hya8 homo sapien Q17969 caenozhabdi	Q51ed6 entamoeba h Q18118 caenorhabdi Q98910 g sorttilin-	P46687 prinkletek P46687 prinkletek Q8s258 drosophila Q9veH drosophila	Q22423 caenorhabdi Q5uq14 mimivirus.	GE 3	Q4zle4 pseudomonas Q61si8 caenorhabdi O6de15 brachydanio	9 9	نرو	נ ע נ	ונונ	4 0 1	mus mu tetrac	O35161 mus musculu O53av9 rattus norv	Q9wdx2 human immun O60ne2 ceenorhabdi	Q6csy3 kluyveromyc	Q86wk8 homo sapien Q4rty8 tetraodon n	bos ta	Q96dnz homo sapien Q4s9d3 tetraodon n	bos tau	ĕ ĕ	caenorh	ັວັບັ
Q8NAV8 HUMAN Q5OLY7 ENTHI Q5OY51 ENTHI Q5CSB3 HUMAN	QBNAU9_HUMAN Q61V24_CAEBR Q86U29_HUMAN	Q81X30 HUMAN Q7QGV0 ANOGA Q4N9US THEPA	Q410Y5 G1BZE Q54KF9 D1CD1 Q9GQ45 G1ALA Q66FG9 M01SE	Q66PY1 MOUSE Q4UE95 THEAN	Q8R4W8_MOUSE O678B7_9VIRU	Q8CFA7 MOUSE Q9D351 MOUSE	Q6P233_MOUSE Q5JSG7_HUMAN Q4UHW4_THEAN	Q8IZO6 HUMAN Q7Z5T8 HUMAN Q5HYA8 HUMAN	QS1EDG_ENTHI O18118_CAEEL SORL_CHICK	GASA3 ARATH GASA3 ARATH QBSZ58 DROME Q9VW81 DROME	Q22423_CAEEL Q22423_CAEEL OSUOL4_MIMIV	Q9VTR9_DROME Q9WEJ8_9HIV1	04ZLE4 PSESY 061SI8 CAEBR 06DEIS BRARE	QSOMS4_ENTHI	Q50S60 ENTHI Q6B534 WHEAT	Q717V9 WHEAT	Q4N3N8 THEPA	OSOSS7 ENTHI	2 Q571L9 MOUSE 2 Q4SVV9_TETNG	L CELRI MOUSE	OSWDX2_9HIV1							2 Q61M00 CAEBR	
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64.5 64.5 64.5	64.5 64.5 64.5 64.5	84.5 84.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8	63.54 63.53 63.53	63.5	366	9 9 8	933	. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6.	62 62 62 63 63 63 63 63 63 63 63 63 63 63 63 63	61.5 61.5 61.5	61.5	61.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	9	09	60	09	09 .	9	0.00 0.00 0.00	. 60 . 60 . 60 . 60 . 60 . 60 . 60 . 60	59.5 59.5
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen	protein search, using sw model	December 21, 2005, 15:56:49 ; Sear (withou	US-10-077-137-1_COPY_1_51 283 1 MLQMAGQCSQNEYFDSLLHATE	BLOSUM62 Gapop 10.0 , Gapext 0.5	2166443 seqs, 705528306 residues	hits satisfying chosen parameters	length: 0 length: 200000000	f: Minimum Match 0% Maximum Match 100% Listing first 300 summaries	<pre>Uniprot_05.80:* 1: uniprot_sprot:* 2: uniprot_tremb1:*</pre>	No. is the number of results predicted by greater than or equal to the score of the derived by analysis of the total score di		* Query Match Length DB ID	100.0 184 1 TNR17 100.0 184 2 Q6PE4	64.0 185 1 27.6 184 2 25.8 718 2	25.8 1113 25.6 499	25.6 1674 2 25.6 2850 2	25.3 74 2 25.3 140 2	25.3 249 1 25.3 249 2	25.1 1150 2	24.9 1877 1	24.7 1025 2 24.6 5374 2	24.6 5376 1	24.2 1569 2	23.9 293 1 23.9 293 2	23.7 135 2	23.7 532 2 23.7 574 2	23.5 1562 2	.3 861 2 .1 1299 2	.0 2551 1 8 484 2
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017970 caenorhabdi Q41f99 gibberella Q5b0c3 aspergillus Q620m9 caenorhabdi Q16363 homo sapien Q5d044 homo sapien Q5arg8 homo sapien Q9enz4 homo sapien Q9enz4 hopatitis c Q9enz4 hepatitis c Q5aylvi candida alb Q61r18 caenorhabdi	human i human i oryza e oryza e drosopk triticu tetraoc theiler	P30432 drosophila P60411 homo sapien P62012 caenorhabdi Q62012 caenorhabdi Q94113 q12	Q9C091 home sapient Q9C091 home sapient Q9C091 home sapient Q9C091 home sapient Q9L1C giardia lae Q5C044 xenopus lae Q5C045 xenopus lae Q5C047 xenopus lae Q6C074 xenopus lae Q8WF4 monosiga br Q5C06 entamoceba hQ5C06 hepatitis CQ5C074 xenopus lae Q8C070 oryza sativ
	1000000000		752 090091 HUMAN 753 2 090091 HUMAN 838 2 027422 CAEEL 838 1 TTC7A HUMAN 911 2 05EE49 XENLA 912 065E47 XENLA 913 2 05EE44 XENLA 1174 2 05EE44 XENLA 1210 2 07EE46 GIALA 1394 2 090E31 DROME 1511 2 090E31 DROME 1540 2 05EE47 XENLA 1170 2 05EE47 XENLA 1184 2 05EE46 XENLA 1170 2 05EE47 XENLA 1180 2 05EE47 XENLA 1180 2 05EE47 XENLA 1180 2 05EE47 XENLA 1180 2 05TRA CHICK 181 2 06TRA CHICK 1883 2 05TRA CHICK 1884 2 05TRA CHICK 1885 2 05TRA CHICK 1885 2 05TRA CHICK 1885 2 05TRA CHICK 1887 2 05TRA CHICK 1888 2 05TRA CHICK 1888 2 05TRA CHICK 1889 2 05TRA CHICK 1880 2 05TRA CHICK 1881 2 05TRA CHICK 1882 2 05TRA CHICK 1883 2 05TRA CHICK 1883 2 05TRA CHICK 1884 2 05TRA CHICK 1885 2 05TRA CHICK 1887 2 05TRA CHICK 1888 2 05TRA CHICK 1888 2 05TRA CHICK 1889 2 05TRA CHICK 1880 2 05TRA CHICK 1880 2 05TRA CHICK 1881 2 05TRA CHICK 1881 2 05TRA CHICK 1882 2 05TRA CHICK 1883 2 05TRA CHICK 1884 2 05TRA CHICK 1885 2 05TRA CHICK 1886 2 05TRA CHICK 1887 2 05TRA CHICK 1888 2 05TRA
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Q5fxf2
Q5fxf9
Q5fxh0
Q4liq3
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Q8muz6
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01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
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 074432_9HIV2
093017_9HIV2
068791_9HEPC
04MLAS_ASPFU
088120_SIVCZ
090827_SIVCZ
090827_SIVCZ
0472W3_AZOVI
0472W3_AZOVI
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050806_BWTHI
050806_BWTHI
050806_BWTHI
060744_BWTHI
060744_BWTRI
250806_BWTHI
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Q4ZJZ2_9VIRU
Q8RYA8_HEVBR
Q50SR1_BRTHI
Q9ENZ5_9HEPC
Q9VEQ0_9HEPC
Q9VE40_BNCME
Q9VE40_BNCME
Q9VE40_BNCME
C9VE95_BNCME
CATB_RAT
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060NE3 CAEBR
027383 CAEEL
06FHS9 HUMAN
093CT0 SHIBO
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Name=TNFRSF17; Synonyms=BCM, BCMA;
Homo sapiens (Human).
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VAL-75, ASN-81 AND SER-165.
Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;
"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20363816; PubMed=10903733;

Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,

Hatzoglou A., Taspis A.,

Thoue J.-I., Devergine O., Taspis A.,

TINE receptor family member ECMA (B cell maturation) associates with

TNF receptor associated factor (TRAF) 1, TRAF2, and TRAF3 and

activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
activated protein kinase.

J. Immunol. 165:1322-1330(2000).
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                                                                                                                                                                                                                                                                                                                      MEDLINE-94218235; PubMed-8165126; Laabi Y., Gras M.P., Tsapis A.; Lazbi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.; "The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed."; Nucleic Acids Res. 22:1147-1154(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;
Lioftus B.J., Kim U.-J., Sneedon V.P., Kalush F., Brandon R.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
Genomics 60:295-308(1999).
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MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.
McCabe S., Qiu W.R., Kornuc M., Xia X. Z., Guo J., Stolina M.,
Boyle W.J., Sarosi I., Hau H., Senaldi G., Theill L.E.;
"APRIL and TALL-I and receptors BCMA and TACI: system for regulating humoral immunity.";
Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
Larsen C.-J., Tsapis A.;
"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
"A new gene, 116) (q26,p13) translocation in a malignant T cell lymphoma.";
EMBO J. 11:3897-3904 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21419161; PubMed-1152852; DOI=10.1038/sj/gene/6363770; Kawasaki A., Teuchiya N., Fukazawa T., Hashimoto H., Tokunaga K., "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65;
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MEDLINE-20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
Shu H.-B., Johnson H.;
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Genes Immun. 2:276-279(2001).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 109545; -.

RIM; 109545; -.

ROGO:0016021; C:integral to membrane; TAS.

ROGO:0005886; C:plasma membrane; TAS.

ROGO:0000823; F:receptor activity; TAS.

ROGO:0007275; P:development; TAS.

ROGO:0007125; P:development; TAS.

ROGO:0007125; P:signal transduction; TAS.

ROGO:0007165; P:signal transduction; Tansmembrane.

ROGO:0000
                                                                                                                                                                                                                                                                                                                                                     DISEASE: A chromosomal aberration involving TNFRSF17 is found in a form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation t(4,16) (qS6;pl3) with l12. SIMILARITY: Contains 1 TNFR-Cys repeat.
"B cell maturation protein is a receptor for the tumor necrosis factor
                                                                                                                                                                                                                O9Y275:TNFSF13B; NbExp=1; IntAct=EBI-519945, EBI-519169;
-!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.
-!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
                      family member TALL-1.",

Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).

-!- FUNCTION: Receptor for TRF8F13B/BLyS/BAFF and TNFSF13/APRIL.

Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK.

-!- SUBUNIT. Associates with TRAFI, TRAF2, TRAF3, TRAF5 and TRAF6.
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FTId=VAR_018758.
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277AF11E2767D932 CRC64;
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EMBL; Z29575; CAA82691.1; -; mRNA.
EMBL; Z29574; CAA82690.1; -; Genomic_DNA.
EMBL; U95742; AA867251.1; -; Genomic_DNA.
EMBL; AX503112; AA867251.1; -; Genomic_DNA.
EMBL; AX503112; AA84240.1; -; Genomic_DNA.
PIR; A34366; S43486.
PDB; 10QD; X-ray; K/L/M/N/O/P/Q/R=8-46.
PDB; 1XU2; X-ray; R/S/T=5-51.
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By similarity.
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Ensembl; ENSG00000048462; Homo sapiens.
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SITE
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Length 184;

DB 1;

Score 283;

100.08;

Query Match

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Straubberg R.L., Feingold B.A., Grouse J.H., Dorge J.G.,

Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max J.L., Wang J., Hsich F.,

Astapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield A.S. John J. J. John J. J. Marra M.A.;

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

Butterfield A.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Marra M.A.;

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                        1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FFB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
Tunor necrosis factor receptor superfamily member 17 (B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                    us-Jul-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor receptor superfamily, member 17.
Name-TNFRSF17;
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                                    ö
   Pred. No. 7.6e-27;
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100.0%; Pred. No. 7.6e-27;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                184 AA
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                                    0; Mismatches
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100.08;
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QGPE46;
05-JUL-2004 (TEMBLEE]. 27,
05-JUL-2004 (TEMBLEE]. 27,
                                    51; Conservative
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FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
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SETRAIN-CSTBL/63; TISSUE=COLON;

REDLINE=23354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=23354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=23354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Nikaido I., Caato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Asaji K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Blake J.A., Bradt D., Bult C., Hume D.A., Quackenbush J.,

RA Garimin L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.M.,

RA Gasterland T., Gariboldi M., Gibsi C., Godzik A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gibsi C., Godzik A., Frazer K.S.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Ronagaya A., Kurochkin I.V., Lee Y., Lehhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lehhard B.L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Raid J., Ring B.Z., Kingwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Verardo R., Wagner L., Wahlested C., Wang Y., Watanabe Y., Walls C.,

Willming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

RA Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Hashizume W., Imotani K., Alakawa T., Romo H., Nakamura M., Sakazume N., Sakazume N., Hashizaki A., Sasaki K., Sasaki D., Shinagawa A.,

RA Yamulshi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C STRAIN-C57BL/60; TISSUE-Mammary gland;

XX MEDLINE-22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

XX MEDLINE-25388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

XX Autaner R.D., Collins F.S., Wagner L., Derge J.G.,

XA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B Astachench M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Richards S.A., McEwan P.J., McKernan K.J., Mallahy S.J.,

A Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Nilalon D.K., Muxny D.M., Sodergren B.J., Lu X., Glabs R.A.,

B Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Amannan A. Schein J.E., Jones S.J.M., Marra M.A.;

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Rodriguez M. J., Hollon B.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schwitz J., Schmutz J., Schmutz J., Schmutz J., Schmutz J.,
                              Name=Infrsf17; Synonyms=Bcm, Bcma;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchoncoglires; Glires; Rodentia; Sclurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                      MEDLINE=99061155; PUDMed=9846698; DOI=10.1093/intimm/10.11.1693; MEDLINE=99061155; PubMed=9846698; DOI=10.1093/intimm/10.11.1693; Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A., Le Coniat M., Mornon J.P., Berger R., Tsapis A.; The characterization of murine BCMA gene defines it as a new member of the tumor necrosis factor receptor superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
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             maturation protein)
                                                                                                                                            NCBI_TaxID=10090;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK (By similarity). SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                 thymus, bone marrow and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terracdon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ediniopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001368; TWFR_c6.
PROSITE; PS0625; TWPR NGFR_1; FALSE_NEG.
PROSITE; PS50050; TNPR_NGFR_2; FALSE_NEG.
Alternative splicing; Immune response; Receptor; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
?
                                                                                                  SUBCELLULAR LOCATION: Type III membrane protein (Probable) ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 181; DB 1; Length 185; Pred. No. 2.9e-14; 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular (Potential).
Signal-anchor for type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VSP_006507.
185 AA; 20442 MW; 8806352B4FD26A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
TNFR-Cys.
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 2 SCAR14738, whole genome shotgun sequence.
ORFNames=GSTENG00024082001;
                                                                                                                                                                                                                                                       ISOId=088472-2; Sequence=VSP 006507;
-!- TISSUE SPECIFICITY: Detected in spleen, thymus heart, and at lower levels in kidney and lung-:- SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q02223; 10QD.
Ensembl; ENSWIGSG000022496; Mus musculus.
MGI; MGI:1343050; Thfrsf17.
GO; GO:0016021; C:integral to membrane; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                            IsoId=088472-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF061505; AAC23799.1; -; mRNA.
EMBL; AK020247; BAB32038.1; -; mRNA.
EMBL; BC027519; AAH27519.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q4S4Q3_TETNG PRELIMINARY;
Q4S4Q3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
36
18
32
36
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70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=99883;
                                                                                    similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pransmembrane
                                                                                                                                                                                         Name=1;
                                                                                                                                                                                                                                         Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPO DOM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPO DOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      removed.
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ORFNāmes=99.t00011;
Entamoeba histolytica HM-1:IMSS.
Eukaryota; Entamoebidae; Entamoeba
     Receptor protein kinase, putative.
                                                                                    NUCLEOTIDE SEQUENCE.
                                                        NCBI_TaxID=294381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rio M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
088714_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Linder P., Lander E.S., Waissenbach J., Roest Crollius H.; Wincker P., Lander E.S., Waissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=21428166; PubMed=11545438;
MILINGET U., Campos-Gongora E., Touzni S., Bruchhaus I., Tannich E.;
Willhoeft U., Campos-Gongora E., Touzni S., Bruchhaus I., Tannich E.;
Willhoeft U., Campos-Gongora E., Touzni S., Bruchhaus I., Tannich E.;
Protist 152:149-186 (2001).
EMBL; AJ409106; CAC34072.1; -; Genomic_DNA.
InterPro; IPR006212; Furin_repeat.
SNART; SM00561; FU; 6.
NNN TER 718
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 ELCGRCNDGSYFDSTTRTCQKCFNNCELCTSSTNCFKCSNKTILTESNG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                    Genoscope: Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                      91 AGQCSSSEFWNSDVDVCVPCE-----SCKKYPKTPSCNTCK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%; Score 73; DB 2; Length 718; 26.5%; Pred. No. 2.5; tive 7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 OMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                              27.6%; Score 78; DB 2; Length 184; 30.4%; Pred. No. 0.15; tive 11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                       5 AGCCSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVK 50
                                                                                                                                                                                                                                                                          preliminary data.
EMBL; CAAE01014738; CAG04379.1; -; Genomic DNA.
SEQUENCE 184 AA; 19133 MW; 3B2167E5E4FB1BB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative cysteine surface protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1113 AA
                                                                                                                                                                   the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Entamoeba histolytica.
Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q511P5
Q511P5
13-SEP-2005 (TEMBLE1.31,
13-SEP-2005 (TEMBLE1.31,
13-SEP-2005 (TEMBLE1.31,
                                                                                                                                                                                                                                                                                                                                               Local Similarity 30.4%
nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BIO7 ENTHI PRELIMINARY;
Q9BIO7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 26.5
Matches 13; Conservative
                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=csp;
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                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                             Matches
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Q511P5 EW
ID Q511
AC Q511
DT 13-S
DT 13-S
DT 13-S
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomasetto C., Masson R., Wendling C., Lefebure O., Chenard M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ELCGRCNDGSYPDSTTRTCQKCFNNCELCTSSTNCFKCSNKTILTESNG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 25.8%; Score 73; DB 2; Length 1113; Local Similarity 26.5%; Pred. No. 3.9; Length 1113; Les 13; Conservative 7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 QMAGQCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1113 AA; 124275 MW; 8F6D9846EFCD4D07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AARBO100356; EAL47552.1; -; Genomic_DNA. GO; GO:0016301; F: Kinase activity; IEA. GO; GO:004872; F: Receptor activity; IEA. InterPro; IPR06512; Furin repeat. InterPro; IPR06512; Furin repeat. InterPro; IPR06512; Furin repeat. InterPro; IPR06213; Ser_thr_pkin AS. InterPro; IPR06229; Ser_thr_pkinase. InterPro; IPR01245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan; PP00069; Pkinase; 1.
ProDom; PD00001; Proc_kinase; 1.
SWART; SW0021; Pru; 7.
SWART; SW00219; TV; 1.
SWART; SW00219; TV; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Muc6; Synonyms=gastric mucin-like;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gastric mucin-like protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OB8714 MOUSE PRELIMINARY;
088714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                           preliminary data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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Mus musculus (Mouse).

Mus musculus (Mouse).

Muscupta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                        Name=Muc6;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                    MEDLINE=22563400; Pubmed=12676567; DOI=10.1016/S0888-7543(03)00036-3;
                                                                                                                                                                                                                                                                                                 conservation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.6%; Score 72.5; DB 2; Length 2850; 48.3%; Pred. No. 12; ive 1; Mismatches 7; Indels 7;
                                                                                                                                                                                                                                                                             Desseyn J.-L., Laine A.; Desseyn J.-L., Laine A.; Conservation "Characterization of mouse muc6 and evidence of conservation gel-forming mucin gene cluster between human and mouse."; gel-forming mucin gene cluster between human and mouse."; Genomics 81:433-436 (2003).

EMBL; AY18438; AAO47735.1; JOINED; Genomic_DNA. EMBL; AY184387; AAO47735.1; JOINED; Genomic_DNA. EMBL; AY184387; AAO47735.1; JOINED; Genomic_DNA. HSSP, O46162; IXJO.

ENSEMB, SENSWINGSO0000048191; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
25.3%; Score 71.5; DB 2; Length 74;
Best Local Similarity 35.3%; Pred. No. 0.36;
Matches 12; Conservative B; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR062019; Prof_Inh_CR_TIL.
InterPro; IPR002919; Prof_Inh_CR_TIL.
InterPro; IPR001846; VWF_D.
Pfam; PF01826; TIL;
Pfam; PF00094; VWD; 3.
SMART; SM0216; VWD; 3.
SMART; SM02125; CTCK 2; 1.
SEQUENCE 2850 AA; 30398 WW; 9CD95F0845C79C9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL646093; CAI25894.1; -; Genomic_DNA.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLFEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Tumor necrosis factor receptor superfamily, member 13b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DABA3B06FE191A26 CRC64;
             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 CSQNEYFDHSEGTCVPC-----APPTT 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 CSQNEYFUSLLHACIPCQLRCSSNTPPLT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Tnfrsf13b; ORFNames=RP23-55I2.2-002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 74
74 AA; 8337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q5SU84 MOUSE
ID Q5SU84 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.33
Matches 14; Conservative
               01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
Holt K.;
                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                        MUC6.
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Best Local Similarity 48.3%; Pred. No. 6.8;
Matches 14; Conservative 1; Mismatches 7; Indels 7;
                                                                                                                                                                                                                                                                                                                                                          25.6%; Score 72.5; DB 2; Length 499; 48.3%; Pred. No. 1.9; tive 1; Mismatches 7; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1674 AA; 181168 MW; 3BC42CB004476309 CRC64;
                                                                            Tomasetto C.L.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJO10752; CAA09343.1; -; mRNA.
HSSP; P56682; ICCV.
HSSP; P56682; ICCV.
MGI; MGI: 2663233; Muc6.
InterPro; IPR002919; Prot Inh_CR_TIL.
InterPro; IPR001946; VWF_D.
Pfam; PF01056; TIL; 1.
Pfam; PF01054; VWD; 1.
   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                             499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escande F., Bulsine M.P.;
"The mouse secreted gel-forming mucin gene cluster.";
Blochim. Blophys. Acts 1676:240-250(2004).
EMBL; AJS11867; CAD54415.1; -; Genomic_DNA.
EMBL; AJS11868; CAD54415.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secreted gel-forming mucin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J;
PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1674 AA
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MGI; MGI:2662233; Muc6.
InterPro; 1PR001919; Prot Inh_CR_TIL.
InterPro; 1PR001846; VWF_D.
Pfam; PP01826; TIL; 2.
SMART; SMO0216; VWD; 3.
NON_TER 1674 1674
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Best Local Similarity 40.-
Best Local 14; Conservative
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QB0T03 MOUSE
ID QB0T03_MOUSE PRELIMINARY;
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Q80Z18;
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                                                                rissum=Stomach;
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MEDLINE-223546813; DubMed=12466851; DOI=10.1038/nature01266;
MEDLINE-222546813; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE-223546813; PubMed=12466851; DOI=10.1038/nature01266;
Nikaido I., Soato M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
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MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
"Identification of a receptor for BLyS demonstrates a crucial role in
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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10-MAY-2005 (Rel. 47, Last annotation update)
Tumor necrosis factor receptor superfamily member 13B (Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                     Tumor necrosis factor receptor superfamily, member 13b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 AA; 15672 MW; 005D8CDF4E8E3D15 CRC64;
                                                                                                                                                                                                                                                                01-FEB-2005 (TrEMBLrel. 29, Last sequence update) 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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35.3%; Pred. No. 0.69;
:ive 8; Mismatches 13;
                         6 CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
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8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC
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                                                                                                                                                                                                                                                                                                                                                                        Name=Tnfrsf13b; ORFNames=RP23-5512.2-003;
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                          Created)
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AC QPETJS; QDBAZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last annota)
DT 10-MAY-2005 (Rel. 41, Last annota)
DT 10-MAY-2005 (Rel. 41, Last annota)
DE CLIVATOR DECORAGE TACTORIORIS
ON Name-Infrafilab; Synonyms-Taci;
ON Name-Infrafilab; Synonyms-Taci;
ON Name-Infrafilab; Synonyms-Taci;
ON Mammaliab; Butheria; Euarchontogli
MATCHORY BENOTE
ON NCBI_TAXID=10090;
NN LI NAME TAXID=10090;
NN MATGHERS SA., Grewal I.R.
NAME I Immunol. 1:37-41(2000).
NN NUCLEOTIDE SEQUENCE (LARGE SCALE STRAIN-CS7BL/6J; TISSUE-LUNG; RENING I. OSATON N., SABLORNA Y., FARAIN C. TOMARU Y., HABSEGRAW Y., RABLIANDE SEQUENCE (LARGE SCALE STRAIN-CS7BL/6J; TISSUE-LUNG; RENING I., OSATON N., SABLORNA Y., RABLIANDE SEQUENCE (LARGE SCALE STRAIN-CS7BL/6J; TISSUE-LUNG; RA NIKAGO I., OSATON N., SABLORNA Y., RABLIANDE SEQUENCE (LARGE SCALE STRAIN-CS7BL/6J; TISSUE-LUNG; RA NIKAGO I., OSATON N., SABLORNA Y., RABLIANDE Y., RA BABRE J.A., BTABL D., BULLC V., RA BABRE J.A., BTABLE V., FLETCHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activator and CAML interactor). Name=Tnfrsf13b; Synonyms=Taci;
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                                                                                                                                                                                  OSSU83 MOUSE PRELIMINARY;
QSSU83;
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 71.5; DB 1; Length 249; Pred. No. 1.3;
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TNFR-Cys 1.

TNFR-Cys 2.

By similarity.
By Englecologous and the second seco
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10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Tumor necrosis factor receptor superfamily, member 13b.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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35.3%; Pred. No. 1.3;
tive 8; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB2F2D61C2931D81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :::|:|| : | : | : | : | : | : | : | CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
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PubMed=15729342; DOI=10.1038/nature03291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Tnfrsf13b; ORFNames=RP23-55I2.2-001;
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Eukaryota; Entamoebidae; Entamoeba.
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ORFNames=359.t00009;
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26947 MW;
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Q5SU82_MOUSE PRELIMINARY;
Q5SU82;
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12; Conservative
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Best Local Similarity
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PubMed=15296755; DOI=10.1016/j.cub.2004.07.029;
Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen J., Meyer E., Sperling L.; "High Coding Density on the Largest Paramecium tetraurelia Somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative surface protein with EGF domains and furin-like repeats.
Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohla A., El-Sayed N.M., Petri W.A., Clark C.G., Singh U., Mukherjee (El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B., "The genome of the protist parasite Entamoeba histolytica."; Nature 431:865-868 (2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paramecium tetraurelia.
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Peniculida,
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                                                                                                                                                                                                 -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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                                                                                                                                                                                                                                                                                                                                                                                                        25.1%; Score 71; DB 2; Length 1150; 35.3%; Pred. No. 7.1; tive 5; Mismatches 17; Indels
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"Paramecium megabase sequencing project.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; CR548612; CAH0366061; -; Genomic_DNA.
InterPro; IPR00658; ZFe2S fd BS.
InterPro; IPR006519; EGF 11ke.
InterPro; IPR006210; IEGF.
SMART; SM00181; EGF.
SMART; SM00261; FU; 29.
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                                                                                                                                                                                                                                                                                                                                                       1150 AA; 128938 MW; 0DBE7051D4B4E286 CRC64;
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                                                                                                                                                                                                                                                              preliminary data.
EMBL; AAFB01000933; EAL43605.1; -; Genomic_DNA.
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PROSITE; PS01186; EGF 2; 12.
SEQUENCE 3005 AA; 343821 MW; DBCCGAZ47876A
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nes 16; Conservative
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Best Local Similarity 35.3
Matches 12; Conservative
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Dev. Genet. 21:75-81(1997).

-1- FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R) R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation
                                                           16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Proprotein convertase subtilishin/kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilishin/kexin-like protease PC5) (Subtilishin/kexin-like protease PC5) (Subtilishin-like protease PC5)
                                                                                                                                                                                                                                                                                                                                     STRAIN=ICR; TISSUB=Intestine; MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-0; Nakagawa T., Murakami K., Nakayama K.; "Identification of an isoform with an extremely large Cys-rich region of PC6, a Rex2-like processing endoprotease.";
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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96293359; PubMed-8698813; DOI=10.1083/jcb.134.1.181; Constam D.B., Calfon M., Robertson E.J.; SpSC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis."; J. Cell Biol. 134:181-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lugson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G., TeDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate proprotein convertase expressed in endocrine and nonendocrine cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and functional expression of a new member of the mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4.";
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MEDLINE-97103178; PubMed-8947550; DOI=10.1083/jcb.135.5.1261;
De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97436919; Pubmed=9291583;
DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;
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                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 330-1877 (ISOFORM PC5B)
  1877 AA
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MEDLINE=93342056; PubMed=8341687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain, and Intestine;
MEDLINE=93224489; Pubmed=8468318;
PCSK5 MOUSE STANDARD; E 004552; 062040; 01-FB1995 (Rel. 31, Created) 16-0CT-2001 (Rel. 40, Last sequino-MAY-2005 (Rel. 47, Last anno-MAY-2005 (Rel. 47, Last anno-MAY-2005 (Rel. 47)
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DEVELOPMENTAL EXPRESSION
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                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakayama K.;
                                                                                                                                                                         Name=Pcsk5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa T
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of growth factors. CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use as long as its content is in no way modified and this statement is not
can be any amino acid and Yaa is Arg or Lys.
SUBCELLUIAR LOCATION: PC5A is secreted through the regulated secretory pathway. PC5B is a type I membrane protein localized to a paranuclear post-Golgi network compartment in communication with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing, Cleavage on pair of basic residues, Direct protein sequencing, Glycoprotein, Hydrolase, Protease, Repeat; Serine protease, Signal; Transmembrane, Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                    reticulum.

DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain boxing information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.

SIMILARITY: Belongs to the peptidase S8 family.

SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proprotein convertase subtilisin/kexin
                                                                         Event-Alternative splicing, Named isoforms=2,
Comment-Additional isoforms seem to exist;
Name=PC5B, Synonyms=Long;
IsoId=Q04592-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS, SOB.076; -.
Ensembl; ENSMUSGG000024713; Mus musculus.
MGI; MGI:97515; PC8K5.
GO; GO:0005615; C:extracellular space; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016021; C:integral to membrane; TAR, InterPro; IPR003460; APP.
InterPro; IPR003460; Pept_S8_S3.
InterPro; IPR000280; Pept_S8_S3.
InterPro; IPR002804; PrproinconvertsP.
Pfam; PF01483; P. proprotein; 1.
Pfam; PF00483; P. proprotein; 1.
PRAM: PF000023; SUBTILISIN.
ProDom; PD000717; PrproinconvertsP; 1.
PROSITE; PS00137; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D17583; BAA04507.1; -; mRNA.
EMBL; D12619; BAA02143.1; -; mRNA.
EMBL; L14932; AAA74636.1; -; mRNA.
                                                  early endosomes.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A48225; A48225.
PIR; S34583; S34583.
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MEROPS; S08.076; -.
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20; Gaps

DOMAIN

REGION MOTIF

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----NTPPLTCORYCNASV 45
                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/Sv;
MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
Wilson M.D., Riemer C., Martindale D.W., Schuupf P., Boright A.P.,
Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Teui L.-C.,
Miller W., Koop B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to zona pellucida; IEA.
19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 90D2D8CFE5DE24EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
Submitted (JUL-2001) to the EMBL/Genbank/DDBJ databases.
EMBL, AR7312033; AAK28824.1; -; Genomic_DNA.
EMBL; AY046055; AAL04416.1; -; Genomic_DNA.
HSSP; Q90248; 1HX2.
                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
8; Mismatches
                              4 MAGQCSQNEYFDSLLHACIPCOLRCSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI; MGI:106656; Zan.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0007339; P:binding of sperm tc
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                           Created)
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InterPro; IPR006209; EGF 1ike.
InterPro; IPR00645; Pol N.
InterPro; IPR006210; IEGF.
InterPro; IPR000998; MAM.
InterPro; IPR003199; Prot Inh CR TII
InterPro; IPR003181; Tila_CysTich.
InterPro; IPR001007; VWF C.
InterPro; IPR001007; VWF C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00022; EGP 1; UNKNOWN 1.
PROSITE; PS01186; EGF 2; 18.
PROSITE; PS50026; EGF 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02345; TIL assoc; 25
Pfam; PF00094; VWD; 4.
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                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-FEB-2005 (TrEMBLrel. 29,
ZAN (Zonadhesin).
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SMART; SMO0774; FOLM; 20.
SMART; SMO0217; MAM; 3.
SMART; SMO0216; VWC; 18.
                                                                                                                                                                                                      Q99NDO_MOUSE PRELIMINARY;
Q99NDO;
15; Conservative
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PS50060; MAM
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                                                                                                                          133 TN 134
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                                                                                              46 TN 47
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SEQUENCE
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ATEESWAEGGFCMLVKKNNLCQRKVLQQLCCKTCTFQG
                                                                                                              AC 1.
AC 2.
Cell attachment site (Potential).
Charge relay system (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen G.J., Sogin M.L.,
"Draft sequence of the Giardia lamblia genome.";
submirted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                       (Potential).
                                                                                                                                                                                                                                                                             (Potential) (Potential)
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N-linked (GloNAc. ) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.
                                                                                                                                                                                                                                                                                                             (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.7%; Score 70; DB 2; Length 1025; 24.2%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gıardia lamblia ATCC 50803.
Bukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
VOLE TaxID=184922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Indels
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EMBL; AACE01000001; EAA43000.1; -; Genomic_DNA.
HSSP; Q9S7B3; 1EHD.
INTEATORY IPROCESTY. Laminin EGF.
PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN 1.
SEQUENCE 1025 AA; 109044 MW; 36281DF3FEZDDB43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW; EC850E2DF20EA1C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (In isoform PC5A). /FIId=VSP_005439.
                  Extracellular (Potential)
                                           Cytoplasmic (Potential)
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Last annotation update)
                                                                                               (Cys-rich motif)
                                                                                                                                                                                                                                                                                                                                                                                                           (GlcNAc. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70.5; DB
Pred. No. 14;
5; Mismatches
                                                                                    Catalytic.
CRM (Cys-1
                                                                                                                                                                                                                                                                                                                                                                            N-linked
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                                   Potentia]
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Local Similarity 34.7%;
les 17; Conservative
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Q7R6J7;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                        CHAIN
 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                 5
                                                                                                                                                                                                                                                                                                  Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98123114; PubMed=9452463; DOI=10.1074/jbc.273.6.3415; Gao Z., Garbers D.L.; "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like
                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-- SIMILARITY: Contains 1 EGF-like domain.
-- SIMILARITY: Contains 3 MAM domains.
-- SIMILARITY: Contains 25 VWFD domains.
 DB 2; Length 5374;
                                 16; Indels
                                                                                 7 QCSQNEYFDSLLHACIP-COLRCSSNTP--PLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U97068; AAC26680.1; -; mRNA.
EMBL; U83190; AAC53125.1; -; mRNA.
PIR; T42215; T42215.
HSPP; Q90248; LHX2.
MGI; MGI:106656; Zan.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR004153; CXCXC_repeat.
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ZAN MOUSE

088647,
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
...v-2005 (Rel. 47, Last annotation update)
Query Match
24.6%; Score 69.5; Di
Best Local Similarity 36.8%; Pred. No. 53;
Matches 14; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domains.";
J. Biol. Chem. 273:3415-3421(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
NUCLEOTIDE SEQUENCE OF 4864-5376.
                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
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EGF-like.
80 X heptapeptide repeats (approximate)
(mucin-like domain).
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                                                                                                                                                                                                                                    PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00146; EGF_2; 18.
PROSITE; PS50026; EGF_3; 1.
PROSITE; PS500740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 3.
CEL1 adding; EGF_1ike domain; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                    Zonadhesin.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential).
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(partial)
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(partial).
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                                               InterPro; IPR002919; Prot Inh CR TIL.
InterPro; IPR003328; TILa_Cysrich.
InterPro; IPR01846; VWF D.
Fram; PF02363; C_triplex; 18.
Fram; PF03128; CXCXC; 11.
Fram; PF00008; EGF; 1.
Fram; PF00629; MAM; 3.
Fram; PF008245; TIL; 25.
Fram; PF01826; TIL; 25.
Fram; PF01826; TIL; 25.
Fram; PF00949; VWD; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAM 2. MAM 3. VWED 2. VWED 2. VWED 2. VWED 3. VWED 4. VWED 4. VWED 6. VWED 9. VWED 110 VWED 112 VWED 112 VWED 115 VWED 115 VWED 116 VWED 116 VWED 116 VWED 117 VWED 217 VWED 217 VWED 22 VWED 22
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EGF 2.
EGF like.
MAM.
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                    InterPro; IPR006209;
InterPro; IPR000998;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 014835; Q726F5;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
13-SBP-2005 (Rel. 48, Last annotation update)
Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
Name=TNFRSF13B; Synonyms=TACI;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                          Gaps
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MEDLINE=97458245; PubMed=9311921; DOI=10.1126/science.278.5335.138;
von Buelow G.-U., Bram R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genomic organization of the human MUC6 and MUC2 mucin
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                                      24.2%; Score 68.5; DB 2; Length 966; 36.2%; Pred. No. 12; tive 10; Mismatches 15; Indel8
                                                                                                                                                                215 QCSQSTVFNSDLNVCVPLAIQNSCDSSTQQPVCS--C-SQVSSSCPG 258
                                                                                                                                     7 QCSQNEYFDSLLHACIPCQLR--CSSNTPPLTCQRYCNASVTNSVKG 51
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PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;
Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,
Toribara N.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1569 AA; 168065 MW; 6AEDEE143ECB855B CRC64;
966 AA; 102461 MW; B565A3CDD25216D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 45.2%; Pred. No. 20; es 14; Conservative 2; Mismarth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 83:936-939(2004).

ENBL; AY312160; AAQ82434.1; -; mRNA.

InterPro; IPR002919; Prot_Inh_CR_TIL.

InterPro; IPR006552; VWC_Out.

InterPro; IPR001846; VWF_D.

Fām; PP01826; TIL; 2.

Fām; PP00094; VWD; 3.

SNART; SN00215; VWC_Out; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mucin glycoprotein (Fragment)
                                                                                                                                                                                                                                                                                                 QEW4X9_HUMAN PRELIMINARY;
Q6W4X9;
                                                                    Local Similarity 36.2
nes 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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SEQUENCE
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                                                   Query Match
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                                                                                              Matches
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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(Potential).
(Potential).
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(Potential)
(Potential)
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Pred. No. 54;
5; Mismatches 16; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                            similarity.
0E44DB77DF2A2620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T10E10.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0666; B KETOACYL SYNTHASE; UNKNOWN 1. PROSITE; PSO0272; SNAKE TOXIN; UNKNOWN 1. Complete proteome; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 QCSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; Vaca''o; Ensembladitis elegans.
Bormanse; Wagene0020421; T10E10.4.
Wormbase; Wagene0020421; T10E10.4.
Wormbep; T10E10.4; CE25989.
GO; GO:000561; C:extracellular region; IEA.
GO; GO:000601; F:chitin binding; IEA.
GO; GO:0006030; P:chitin binding; IEA.
InterPro; IPR001555; Chitin bind PerA.
InterPro; IPR001549; EB_region.
InterPro; IPR001794; Ketoacyl_synth.
InterPro; IPR001571; Snake_toxin.
InterPro; IPR001571; Snake_toxin.
InterPro; IPR06150; Worm_repeat_1.
Pfam; PF01683; EB; 1.
                                                                                                   (GlCNAC.
                                                       (GlcNAc
                                                                                (GlcNAc
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similarity.
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MEDLINE=99069613; PubMed=9851916;
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Q22378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
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SMART; SM00289; WR1; 12
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34292
44284
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                                                                             Best Local Similarity
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AC 02237
AC 02237
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DE Hypot
OC Caeno

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MIM; 604907; -.

R MIM; 604907; -.

R GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.

DR RITEPRO; IRPRO01368; TNFR_C.

DR PROSITE; PSO052; TNFR_NGFR_1; I.

DR PROSITE; PSO0505; TNFR_NGFR_1; I.

DR PROSITE; PSO0505; TNFR_NGFR_1; I.

RRCEPTO: IRPRO01368; TARE_NGFR_2; I.

RRCEPTO: IRPRO01368; TARE_NGFR_2; FALSE_NEG.

KW Receptor; Repeat; Signal-anchor; Transmembrane.

TOPO DOM 1 165 Signal-anchor for type III membrane protein (Potential).

FT TOPO DOM 187 293 Cytoplasmic (Potential).

FT TRANSMEM 166 186 Signal-anchor for type III membrane protein (Potential).

FT TRANSMEM 17 293 Cytoplasmic (Potential).

FT REPEAT 33 67 TNFR-Cys 1.

FT REPEAT 34 47 By similarity.

FT DISULFID 50 62 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS
              EMBL; AF023614; AAC51790.1; -; mRNA.
EMBL; AX302137; AAP57629.1; -; mRNA.
PDB; 1XU1; X-ray; R/6/T=68-109.
PDB; LXUT; NMR; A=68-109.
INLACC; OL4836; -.
Ensembl; ENSG0000108516; Homo gapiens.
                                                                                                                                                          HGNC, HGNC:18153; TNFRSF13B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 AA; 31816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
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133
138
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171
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189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTIONS WITH TRAF2 AND TRAF5.

MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;

MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;

Xia X.-Z., Trandor J., Senaldi G., Khare S.D., Boone T., Kelley M.,

Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,

Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,

Meng S.-Y., BOYLE W.J., Hsu H.;

"TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
factor family member involved in B cell regulation.";

J. Exp. Med. 192:137-143(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isoid=014836-2; Sequence=VSP_013798;
TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
intestine and peripheral blood leukocytes. Expressed in resting B-
cells and activated T-cells, but not in resting T-cells.
SIMILARITY: Contains 2 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
"APRIL and TALL-I and receptors BCMA and TACI: system for regulating humoral immunity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=15542592; DOI=10.1074/jbc.M411714200; Hymowitz SG., Patel D.R., Wallweber H.J., Runyon S., Yan M., Yin J., Shriver S.K., Gordon N.C., Pan B., Skelton N.J., Kelley R.F., Starovasnik M.A.;
'NF-AT activation induced by a CAML-interacting member of the tumor
                                                                                                                                                                                                  MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200; Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinke D., LaFleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.; "Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLyS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 68-109, AND STRUCTURE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O75888 TNFSF13; NbExp=1; IntAct=EBI-519160, EBI-519208; Q92275:TNFSF13B; NbExp=4; IntAct=EBI-519160, EBI-519169; SUBCELLULAR LOCATION: Type III membrane protein. ALTERNATIVE PRODUCTS:
                                                                                     NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=014836-1; Sequence=Displayed;
                       necrosis factor receptor superfamily.";
Science 278:138-141(1997).
                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 275:35478-35485(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Immunol. 1:252-256(2000).
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X-RAY

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Gaps

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DB 1; Length 293; 15; Indels

23.9%; Score o..., 30.6%; Pred. No. 4.6; -ive 9; Mismatches

PPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRT

293 67 104 128 47 47 65 66 100 100 67

FUNCTION.

CAAFCR -> W (in isoform 2) /FIId=VSP_013798.

411799F3DE17A5EB CRC64;

MW;

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TISSUE=Small intestine;
Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
"Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Oligo-capping : a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";
                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Tumor necrosis factor receptor 13B variant (Fragment).
          293 AA.
      PRT;
OS3F36 HUMAN PRELIMINARY;
QS3F36;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 138:171-174(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 200:149-156(1997)
                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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removed.

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                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis briggeae.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota, Metazoa, Nematoda, Chromadorea, Ascaridida, Ascaridoidea,
Ascarididae, Ascaris.
           Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AK223453; BAD97173.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The C.briggaae Sequencing Consortium; Submitred (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                    Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 67; DB 2; Length 135; 34.8%; Pred. No. 2.4; ive 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 QCSQNEYFDSLLHACIP-CQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 135 AA; 14981 MW; 74B21060EAF539B6 CRC64;
                                                                                                         NON TER 1 1 SEQUENCE 293 AA; 31846 MW; D9EA2F28B33BF466D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG19174.
                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                    8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.

EMBL; CAAC01000098; CAF21086.1; -; Genomic_DNA.

InterPro. IPR006209; EGF_like.

InterPro; IPR002919; Prot_Inh_CR_TIL.

Pfam; PF01826; TIL; 2.

PROSITE; PS01186; EGF_2; UNKNOWN_2.
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                                                                                                                                                                  Score 67.5; Di
Pred. No. 4.6;
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Q60WC9;
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TISSUE=Small intestine;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=CBG19174;
                                                                                   Receptor.
NON TER
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STRAIN=AX4;

A Elchinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,

A Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,

Buchinger L., Perriman M., Song J., Olsen R., Szafranski K., Xu Q.,

Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

A Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

By Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,

Ra Frbornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Rarborcher P., Desany B., Just E., Morio T., Rost R., Churcher C.,

A Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

An Arany D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,

Anardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,

A House H., Mungal K., Oliver K., Price C., Quail M.A.,

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A J., Kohara Y., Sharp S., Simmonds M., Schegler S., Tivey A.,

A Sugano S., White B., Walker D., Woodward J., Winckler T., Transka Y.,

Chisholm R.L., Glibbs R., Loomis W.F., Platzer M., Kay R.R.,

Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;

Nature O:0-0(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -: SINDELLUJAR LOCATION: Integral membrane protein (By similarity).
-: SINDELLUJAR LOCATION: Integral membrane protein (By similarity).
-: SINDELLUJAR LOCATION: Integral compled receptor 1 family.

GO; GO:0004602; C:integral to membrane; IEA.

GO; GO:0004802; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001885; F:G-protein coupled receptor protein signalin. .; IEA.

GO; GO:0007185; P:signal transduction; IEA.

InterPro; IRR000276; GPRR Rhodpsn.
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      MEDLINE=22311325, PubMed=12423236;
Huang X., Xiao H., Rex E.B., Hobson R.J., Messer W.S.,
Komuniecki P.R., Komuniecki R.W.;
"Functional characterization of alternatively spliced 5-HT2 receptor
lsoforms from the pharynx and muscle of the parasitic nematode,
Ascaris suum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60141 MW; 4D795D1C249D55F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
14)
15-SEP-2005 (TrEMBLrel. 31, Last annotation update)
17-SEP-2005 (TrEMBLREL 31)
18-SEP-2005 (TR
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
G-prosite; PS50262; G-pROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Trans
SEQUENCE 532 AA; 60141 MM; 4D795DIC249;

    Neurochem. 83:249-258(2002).

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Best Local Similarity 23.84
Matches 15; Conservative
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NUCLEOTIDE SEQUENCE.
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489 SLQ 491
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Gaps

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GO:0015020; C:membrane; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0008234; F:peptidase activity; IEA.
GO:0004289; F:subtilase activity; IEA.
GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                               Cryptococcus neoformans var. neoformans B-3501A.
Bukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
                                                                                                   233 GLCYRRKFFINVKGSNVLNVCNSVLHSCSP-ESKCSEN--PLYCPARRFQNSDIT 284
                                                                                                                                                                                                                                                                                                                                                                                                                  ------DSLLHACIPCQLRCSSNTPPLTC--QRYCNASVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                             9; Indels 17;
             Length 1562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 23.3%; Score 66; DB 2; Length 861;
1 Similarity 34.8%; Pred. No. 22;
16; Conservative 6; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Sf9;
Cieplik M., Klenk H.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z68989; CAA93116.1; -; mRNA.
PIR; T43251; T43251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GOCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 861 AA; 93346 NW; 8745729FBD869366 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
EMBL; AAEY01000041; EAL19380.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1299 AA
             23.5%; Score 66.5; D
30.9%; Pred. No. 35;
ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spodoptera frugiperda (Fall armyworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QZ6489 SPOFR PRELIMINARY;
Q26489;
                                                                                                                                                                                               Q55NLS CRYNE PRELIMINARY;
Q55NLS;
             Query Match 23.5
Best Local Similarity 30.9
Matches 17; Conservative
                                                                                                                                                                                                                                                                                 Hypothetical protein.
ORFNames=CNBH0730;
                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                              6 GQCSQNEYF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=283643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=FURIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                   CRYNE
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                                                                                                                                                                   RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N., Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Sato S., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R., Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C., Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L., Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C., Submitted (JUN-2005) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         359 QAKKNNYIVSHLLHGLTPCEDRYRESMSPASSNTPSPDSSRPSSPEHYNHGNVVNS 414
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      7 OCSONEYFDS-LLHACIPCOLR-----CSSNTP-----PLTCORYCNASVTNS 48
                                                            GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004524; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:000468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
             EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                Score 67; DB 2; Length 574;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
,; AAGK01000002; EAN32674.1; -; Genomic DNA.
ENCE 1562 AA; 179264 MW; 44A17485D05BFBAO CRC64;
 CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                  574 AA; 64223 MW; 9D344378077A91C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                               preliminary data.
EMBL; AAF101000053; EAL68033.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1562 AA
                                                                                                                                                                               Pfam; PF00069; Pkinase; 1.

PKNTAS; PR00109; TYRKINASE.

ProDom; PD000001; Proc. Kinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00219; TYKC; 1.

PROSTTE: PSS0011; PROTEIN_KINASE_DOM; 1.

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 309:134-137(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transporter, putative.
Names=TP02_0391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q4N599 THEPA PRELIMINARY, Q4N599;
                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theileria parva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Muguga;
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                                                                                                                                                                                                                                                                                                      SEQUENCE
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EMBL;
EMBL;
EMBL;
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 GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                      STAB2 HUMAN STANDARD; PRT; 2551 AA.

GBWWQB; QGZMKZ; Q7Z5N9; QBGUR4; QBIUG9; QBTES1; Q9H7H7; Q9NRY3;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Stabilin-2 precursor (FEEL-2 protein) (Fasciclin EGF-like laminin-type EGF-like and link domain-containing acavenger receptor-1) (FAS1 EGF-like and X-link domain containing adhesion molecule-2) (Hyaluronan receptor for endocytosis) (Contains: 190 kDa form stabilin-2 (190 kDa hyaluronan receptor for endocytosis):
Name-STAB2; Synonyms=FEEL2, FELL, FEX2, HARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE, AND FUNCTION.
MEDLINE=22206516; PubMed=12077138; DOI=10.1074/jbc.M204277200;
Adachi H., Tsujimoto M.;
"FEEL-1, a novel scavenger receptor with in vitro bacteria-binding and "FEEL-1, a novel scavenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park S.-Y., Kim I.-S., "FEX2, a novel cell adhesion molecule of Fas-1 superfamily mediates cell-cell interaction.";
                                                                                                                                                                                                                                                                                                      1150 CSRPLRIDALANQCVPC---CSERGVTNSTPPTDC-CHCNPENGECINSSVAG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMod=14702039; DOI=10.1038/ng1285; T., Sugiyama T., Irie R., Ota T., Suzuki Y., Nishikawa T., Oteuki T., Sugiyama T., Irie R., Ota T., Suzuki Y., Makita H., Sakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S. Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-11818465; PubMed=11829752; DOI=10.1042/0264-6021:3620155; Politz O., Gratchev A., McCourt P.A.G., Schledzewski K., Guillot P. Politz O., Gratchev A., McCourt P.A.G., Schledzewski K., Guillot P. Polansson S., Sonneng G., Franke P., Kannicht C., Kzhyshkowska J., Longati P., Velten F.W., Johansson S., Goerdt S.; "Stabilin-1 and -2 constitute a novel family of fasciclin-like
                                                                                                                                                                                                                                                                                       8 CSQNEYPDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKG
                                                                                                                                                                                                                             23.1%; Score 65.5; DB 2; Length 1299;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                  1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 35-2551.
                                                                                                                                                                                                                                            Pred. No. 38;
8; Mismatches
                                                                                                                                              UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE, AND VARIANT PRO-510.
                                         InterPro; IPR006212; Furin repeat.
InterPro; IPR00209; Pept S8 553.
InterPro; IPR002884; PrprotnconvertsP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis-modulating activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 277:34264-34270(2002).
                                                                                                                                           PROSITE; PS00136; SUBTILASE ASP; UN PROSITE; PS00137; SUBTILASE HIS; 1. PROSITE; PS00138; SUBTILASE SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyaluronan receptor homologues.";
Biochem. J. 362:155-164(2002).
                                                                                     Pfam; PF01483; P_proprotein; 1.
Pfam; PF00002; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
SWART; SM00261; FU; 10.
                                                                                                                                                                                                                                              1 Similarity 34.0%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                        Protease.
SEQUENCE
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                              Matches
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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A Shiratori K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Atanaka M., Matanaba B., Hiraoka S., Chiba Y., Raishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Rusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., R. Inoiga S., Komai F., Hara R., Takeuchi K., Arla M., Hotuta T., Rasano J., Kanehori K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Romiyama H., Satoh N., Takami S., Tersahima S., Sanoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., R. Maranabe T., Sujiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Ramadaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Ramadaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Rwabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Matani R., Rawakami T., Oyama M., Hata H., Watanabe M., Komatsu T., Sangani T., Oyama M., Hata H., Watanabe M., Komatsu T., Shigeta K., Sanba T., Atsushima-Sugano J., Satoh T., Shigata K., Sanba T., Rakabani Y., Nakajima Y., Matanabe M., Komatsu T., Shigeta K., Sanba T., Rakabani Sugano J., Satoh T., Shigata K., Sanba T., Rakashita R., Nakai M., Nakai K., Yada T., Nowura Y., Ohara O., Isogai T., Sugano S.; R., Complete sequencing and characterization of 21,243 full-length human R., Anna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Hyaluronan receptor that binds to and mediates endocytosis of hyaluronic acid. May serve to maintain tissue integrity by supporting extracellular matrix turnover or it may contribute to maintaining fluidity of bodily liquids by resorption of hyaluronan. Binds to both Gram-positive and Gram-negative bacteria and may play a role in defense against bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rao Q., Zhang W., Cao X.;
'Molecular cloning and characterization of human FELL sharing homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CAUTION: Ref.4 (BAB84877) sequence differs from that shown due to a frameshift in position 1367.
-!- CAUTION: Ref.4 (BAD18723) sequence differs from that shown due to frameshifts in positions 240, 253, 588 and 1586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1257-1269; 1597-1605; 1623-1645; 1652-1660; 1813-1817; 1834-1843;
1914-1918; 1953-1957; 2204-2217; 2211-2215 AND 2355-2367, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1. SUBCELLULAR LOCATION: Type I membrane protein. Cell surface.
-1. TISSUE SPECIFICITY: Highly expressed in sinusoidal endothelial
cells of liver, spleen and lymph nodes.
-1. PTH: Proteclytically processed to yield a 190 kDa protein.
-1. SIMILARITY: Contains 17 EGF-like domains.
-1. SIMILARITY: Contains 2 laminin EGF-like domains.
-1. SIMILARITY: Contains 2 laminin EGF-like domains.
-1. SIMILARITY: Contains 1 Link domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 1136-2551, PROTEIN SEQUENCE OF 1136-1144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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Glycobiology 13:339-349(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB052958; BAC15608.1;
AY311388; AAP74958.1;
AK024503; BAB15793.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Genet. 36:40-45(2004).
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Gaps

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RESULT 32
QBNAV8 HUMAN
D OBNAV8 HUMAN
TO GBNAV8 HUMAN
TO GBNAV8 HUMAN
C BNAV8
TO 1-0CT-2002 (TrEMBLrel. 22, Created)
DT 01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DF Hypothetical protein FLJ34691.
S Homo sapiens (Human)
OC Eukaryota, Metazoa; Chordeta, Craniata, Vertebrata, Buteleostomi;
OC Eukaryota, Metazoa; Chordeta, Craniates, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2005 (TYEMBLrel. 30, Created)
10-MAY-2005 (TYEMBLrel. 30, Last sequence update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp686D20108 (Fragment).
Name=DKFZp686D20108;
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bloecker H., Beccher M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (FRB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CR936873; CAIS9785.1; -; -.
InterPro; IPR0106859; CUB.
InterPro; IPR011641; GCC2_GCG3.
Pfram; PF00491; CUB; 1.
Pfram; PF00491; CUB; 1.
PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                         22;
                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                        -----CQRYCNASV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.8%; Score 64.5; DB 2; Length 484; 30.8%; Pred. No. 18; tive 5; Mismatches 9; Indels 1:
                                                                                                                                                     Score 65; DB 1; Length 2551;
Pred. No. 89;
4; Mismatches 9; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 484 AA; 53895 MW; 8895A663E9DB369C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 QCSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 278
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        FAS1 5.
FAS1 6.
Laminin EGF-like 2.
EGF-like 15.
EGF-like 16.
                                                                                                                                                                                                                                                                                                                                            484 AA
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                                                                                                          Link.
FAS1 7.
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                          23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The German cDNA Consortium;
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QSCZ68;
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Best Local Similarity 30.89
Matches 12; Conservative
                                                                                                                                                                         Best Local Similarity 30.0
Matches 15, Conservative
          1724
1881
2022
2081
2122
2165
2291
2446
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TISSUE=Fetal kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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[1]
          1596
1740
1957
2047
2082
2123
2123
2198
                                                                                                                                                            Query Match
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HUMAN
      DOMAIN
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Q5CZ68
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R SMART; SM00181; EGF, CA; 8.

R SMART; SM00180; EGF_Lam, 5.

R SMART; SM00180; EGF_Lam, 5.

R SMART; SM00180; EGF_Lam, 5.

R SMART; SM00445; LiNK; 1.

R SMART; SM00445; LiNK; 1.

R PROSITE; PS00186; EGF_2; 16.

R PROSITE; PS0186; EGF_1AM_1; 2.

R PROSITE; PS01848; EGF_LAM_1; 2.

R PROSITE; PS01821; EGF_1AM_1; 2.

R PROSITE; PS01821; LINK 1: 1.

R PROSITE; PS01821; LINK 2: 1.

R PROSITE; PS01821; LINK 2: 1.

R PROSITE; PS0184; EGF_LAM_1; 1.

R PROSITE; PS0184; EGF_LAM_1; 1.

R PROSITE; PS0184; EGF_LAM_2; FALSE_NEG.

M Direct protein sequencing; EGF-like domain; Endocytosis; Glycoprotein; M Hyaluronic acid; Laminin EGF-like domain; Polymorphism; Proteoglycan; R PCOPUTE; EGF CANT.
EMBL; AK074051; BAB84877.1; ALT_FRAME; mRNA.

EMBL; AK160380; BAD18723.1; ALT_FRAME; mRNA.

EMBL; AK160444; AA039681.1; -; mRNA.

BENGL; AF160476; AAF82398.1; ALT_FRAME; mRNA.

BENGL; AF160476; AAF82398.1; ALT_INIT; mRNA.

HSSP; P16109; 1FSB.

HGNC; HGNC:18629; STAB2.

MIM; 608561; Cintegral to plasma membrane; ISS.

GO; GO:0009897; C:external side of plasma membrane; IDA.

GO; GO:0003587; C:integral to plasma membrane; IDA.

GO; GO:0003587; C:external side of plasma activity; IDA.

GO; GO:0003587; C:integral to plasma membrane; IDA.

GO; GO:0003587; C:protein binding; MSS.

GO; GO:0005541; F:protein binding; MSS.

GO; GO:0005541; F:protein binding; MSS.

GO; GO:0005542; F:protein disulfide oxidoreductase activity; IDA.

GO; GO:0005515; P:protein binding; MSS.

GO; GO:0001503; P:protein binding; MSS.

GO; GO:0001503; P:protein binding; MSS.

GO; GO:0001503; P:protein binding; TAS.

InterPro; IPR000742; EGF 2.

InterPro; IPR000742; EGF 2.

InterPro; IPR000742; EGF 2.

InterPro; IPR000742; EGF 2.

InterPro; IPR0006210; IEGF.

InterPro; IPR000739; Laminin_EGF.

InterPro; IPR000739; Prot_inh_squash.

Refam; PP00199; Kilnk; 1.

Refam; PP00199; Kilnk; 1.
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190 kDa form stabilin-2.
Extracellular (Potential)
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EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4.
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FAS1 4.
Laminin BGF-like 1.
EGF-like 11.
EGF-like 12.
EGF-like 13.
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FAS1 2.
EGF-like 6.
EGF-like 9.
EGF-like 9.
EGF-like 9.
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preliminary data
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    RAUGEDOTIDE SEQUENCE.

RA WARGHAGE SEQUENCE.

RA WARGHAGE NO. 1018 MINISTER.

RA WARGHAGE NO. 1018 MINISTER.

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RA SEKINE M., Dayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Magasauma M.,

RA Sekine M., Dayashi M., Kawai Y., Isono Y., Nakamura Y.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Rondo H.,

RA Shiratori A., Sudo H., Mimara K., Katesuta M., Sato K., Tanikawa K.,

RA Tanana H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

RA Tunano J., Xanehori K., Takahashi-Fuji A., Hara H., Murakawa K.,

RA Kusano J., Kanehori K., Takahashi-Fuji A., Hara H., Tanasa T.,

RA Nomura Y., Abersunawa H., Ichihara T., Shiohata M., Botuka S.,

ROSHIKAWA Y., Matsunawa H., Ichihara T., Shiohata M., Sano M.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Yamazaki M., Watanabe K., Kunagai A., Tarkemoto M., Kawakami B.,

RA Tanabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Kawabata A., Hikiji T., Kobateke N., Inagaki H., Ikema Y., Okamoto S.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Kawabata A., Hikiji T., Kobateke N., Inagaki H., Ikema Y., Okamoto S.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Togashi T., Oyama M., Hata H., Shirai Y., Takahashi Y., Yamashita R.,

RA Togashi T., Oyama M., Hata H., Shirai Y., Takahashi Y., Wanatali Y., Wadanic Y., Wadanic Y., Watanic W., Yanashita R.,

RA Togashi T., Oyama M., Hata H., Shirai Y., Takahashi Y., Wanati Y., Wada T., Nakamura Y., Ohara O., Isogai T., Shirai Y., Takahashi Y., Yanashita R.,

ROMPILL Y., Wada T., Nakamura Y., Ohara O., Isogai T., Suyano S.,

RA Ocomplete sequencing and characterization of 21,243 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.8%; Score 64.5; DB 2; Length 581; 30.8%; Pred. No. 22; Live 5; Mismatches 9; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01180; CUB; 1.
SEQUENCE 581 AA; 64343 MW; D17BC28CDA1E4EE1 CRC64;
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13.5EP-2005 (TrEMBLrel. 31, Last sequence update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
Protein kinase, putative (Fragment).
Protein kinase, putative (Fragment).
Entamobe
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PubMed=15729342; DOI=10.1038/nature03291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Genet. 36:40-45(2004).

EMBL, AK092010; BAC03789.1; -; mRNA.

InterPro; IPR010859; CUB.

InterPro; IPR011641; GCC2_GCC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; CUB; 1. Pfam; PF07699; GCC2 GCC3; 3. SMART; SMORT; CUB; 1.
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QSOLY7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 30.8 nes 12; Conservative
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 NUCLEOTIDE SEQUENCE
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STRAIN=HM-11MSS;
Pubmed=15729342; DOI=10.1038/nature03291;
Pubmed=15729342; DOI=10.1038/nature03291;
Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Loftus B., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
Ander M., Burchhaus I., Willhoeft U., Bhattacharya A.,
Ander M., Burchhaus I., Willhoeft U., Bhattacharya A.,
Ander M., Rabbinowitsch E., Norberczak H., Price C., Wang Z.,
Andels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
Andels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
Andels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
Andels M., Rabbinowitsch E., Norberczak H., Price C., Wang Z.,
Rollen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
Roster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
R. El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
Rraser C.M., Hall N.;
The genome of the protist parasite Entamoeba histolytica.";
Nature 433:865-868(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Quail M.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohla A., Foster P.G., Scheritz-Ponten T., Weber C., Singh U., Mukherjee (El.Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B., Fraser C.M., Hall N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                            preliminary data.

-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. BMBL, AAFBO1001427; EAL42605.1; -; Genomic_DNA.
GO; GO:0016301; F: kinase activity; IEA.
InterPro; IPR008712; Purin repeat.
InterPro; IPR008713; Prot_Kinase.
InterPro; IPR008719; Prot_Kinase.
InterPro; IPR008719; Tyr_Dkinase.
PF00069; Pkinase: 1.
PF00069; Pkinase: 1.
                                                                                                                                                                                                                                                                       -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.8%; Score 64.5; DB 2; Length 799; Best Local Similarity 34.3%; Pred. No. 31; Matches 12; Conservative 6; Mismatches 14; Indels 3
                                                                                                                                                                                          "The genome of the protist parasite Entamoeba histolytica."; Nature 433:865-868(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 799 AA; 91662 MW; D8BFE2F2E235989E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMIS; PRO0109; TYRKINASE.
ProDom; PD000001; Proc_kinase; 1.
SMART; SM00210; FU; 4.
SMART; SM00219; TYRC; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 QCSQNEYFDSLLHACIPCQ---LRCSSNTPPLTCQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               802 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Entamoeba histolytica HM-1:IMSS.
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CXXC-rich protein (Fragment).
ORFNames=141.t00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSOYS1_ENTHI PRELIMINARY;
QSOYS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=294381;
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Mewes H.W., Well B., Ambert R., Moosmayer P., Schupp I., Wellenreuther R., Newes H.W., Well B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.; Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

EMBL: CR936607; CAI56752.1; -; mRNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:00075509; F:calcium ion binding; IEA.

RO; GO:0007596; P:blood coagulation; IEA.

RILEPPC: IPR000152; Asx_hydroxyl_S.

RILEPPC: IPR00181; EGF_Z.

RILEPPC: IPR00181; EGF_Z.

RILEPPC: IPR00181; EGF_Z.

RILEPPC: IPR001611; IEGF_Z.

RILEPPC: IPR001641; GCCZ GCC3.

RILEPPC: IPR001641; GCCZ GCC3.

RILEPPC: IPR001641; Thrmbomoduln.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                  Length 802;
                                                                                                                                                                              Indels
                                                      802 AA; 90126 MW; 1425BF8514DED237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514918C0D126C7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 QCSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 OCSONEYFDSLLHACIPCOL------RCSSNT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKF2p686B1223 (Fragment).
Name-DKF2p686B1223;
                                                                                                               / Match 22.8%; Score 64.5; DB 2; Local Similarity 34.3%; Pred. No. 31; Nes 12; Conservative 6; Mismatches 14;
                                                                                                                                                                                                                                                                                                 653 RCODNYYYDKELOSCVGCSSECLTCSNKDICFTCK 687
                                                                                                                                                                                                                                           7 OCSONEYFDSLLHACIPCO ---LRCSSNTPPLTCQ 38
EMBL; AAFB01000471; EAL46536.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             852 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF07645; EGF_CA; 1.
Pfam; PF07645; EGF_CA; 1.
Pfam; PF07699; GCC2 GCC3; 3.
PRINTS; PR00907; THRMBOMODULN.
SMART; SM00042; CUB; 1.
SMART; SM00181; EGF; 7.
SMART; SP000181; EGF; 7.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 3.
PROSITE; PS01187; EGF_3; 3.
PROSITE; PS01187; EGF_3; 3.
EGF_1ike domain; Hypochetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93812 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The German cDNA Consortium;
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Best Local Similarity 30.0.
These 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSCZB3_HUMAN PRELIMINARY;
QSCZB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00431; CUB; 1.
Pfam; PF00008; EGF; 5.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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SEQUENCE
                                               SEQUENCE
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 35
10.079 Hum
10.079 Hum
10.079 Hum
10.079 Hum
10.079 Hum
10.070 Hum
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Matches

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
13-SBP-2005 (TrEMBLrel. 31, Last annotation update)
CUB and EGF contraining protein (Signal peptide, CUB and EGF-like domain containing protein 3 precursor) (OTTHUMP00000016250).
Name=SCUBE3; Synonyms=CEGF3; ORFNames=RP3-329A5.4-001;
              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pancreas;
Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO522563; AAH52263.2; -; mRNA.
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109165 MW; 24093050738932E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 QCSQNEYFDSLLHACIPCQL------RCSSNT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO: 0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000152; GUB.
InterPro; IPR000742; BGF_Ca.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR01481; BGF_Ca.
InterPro; IPR01481; GGF_GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.8%; Score 64.5; E
30.8%; Pred. No. 38;
Live 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fram; PP00431; CUB; 1.

Pfam; PP00408; EGF CA; 4.

Pfam; PP07699; GCCZ GCC3; 3.

SMART; SM00042; CUB; 1.

SMART; SM00119; EGF CA; 7.

SMART; SM00119; EGF CA; 7.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01180; EGF 2; 7.

PROSITE; PS01181; EGF 2; 7.

PROSITE; PS01187; EGF CA; 6.

SEQUENCE 992 AA; 109165 MW; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBIX30 HUMAN PRELIMINARY;
Q8IX30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 30.8
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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Matches
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
81gnal peptide, CUB domain, EGF-like 3.
Name=SCUBE3;
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                          Gaps
                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 QCSQSTVFNAELSVCVPLAIQNSCDSSTQQPVCS--C-SQVSSSCPG 206
                                                                                            Length 880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L Chiggsae Sequencing Consortium;
L Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0000576; Carellular region; IEA.
R GO; GO:0008061; F:chitin binding; IEA.
R GO; GO:0008061; F:chitin binding; IEA.
R GO; GO:0008061; F:chitin metabolism; IEA.
R InterPro; IPR002557; Chitin bind PerA.
R InterPro; IPR006149; BB region.
R InterPro; IPR006159; Ketoacyl_synth.
R InterPro; IPR006150; Worm_repeat_1.
R Ffam; PF01607; CBM_14; 2.
R Ffam; PF01607; CBM_14; 2.
R Ffam; PF01683; BB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCSQNEYFDSLLHACIPCQLR--CSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches 16; Indels
                                                                                                                                          Indels
  PROSITE; PS50026; EGF 3; 3.
PROSITE; PS01187; EGF CA; 3.
SEQUENCE 880 AA; 97239 MW; FOBDEGE85266FD60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 919 AA; 96816 MW; BE3EFC096CE53DFD CRC64;
                                                                                                                                                                                                                  635 QCSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 673
                                                                                                                                                                                     7 QCSQNEYFDSLLHACIPCQL------RCSSNT 32
                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Hypothetical protein CBG05036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00289; WR1; 14.
PROSITE; PS00606; B KETOACYL SYNTHASE; UNKNOWN_1.
PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
                                                                                         / Match 22.8%; Score 64.5; DB 2; Local Similarity 30.8%; Pred. No. 34; hes 12; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBGUZ9 HUMAN PRELIMINARY;
Q8GUZ9;
                                                                                                                                                                                                                                                                                                                                                   QEIV24 CAEBR PRELIMINARY;
QEIV24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis briggsae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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les 16; Conserv
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                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                  CAEBR
                                                                                                                                                                                                                                                                                                          RESULT 37
Q61024 CAE
D0 1025-0C
DT 25-0C
DT 105-0C
DT 10
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7

Gapa

13;

Q86UZ9 11D Q8 Q8 Q0 D7 Q01 D7 Q01 D7 Q01 D8 Q0 D8 Q0 D8 Q0 D9 D

g

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13-SEP-2005 (TrEMBLrel. 31, C)
13-SEP-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, Le
AGC transporter, putative.
ORFNames=TP01_0011;
Theileria parva.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01209; LDLRA_1; 5.
PROSITE; PS50068; LDLRA_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.8*;
Best Local Similarity 31.0*;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS THEPA
QAN9US THEPA PRELIMINARY;
Q4N9US;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 309:134-137(2005)
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                                                                                                                         NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Muguga;
                                                                                                                                                 STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lymphocytes
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q4N9U5
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                              Pfarr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R., Hankeln T., Winterpacht A.; "Novel human gene family (CEGF) encoding mosaic proteins with EGF-like, STT2R and a CUB module: cloning and expression analysis."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP0000012534 (Fragment).
ORPNAMES-ENSANGG000010045;
Anophales Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophalinae; Anopheles.
101
                                                                                                                                                                                                                           PubMed=15234972; DOI=10.1074/jbc.M405912200; Wu B.T., Su Y.H., Tsai M.T., Wasserman S.M., Topper J.N., Yang R.B.; "A novel secreted, cell-surface glycoprotein containing multiple epidermal growth factor-like repeats and one CUB domain is highly expressed in primary osteoblasts and bones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 993;
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                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Williams S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AF45294; AAN76608.1; -; mRNA.
EMBL; AZ7939.608; AAU08347.1; -; mRNA.
EMBL; AZ7939.; CAIZ0187.1; -; Genomic_DNA.
HSSP; P35555; IEMN.
Ensembl; ENSG0000146197; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 Potential.
109282 MW; 19BBE0E5627EEAF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             748 QCSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 OCSQNEYFDSLLHACIPCQL------RCSSNT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P35351 IERM.
Buneambl; P35351 IERM.
Buneambl; P35351 IERM.
HGNC; HGNC:13655; SCUBE3.
GO; GO: GO: GO: SCUBE3.
GO; GO: GO: F: calcium ion binding; IER.
InterPro; IPR00152; Asx_hydroxyl_S.
InterPro; IPR001891; EGF_Z.
InterPro; IPR001891; EGF_Z.
InterPro; IPR001891; EGF_Z.
InterPro; IPR011641; GCCZ_GCC3.
Ffam; PF00431; CUB; 1.
Pfam; PF00409; EGF; 6
Pfam; PF00409; EGF; 6
Pfam; PF00409; EGF; 6
Pfam; PF00409; EGF CA; 3.
SMART; SM00042; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00179; EGF CA; 6.
PROSITE; PS01180; CBF; 1.
PROSITE; PS01180; EGF_Z; 7.
PROSITE; PS01180; EGF_Z; 7.
PROSITE; PS01187; EGF_ZA; 6.
SFGA11E; PS01187; EGF_ZA; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.8%; Score 64.5; D
30.8%; Pred. No. 38;
iive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7QGV0 ANOGA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 30.8
nes 12; Conservative
                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 993 AA;
                     NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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070GV0 ANG
1D 070GVV
AC 070GVV
DT 01-MF
DT 01-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                    C. The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

C. The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

C. -I - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

C. EMBL; AAAD01008823; EAA05574.2; -; Genomic_DNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008656; F:protein transport; IEA.

RO; GO:0008666; F:protein transport; IEA.

RICHEPRO; IPR002617; LDL_receptor_A.

InterPro; IPR002617; LDL_receptor_A.

InterPro; IPR002617; LDL_receptor_A.

RICHEPRO; IPR000531; Ldl_receptor_Tep.

REAM; PR00054; Ldl_recept b; 4.

RINTS; PR001261; LDLRECEPTOR.

SMART; SM00121; LDLs; 7.

SMART; SM00121; LDLs; 7.

SMART; SM00125; LLS.

SMART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64.5; DB 2; Length 1294;
Pred. No. 51;
9; Mismatches 13; Indels 7,
The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1294 AA; 146748 MW; 10C251750A3F0586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 QCSQNEYFDSLLHACIPCQLRCSS-----NTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Query Match
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                                                                                                                RESULT
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PubMed=15077118; DOI=10.1038/nbt959;
Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Rolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
Deterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
The genome sequence of the anaerobic, sulfate-reducing bacterium
                                        Carlton J.M., Hall N.,
                    STRAIN=Muguga;
Gardnar M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.
Gardnar M., Bishop R., Pain A., Berriman M., Wilson R.J.M., Sato S.,
Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
Lynn J., Waever B., Shoalbi A., Wasawo D., Crabtree J., Wortman J.R.,
Lynn J., Waever B., Shoalbi A., Wasawo D., Crabtree J., Wortman J.R.,
Uterback I., Roldblyum T., Pertea M., Allen J., Taracha E.L.,
Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
Submitted (JUN-2005) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GOCSQNEYFDSL-----LHACIPCQLRCSSNTPPLTC--QRYCNASVT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.
NCBI_TaxID=882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hydrogenase, iron-sulfur cluster-binding subunit, putative.
OrderedLocusNames=DVU3401;
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                             -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, AAGKO1000001; BAN31255.1; -; Genomic DNA.

SEQUENCE 1532 AA; 175403 MW; 33C652005EAD2774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54143 MW; 904B524BF3BB118E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.6%; Score 64; DB 2; ilarity 31.8%; Pred. No. 22; Conservative 7; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desulfovibrio vulgaris Hildenborough.";
Nat. Biotechnol. 22:554-559(2004).
EMBL; AE017317; AAS96874.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                              22.8%; Score 64.5; Di
32.7%; Pred. No. 60;
ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00421; THIOREDOXIN.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q729F0 DESVH PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 32.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00037; Fer4; 1
Pfam; PF02662; FlpD; 1
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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O729F0 DES
ID Q729F0
DT Q729F0
DT 05-JU
DT 05-J
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SOCCERARARA
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RA BIXTON-EN-1;

RA Arachol H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

RA Arachol H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

RA Arachol H.M., Barna N., Calvo S.E., Camarata J., Chang J.,

RA Choepel Y., Collymore A., Cooke P., Cooke P., Chang D.,

RA Choepel Y., Collymore A., Cooke P., Corum B., DeArellano K.,

RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,

RA Gardyna S., Gnerrer S., Graham L., Grand-Pierre N., Hafez N.,

RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Illev I.,

RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,

RA Matchews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

RA Milvor T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,

RA Nolsen C.B., Norbu C., O'Connor T., O'Donnell B., O'Neil D.,

RA Roman J., Schauer S., Schubber R., Seaman S., Severy P., Smirnov S.,

RA Roman J., Schauer S., Schubber R., Seaman S., Severy P., Smirnov S.,

RA Talams J., Tesfaye S., Theodore J., Topham K., Travers M.,

RA Lander R., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,

RA Lander E., Stander R., Seman S., Simer R., Zody M.,

RA Lander E., Stander R., Seman S., Simer R., Zody M.,

RA Lander E., Stander R., Sembek L., Zimmer A., Zody M.,

RA Lander E., Stander S., Scholler S., Sembek L., Zimmer A., Zody M.,

RA Lander E., Stander S., Scholler S., Sembek L., Zimmer A., Zody M.,

RA Lander E., Stander S., Scholler S., Sembek L., Zimmer A., Zody M.,

RA Lander E., Stander S., Scholler S., Sembek L., Zimmer A., Zody M.,

RA Lander E., Stander S., Scholler S., Sewer S.,

RA Lander E., Stander S., Scholler S., Sewer S.,

RA Lander R., Stander S., Scholler S., Sewer S.,

RA Lander R., Stander S., Scholler S., Scholler S., Scholler S., Scholler S., Scholer S., Scholler S., Scholler S., Scholler S., Scholler S., Scholer S., Scholler S., Scholler S., Scholler S., Scholler S., Scho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Fusarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypochetical protein.
ORFNames=FG09123.1;
Glibberella zeae PH-1.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Glibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 762;
                                                                     Indels
45
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SEQUENCE 762 AA; 84756 MW; 55825D037F21A35A CRC64;
2 LOMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-5RP-2005 (TrEMBLrel. 31, Created)
13-5RP-2005 (TrEMBLrel. 31, Last sequence update)
13-5RP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=DB0219228;
Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
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EMBL; AACM01000370; EAA78173.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                762 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.6%; Score 64; DB 43.3%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 ACIPCO---LRCSSNTPPLTCOR----YC 41
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Q54KF9;
                                                                                                                                                                                                                                                                                                                                                                       (5 GIBZE
Q4IOY5 GIBZE PRELIMINARY;
Q4IOY5;
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Matches 13; Conservative
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100 AC OST
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00 DT 0
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InterPro; IPR000859; CUB.
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PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000742; BGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR011641; GCG_GCS
InterPro; IPR011641; GCG_GCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00431; CUB; 1.
Pfam; PF00008; EGF; 5.
Pfam; PF07645; EGF CA; 3.
Pfam; PF07699; GCCZ GCC3; 2.
SMART; SM00042; CUB; 1.
SMART; SM00181; EGF; 9.
SMART; SM00199; EGF; 9.
                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                                                                                                                                               Scube3 protein (Fragment).
Name=Scube3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
                                                                                                                                                           Q68FG9 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                              Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q., Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F., A Bunkler A.T., Lehmann R., Hamiln N., Davies R., Gaudet P., Fey P., Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., Rarborner P., Desany B., Just B., Norio T., Rost R., Churcher C., Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R., Mardroper A., Felder M., Thangavelu M., Johnson D., Knights A., Loulseged H., Mungall K., Oliver K., Price C., Quail M.A., Loulseged H., Mungall K., Oliver K., Price C., Quail M.A., Mushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M., Ma J., Kohlara Y., Sharp S., Simmonds M., Spiegler S., Tivey A., Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C., A Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C., Millem J., Dear P.H., Noegel A.A., Barrell B., Kuspa A., The genome of the social amoeba Dictyostelium discoideum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 LIQSMSRCNQPSVFKTLCSYLFPECQLYTNNKVVVAVPVLTCYEECTQSVS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 0:0-0(2005).
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MIQMAGQCSQNEYFDSLLHACIP-CQLRCSSN----TPPLTCQRYCNASVT 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 22.4%; Score 63.5; DB 2; Length 548; 1 Similarity 30.4%; Pred. No. 28; 17; Conservative 4; Mismatches 20; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.4%; Score 63.5; DB 2; Length 300; Best Local Similarity 31.4%; Pred. No. 15; Matches 16; Conservative 8; Mismatches 22; Indels
                                                                  Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giardia lamblia (Giardia intestinalis).
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mansouri M., Ey P.L.;
Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF298662; AAG37862.1; -; Genomic_DNA.
HSSP; O16119; 1EZG.
HSSP; O16119; 1EZG.
InterPro; 1PR0060519; 2FeZS, £d BS.
InterPro; 1PR0062112; Furin_repeat.
InterPro; 1PR005210; 1EGF.
InterPro; 1PR005210; 1EGF.
SWART; SM00111; EGF.
SWART; SM00261; FU; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 AA; 34482 MW; 9D863B38B2007E61 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Variant-specific surface protein M21-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.

EMBL; AAF10100151; EAL63792.1; -; Genomic_DNA.

SEQUENCE 300 AA.
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PROSITE; PS00282; KAZAL; UNKNOWN_1.
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09G045_GIALA PRELIMINARY;
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Matches 17; Conserva
[1]NUCLEOTIDE SEQUENCE.
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A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,

A Depkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,

A Distchento M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McEwan P.C., Hale S., Garria A.M., Gay L.J., Hulyk S.M.,

R And S.A., McEwan P.C., McKernan K.J., Male W. G., Glubs R.A.,

R Norley K.C., Hale S., Garria A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R And Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Utterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
                                                           209 AGGCDQGTYADPTTGQCKPCGI-----TDCATCEYNATISQPQCKTCSTSSNKMVK 259
5 AGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ------RYCNASVTNSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC79849; AAH79849.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90870 MW; DF6BB3337B4CE91D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI; MGI:3045253; Scube3.
GO; GO:0005509; F:calcium ion binding; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDDINE-21475520, PubMed=11591325, DOI=10.1016/S0960-9822(01)00481-X; Yan M., Brady J.R., Chan B., Lee W.P., HBu B., Harless S.M., Canacro M.P., Grewal I.S., Dixty V.M., "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "BAFF-R, a newly identified TNF receptor that specifically interacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor (B-cell maturation defect).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 GLCYRRSFFNNVKGANVLNVCNSVLHSCSP-DSKCSEN--PLYCPARRPQNSDIT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GQCSQNEYF-----DSLLHACIPCQLRCSSNTPPLTC--QRYCNASVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
STRAIN=BALB/c; TISSUE=B-cell lymphoma;
MEDLINE=21442025; PubMed=11509652; DOI=10.1126/science.1061965;
Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
                                                                                                    Eukaryota, Alveolata, Apicomplexa, Piroplasmida, Theileriidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.4%; Score 63.5; DB 2; Length 1563; Best Local Similarity 30.9%; Pred. No. 82; Matches 17; Conservative 10; Mismatches 11; Indels 17
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
(Subtelomeric) ABC-transporter family member, putative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:2108-2111(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                              Theileria annulata.
                                                                         ORFNames=TA12925;
                                                                                                                                               NCBI_TaxID=5874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ambrose C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TR13C MOUSE
Q9D8D0;
                    13-SEP-2005
13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with BAFF
                                                                                                                                  Theileria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 49
TR13C MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1524972; DOI=10.1074/jbc.M405912200; PubMed=15234972; DOI=10.1074/jbc.M405912200; PubMed=15234972; DOI=10.1074/jbc.M405912200; PubMed=15234972; DOI=10.1074/jbc.M405912200; PubMed=15234972; DOI=10.1074/jbc.M40; M4., Topper J.N., Yang R.B.; Manovel secreted, cell-surface glycoprotein containing multiple epidermal growth factor-like repeats and one CUB domain is highly expressed in primary osteoblasts and bones."; Diol. Chem. 279:37486-1749012049. EMBL, AX639609; ANU08348.1; -; mRNA. MGI; MGI:3045253; Scube3. GO; GO:005509; F:calcium ion binding; IEA. InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.4%; Score 63.5; DB 2; Length 993; 30.8%; Pred. No. 51; tive 5; Mismatches 9; Indels 13
                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal peptide, CUB and EGF-like domain containing protein 3
                      Length 827;
                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           993 AA; 108983 MW; E43989ACACCC345F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               748 QCSPGHYYNTSIHRCIRCAVGSYQPDFRQNFCTRCPGNT 786
                                                                                                                       7 QCSQNEYFDSLLHACIPCQL------RCSSNT 32
                                                                                                QCSQNEYFDSLLHACIPCQL------RCSSNT 32
                          DB 2;
                                                                                                                                                                                                                           993 AA
                          Score 63.5; Di
Pred. No. 42;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PÉAM; PROQUAI; CUB; 1.
PÉAM; PROODOB; EGF; 5.
PÉAM; PROOT645; EGF CA; 4.
PÉAM; PROOT645; EGF CA; 4.
SMART; SMO0142; CUB; 1.
SMART; SMO0141; EGF; 10.
SMART; SMO0179; EGF CA; 8.
PROSITE; PSO1180; EGF CA; 8.
PROSITE; PSO1186; EGF Z; 7.
PROSITE; PSO1186; EGF Z; 7.
PROSITE; PSO1187; EGF Z; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000742; EGF. 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001801; EGF Like.
InterPro; IPR011641; GCCZ GCC3
InterPro; IPR01641; GCCZ GCC3
                                                                                                                                                                                                                                                                                                                                                        Name=Scube3; Synonyms=SCUBE3;
Mus musculus (Mouse).
                            22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4UE95 THEAN
ID Q4UE95 THEAN PRELIMINARY;
AC Q4UE95;
         Query Match
Best Local Similarity 30.0.
Best Local 2; Conservative
                                                                                                                                                                                                                     QG6PY1_MOUSE PRELIMINARY;
Q66PY1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                           precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gnal
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RESULT 47

066PY1 MOU

1066PY1 MOU

1066PY1 MOU

066PY1 MOU

0766PY1 MOU

076PY1 MOU

076P

PRT; 1563 AA

RESULT 48

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4

17;

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175 AA.
                                                                                                                                                                                                                                                                                                    By similarity. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 QCSQNEYFDSLLHACIPCQL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 OCNOTECFDPLVRNCVSCEL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 OCSQNEYFDSLLHACIPCOL 26
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                                                                                                                                                                                                                                                                                                                                                                                                              22.3%;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity Surve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 50
QBR4WB MOUSE PRELIMINARY;
AC QBR4WB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                175
38
23
35
38
143
                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAF3 binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Tnfrsf13c;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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O
                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                        NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

STRAIN=C57BL/6J; TISSUE=Small intestine;

A CRAZAKI Y. Furunch M., Kasukawa T., Adachi J., Bono H., Kondo S.,

NIKaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

NASIK, Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P. Bult C., Hume D.A., Glondbach C., Gojobori T.,

A Bake J.A., Bradt D., Brusic V., Chochia C., Corbush S.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Gough J.,

A Crimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jazvis E.D.,

Ramai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanajaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Pertea G., Percla G.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagashima T., Numata K., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.V.,

Ravardo R., Wahleatedt C., Serphe C.J., Setou M., Shimada K.,

A. Varardo R., Wahleatedt C., Serphe C.J., Rathanbe Y., Wahlester C., Serou M., Shimada K.,

Ravardo R., Wahlester T., Wahlester C., Serou M., Shimada K.,

Ravardo R., Wahlester T., Wahlester C., Serou M., Shimada A.,

Huming L.G., Wynshaw Boris A., Yangaisawa M., Yang I., Yang I.,

Ravaraki T., Wakai K., Kawai J., Aizawa K., Atakawa T.,

Rayazaki A., Sasaki K., Sasaki D., Sasaki D., Pertea G., Per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISOId-0908D0-2; Sequence=VSP_006506;
TISSUE SPECIFICITY: Highly expressed in spleen and testis;
detected at lower levels in lung and thymus block at lower levels in lung and thymus block at lower block in Thirstild are a cause of severe B-cell deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion in the BAFFR gene leading to an altered C-terminus. The mutant RNA is not detectable. B-cell simphopolesis is normal, but the life span of peripheral B-cells is much reduced.
SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X; Harless S.M., Lentz V.M., Sah A.P., Hau B.L., Clise-Dwyer K., Halbert D.M., Hayes C.E., Cancro M.P.; "Competition for BLyS-mediated signaling through Bcmd/BR3 regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peripheral B lymphocyte numbers.";

Curr. Biol. 11:1986-1989 (2001).

-I- FUNCTION: B-cell receptor specific for TNFSF13B/TALLI/BAFF/BLyS.

Promotes the survival of mature B-cells and the B-cell response.

-I- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

-I- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q96KJ3; 100E.
MGI; MGI:1919299; Thirsfl3c.
GO; GO:0009897; C:external side of plasma membrane; IDA.
GO; GO:001021; C:integral to membrane; TAS.
GO; GO:0011296; P:B cell costimulation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing, Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9D8D0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF373847; AAK91827.1; -; mRNA.
EMBL; AK008142; BAB25490.1; -; mRNA.
Curr. Biol. 11:1547-1552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION.
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                                                                   .; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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MGI; MGI:1919299; Tnfrsfl3c.

GQ; GQ:0009897; C:sxternal side of plasma membrane; IDA.

GQ; GQ:0016021; C:integral to membrane; TAS.

GQ; GQ:0016021; C:integral to membrane; TMP.

GQ; GQ:001782; P:B-cell homeostasis; IMP.

GQ; GQ:0045078; P:positive regulation of interferon-gamma bio. . .;

GQ; GQ:0042102; P:positive regulation of T-cell proliferation; IDA.

GQ; GQ:0042102; P:positive regulation of T-cell proliferation; IDA.

GQ; GQ:0050776; P:regulation of immune response; IMP.

GQ; GQ:0050776; P:regulation of immune response; IMP.

SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;
GO, GO:0001782, P:B cell homeostasis; IMP.
GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
GO; GO:0045078; P:positive regulation of interferon-gamma bio. . .;
GO; GO:0045078; P:positive regulation of T cell proliferation; IDA.
GO; GO:0050776; P:regulation of immune response; IMP.
GO; GO:0050776; P:regulation of immune response; IMP.
InterPro: IPR001385; P:TRE_G.
PROSITE; PS00652; TNFR_GC.
PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
Alternative splicing; Glycoprotein; Immune response; Receptor;
Topo_DOM 1 71
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
TNFR-Cys (incomplete).
N-linked (GlCNAC. . .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63, DB 1; Length 175;
Pred. No. 9.8;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Signal-anchor for type III protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Mixuno K., Irie S., Sato T.-A.;
Submitted (FBS-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF350257; AAL83914.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28BC7C1A02FB87EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 2). /FTId=VSP_006506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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RESULT 51 Q678B7_9VIRU

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Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Zfp393;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/Sv x C57BL; TISSUE-Testis; MEDINE-129/Sv x C57BL; TISSUE-Testis; MEDINE-2239718; PubMed=12351194; DOI=10.1016/S0925-4773(02)00258-7; WAR W., Burns K.H., Ma L., Matzuk M.M.; and W., Burns K.H., and L. Tissue M. Strain of Zfp393, a germ cell-specific gene encoding a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pubmed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
"Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Lymphocystis disease virus - isolate China.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
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Ensembl; ENSWUSG0000048626; Mus musculus.
MG1; MG1: MG1: 181068; Zfp393.
MG1; GC1007276; P: gametogenesis; IDA.
InterPro; IPR007087; Znf C2H2.
Fram; PF00096; Zf-C2H2; 3.
ProDm; PD000003; ZnF CZH2; 3.
PROSITE; PS00028; ZinC FINGER C2H2 1; 3.
PROSITE; PS00187; ZINC FINGER C2H2 1; 3.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 341 AA; 38074 MW; AC82D4C0472B054C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.3%; Score 63; DB 2; Length 289; 39.4%; Pred. No. 16; ive 1; Mismatches 19; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Germ cell specific zinc finger protein.
Name=Zfp393; Synonyms=Gzf;
                                                                                                                                         (TrEMBLrel. 28, Last sequence update) (TrEMBLrel. 28, Last annotation update)
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EMBL, AY380826; AAU19940.1; -; Genomic DNA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR006209; EGF like.

InterPro; IPR001368; TNFR_C6.

Pfam; PF00020; TNFR_C6; 2.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01060; TNFR_NGFR_1; 1.
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                 289 AA
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Mech. Dev. 118:233-239(2002).
EMBL; AF508984; AAN31656.1; -; mRNA.
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                 PRT;
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                                                                                                     25-OCT-2004 (TrEMBLrel. 28,
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QBCFA7;
Q678B7_9VIRU PRELIMINARY;
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=256729;
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                                                                                                                                                  25-OCT-2004
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QBCFA MOU
DD GBCFA MOU
DD O1-MP
DT O1-OC
OB CREW
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KEY ENLEGITURE SEQUENCE.

KAYAIN-C57BL/63; TISSUE=In vitro fertilized eggs;

KAYAIN-C57BL/63; TISSUE=In vitro fertilized eggs;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishinagawa A., Shibata K., Yoshino M., Itoh M., Ishinagawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ratel P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Rachl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Rachl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Bakai K., Okido T., Fletcher C., Fujita M., Gariboldi M., Bankai K., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Andriber J., Mordone P., Ring B., Ringwald M., Rodríguez I., Sakameto N., Asuanki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Andribaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S., Wandhiayai, V., Wangi, V., Kawaji H., Rohtsuki S.,
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                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Mus masculus in vitro fertilized eggs cDNA, RIKEN full-length enriched
11brary, clone:7420700M05 product:weakly similar to D4675G8.1 (NOVEL
ZINC FINGER PROTEIN).
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STRAIN=CS7BL/6J; TISSUB=In vitro fertilized eggs;
MEDLINE=99279213; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                            Gaps
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22.3%; Score 63; DB 2; Length 341; 28.2%; Pred. No. 19; ive 9; Mismatches 19; Indels
                                                                                         45
                                                                                                                         STRAIN=C57BL/6J, TISSUE=In vitro fertilized eggs;
The FANTOM Consortium,
                                                                                           7 QCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
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                                                                                                                                                                                                                                                      Q9D351_MOUSE PRELIMINARY;
                                                 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Mouse)
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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Rabas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rogak S.A., McKernan R.J., Maraman P.J., McKernan R.J., Maraman P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rabergeley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
113-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation converted subjects (Fragment).

Name=PCSK5; ORFNames=RP11-422N19.4-002;

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.3%; Score 63; DB 2; Length 341;
Best Local Similarity 28.2%; Pred. No. 19;
Matches 11; Conservative 9; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC064748; AAH64748.1; -; mRNA. Ensembl. BNSMUSG00000048626; Mus musculus. MGI: AMGI: ALBIOGS; Epsembles in IDA. GO; GO:0007276; P:gametogenesis; IDA. InterPro; IPR007087; Znf C2H2. Ffam; PF00006; Zf C2H2; 3. Probom; PD000003; Znf C2H2; 3. SMART; SM00355; Znf C2H2; 3.
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Metal-binding; Nuclear protein; Zinc; Zinc_finger.
SEQUENCE 341 AA; 38046 MW; 62BB8FS059125A2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 QCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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EMBL, AL589653; CAI40809.1; -; Genomic_DNA.
EMBL, AL353607; CAI41234.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
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Q5JSG7;
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R HSSP, PO8047, ISPI.
     NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

STAIN-C578L/6J; TISSUE-In vitro fertilized eggs;

STAIN-C50530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasati N., Carminci P., Shibata K., Itoh M., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Hashia A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Inoue K., Togawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Awarated S., Kawai J., Natsuura S., Kawai J., Requencing pipeline with 384 multicapillary sequencer.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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MGI; MGI:2181068; Zfp39.
GO; GO:0007276; P:gametogenesis; IDA.
InterPro; IPRO00087; Znf_CZH2.
Pfam; PF00008; Znf_CZH2; Z.
SMART; SM00355; Znf_CZH2; Z.
SMART; SM00355; Znf_CZH2; Z.
PROSITE; PS00028; ZINC_FINGER_CZH2, J; Z.
PROSITE; PS0157; ZINC_FINGER_CZH2, Z; Zinc-finger.
Metal-binding; Nuclear protein; Zinc-finger.
SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFFC CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Juery Match
Best Local Similarity 28.20,
Best Local 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGP233 MOUSE PRELIMINARY;
O6P233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc finger protein 393.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 54
06 P233 MOU
07 P2 O6 P23
AC 06 P23
AC 06 P23
AC 06 P23
DT 05 JU
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MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlauener R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Bopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Hilalon D.K., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,
A Mhiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                      MGC26979 protein.
Name=MGC26979;
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 OMAGQCSQNEYFDSLLHACIPC------OLRCSSNTPPLTCQR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.1%; Score 62.5; DB 2; Length 985; 21.4%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022815; AAH32835.1; -; mRNA. Ensembl; ENSG0000164953; Homo sapiens. InterPro; IPR000126; Hypothet cof. PROSTIE; PS01228; COF 1; UNKNÖWN 1. SEQUENCE 985 AA; 1I0872 MW; 971B5626C726B3B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-2003 (TrEMBLrel. 25, Created)
01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein MGC26979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.1%; Score 04.5; Lu Best Local Similarity 21.4%; Pred. No. 67; Matches 12; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  985 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q725T8 HUMAN PRELIMINARY;
Q725T8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7Z5T8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Ankara isolate clone C9;
Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
Hall N., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 QLGGSASASSIAEALLRGCRCIELDCQDGSEEPVLCHAWKNCHLTGSV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.1%; Score 62.5; DB 2; Length 974;
29.2%; Pred. No. 67;
tive 9; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 OMAGQCSQNEYFDSLLHACIPCQLRCSSNT-PPLTCQRYCNASVTNSV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.3%; Score 63; DB 2; Length 1560; Best Local Similarity 32.6%; Pred. No. 94; Matches 14; Conservative 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
1-phosphatidylinositol-4,5-bisphosphatephosphod ie sterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1154 KCSPSEYWDEDAPGCKPCHVKCFHCMGPAEDQ--CQTCPMNSL 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1560 AA; 173890 MW; 7211FBC127A8A08C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The chromosome 1 sequence of Theileria annulata.";
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CR940347; CAI73325.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 OCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         974 AA; 110873 MW; 0E4988BA23DBAE41 CRC64;
    EMBL; AL353607; CA140675.1; JOINED; Genomic_DNA.
EMBL; AL353607; CA140809.1; JOINED; Genomic_DNA.
EMBL; AL599653; CA140809.1; JOINED; Genomic_DNA.
EMBL; AL591868; CA140809.1; JOINED; Genomic_DNA.
EMBL; AL391868; CA141234.1; JOINED; Genomic_DNA.
EMBL; AL391868; P: Al41234.1; JOINED; Genomic_DNA.
EMBL; AL99689; P: Subtilase activity; IEA.
GO; GO:0006508; P: Subtilase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
                                                                                                                                                                                                                                                                                                                                  ...cetc., irov.zoos; ripioliconveribr.
Pfam; PF02420; APP; 1.
Pfam; PF03460; DUF326; 2.
Pfam; PF01483; P_proprotein; 1.
ProDom, PD00017; ProproteconvertsP; 1.
SMART; SM00181; EGF; 16.
                                                                                                                                                                                                                                                                      InterPro; IPR006210; IEGF.
InterPro; IPR00209; Pept S8 S53.
InterPro; IPR002884; PrprotnconverteP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00138; SUBTILASE SER; 1.
                                                                                                                                                                                                                                                    InterPro; IPR006212; Furin_repeat.
                                                                                                                                                                                                  InterPro; IPR003460; AFP.
InterPro; IPR005560; DUF326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBIZO6_HUMAN PRELIMINARY;
QBIZO6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 THEAN
Q4UHW4 THEAN PRELIMINARY;
Q4UHW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 29.2
nes 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 3.1.4.11).
ORFNames=TA06965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theileria.
NCBI_TaxID=5874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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RESULT 56
OQUIMA THE
DQ OQUIMA
AC QQUIMA
DT 13-SE
DT 13-S

RESULT 57 Q81Z06 HUM 1D Q81Z0 AC Q81Z0 DT 01-MA DT 01-MA

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STRAIN=HM-1:IMSS;
PubMed=15729342; DOI=10.1038/nature03291;
Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.
Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
Chillingworth T., Churcher C., Harris B., Harris D.,
Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012; The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.1%; Score 62.5; DB 2; Length 999; Best Local Similarity 42.5%; Pred. No. 68; Matches 17; Conservative 2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris B.R.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete protecome; Hypothetical protein.
SEQUENCE 999 AA; 114888 MW; 8B46A4EB375357C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 YEDSLLKTCIGRAFERVKKMTPPLRIQSYFVSSTPNGLDG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 YFDSLLHACIPCOL-RCSSNTPPLTCORYCNASVTNSVKG 51
                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein F34D10.2.
0RFNames=F34D10.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0006270; P:DNA replication initiation; IEA.
GO; GO:0000074; P:regulation of cell cycle; IEA.
InterPro; IPR003874; CDC45_like.
PANTHER; PTHR10507; CDC45_like; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; 237139; CAA84594.1; -; Genomic_DNA.
EMBL; 234799; CAA84320.1; -; Genomic_DNA.
EMBL; 234799; CAA85494.1; JOINED; Genomic_DNA.
EMBL; 234199; CAA85494.1; JOINED; Genomic_DNA.
EMBL; 234199; CAA85494.1; JOINED; Genomic_DNA.
ENER; 719275; T19275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1917 AA.
                                                                                                 999 AA
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormBase; WBGene00009372; F34D10.2.
WormPep; F34D10.2; CE01570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entamoeba histolytica HM-1:IMSS.
Eukaryota; Entamoebidae; Entamoeba
                                                                                                 Q17969 CAEEL PRELIMINARY;
Q17969; Q19998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSIED6 ENTHI PRELIMINARY;
QSIED6;
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ORFNames=10.t00040;
                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
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051ED6 ENT
10 Q51ED
AC Q51ED
DT 13-SE
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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Brange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rodens P.J., McKernan K.J., Malek J.A., Gunzartne P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., A Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 OMAGOCSONEYFDSLLHACIPC-------QLRCSSNTPPLTCQR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 QQPEKCDNNQYFDISALSCVPCGANQRQDARGTSCVCLPGFQMISNNGGPAIICKK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QLRCSSNTPPLTCQR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 22.1%; Score 62.5; DB 2; Length 985; Local Similarity 21.4%; Pred. No. 67; los 12; Conservative 10; Mismatches 15; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Lung;
Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC05438, AAH5438.1; -; mRNA.
InterPro; IPR000150; Hypothet_cof.
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InterPro; IPR000150; Hypothet cof.
PROSITE; PS01228 COF_1; UNKNÖWN_1.
Hypothetical protein.
SEQUENCE 995 AA; 111730 MW; AEBD4A6B84F759A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110858 MW; 711109F095C12E89 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp686F1937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local Similarity 21.4%; Pred. No. 68;
Matches 12; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 QMAGQCSQNEYFDSLLHACIPC------
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Hypochetical protein.
SEQUENCE 985 AA; 110858 MW; 711
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QSHYA8;
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QSHYAB HUM
DD 10-MA
DT 10-MA

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Nozaki T.

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P05690:vit-2; NbExp=1; IntAct=EBI-326590, EBI-313756;
                                                                               Intact; Oldila:
Intact; Oldila:
Ensembl; T23F1.6; Caenorhabditis elegans.
Wormbeae; WBGene00004153; T23F1.6.
WormPep; T23F1.6: Cae14080.
InterPro; IPR003475; DUF1096.
InterPro; IPR003341; DUF139_Cys_rich.
Pfam; PF02363; C_triplex; 8.
Pfam; PF06493; DUF1096; 1.
Complete protecome; Hypothetical protein.
SEQUENCE 330 AA; 36605 MW; F043B1A90D3A8FE9 CRC64;
                           EMBL; Z81129; CAB03405.1; -; Genomic_DNA PIR; T25169; T25169.
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Matches 14; Conserv
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SORL CHICK
ID SORL CHICK
AC Q98930;
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         SKARBRARBRARS
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
   Quail M.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A., Poster P.G., Sicheriz-Ponten T., Weber C., Singh U., Mukherjee C., Fraser G.M., Hall N., Clark C.G., Embley T.M., Barrell B., Traser C.M., Hall N.;

"The genome of the protist parasite Entamoeba histolytica.";

Nature 433.865-868(2005).

-I. CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.1%; Score 62.5; DB 2; Length 1917; 31.0%; Pred. No. 1.3e+02; ive 7; Mismatches 21; Indels 1;
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denome sequence of the nematode C. elegans: a platform for
investigating blology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1917 AA; 212684 MW; 4AD7144F6A3CF30D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CSQNEYFDSLLHACIPCQLRCSSNTPPLT-CQRYCNASVTNS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein pqn-71.
Name-pqn-71; ORFNames=T23F1.6;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                           EMBL; AFB0100051; EAL51211.1; -; Genomic_DNA.
GO; GO:0016301; F: Kinase activity; IEA.
InterPro; IPR01226; Fcc3 N_cyt.
InterPro; IPR016212; Furin repeat.
InterPro; IPR006212; Furin repeat.
InterPro; IPR006212; Furin repeat.
InterPro; IPR00610; IEGE.
InterPro; IPR00619; Prot inh antistn.
InterPro; IPR000719; Prot inh antistn.
InterPro; IPR000719; Prot inh antistn.
InterPro; IPR000719; Prot inh antistn.
InterPro; IPR0002290; Ser thr pkinase.
InterPro; IPR001369; TNFR_c6.
InterPro; IPR001369; TNFR_c6.
InterPro; IPR001369; TNFR_c6.
InterPro; IPR001369; TNFR_c6.
InterPro; IPR001099; TNFR_C6.
Pfam; PF07699; GCC2 GCC3; 2.
Pfam; PF07699; GCC2 GCC3; 2.
Pfam; PF07699; GCC2 GCC3; 2.
Probom; DD000001; Prot Kinase; 1.
SWART; SW00226; FU; 17.
SWART; SW00226; FU; 17.
SWART; SW00226; FU; 17.
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PROSITE; PS50011, PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O18118 CAEEL PRELIMINARY;
018118;
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                                                                                                                                                                                                                                                                               preliminary data
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morvald S., Yamazaki H., Bujo H., Kubunoki J., Kanaki T., Seimiya K., Moriaki N., Nimpf J., Schneider W.J., Saito Y.; Amazaki N., Nimpf J., Schneider W.J., Saito Y.; Anoval mosaic protein containing LDL receptor elements is highly conserved in humans and chickens."; Thromb. Vasc. Biol. 17:996-1002(1997).

Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).

L. FUNCTION: Likely to be a multifunctional endocytic receptor, that may be implicated in the uptake of lipoproteins and of proteases. Binds LDL, the major cholesterol-carrying lipoprotein of plasma, and transports it into cells by endocytosis. Binds the receptor-sesociated protein (RAP). Could play a role in cell-cell interaction. Both estrogen status and cholesterol levels lack regulatory effects on this receptor.

C. -- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

C. -- TISSUE SPECIFICITY: Expressed abundantly in brain. Present in the testes, adrenal glands and detectable in the lung.

C. -- SIMILARITY: Contains 5 BNR repeats.

C. -- SIMILARITY: Contains 1 EGF-like domains.

C. -- SIMILARITY: Contains 2 Libronectin type-III domains.

C. -- SIMILARITY: Contains 5 Libronectin class A domains.

C. -- SIMILARITY: Contains 5 Libronectin class B repeats.
                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
113-SBP-2005 (Rel. 48, Last annotation update)
Sortilin-related receptor (Sorting protein-related receptor containing LDLR class A repeats) (SorLA) (SorLA-1) (Low-density lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR relative with 11 ligand-binding repeats) (LDLR relative with 11 ligand-binding repeats)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                              Gaps
                                              9
                                                                                                                         47
21.9%; Score 62; DB 2; Length 330; 29.2%; Pred. No. 25; ive 7; Mismatches 19; Indels
                                                                                          8 CSQNEYFDSLLHACIP----CQLRCSSNTPPL---TCQRYCNASVTN
                                                                                                                                                                                                                                                                  PRT; 1592 AA.
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HSSP; P01130; 1AJJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paramecium tetraurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
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NUCLECATIOE SEQUENCE.

NOVARA J. K., Migdalski A., Gromadka R., Zagulski M.;

NOVARA J. K., Migdalski A., Gromadka R., Zagulski M.;

NOVARA J. K., Migdalski A., Gromadka R., Zagulski M.;

NOVARA J. K., Migdalski A., Gromadka R., Zagulski M.;

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, CR48612, CAH03135.1; -; Genomic DNA.

GO; GO:0005489; F'electron transporter activity; IEA.

GO; GO:0006118; P:electron transport, IEA.

R GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0006118; PR006202; Furin repeat.

R InterPro; IPR006212; Furin repeat.

R InterPro; IPR001369; TEGF.

R InterPro; IPR001369; TURR C6.

R SMART; SM00181; EGF; 16.

R SMART; SM00181; EGF; 16.

R SMART; SM00181; EGF; 16.

R PROSITE; PS01186; EGF 2; UNKNOWN 2.

R PROSITE; PS01186; EGF 2; TURKNOWN 1.

R PROSITE; PS00652; TURE NGFR_1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.9%; Score 62; DB 1; Length 1592; Best Local Similarity 33.3%; Pred. No. 1.3e+02; Matches 15; Conservative 6; Mismatches 18; Indels
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                                                                                                                                                                                                                                                    1592 AA; 178411 MW; 24EDAA5BA231B203 CRC64;
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           R InterPro; IPR000742; EGF_1ike.

R InterPro; IPR000742; EGF_2ike.

R InterPro; IPR000742; EGF_2ike.

R InterPro; IPR0003961; FM_III.

R InterPro; IPR0003961; FM_III.

R InterPro; IPR00031; Ldl_receptor_A.

R InterPro; IPR00031; Ldl_receptor_A.

R Pfam; PF00061; Ed; I.

R Pfam; PF00057; Ldl_recept_b; 5.

R Pfam; PF00058; Ldl_recept_b; 5.

R RPR0011E; PS00186; EGF_2; 1.

R RRINTS; PR00261; LDLRRCEPTOR.

R RRINTS; PS00186; EGF_2; 1.

R RROSITE; PS50068; LDLRA_1; 11.

R RROSITE; PS50068; LDLRA_1; 11.

R RROSITE; PS510209; LDLRA_1; 11.

R RROSITE; PS51040; LDLRA_2; 11.
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BNR 2.

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BNR 3.

BNR 4.

BNR 5.

LDL-receptor class B 1.

LDL-receptor class B 3.

LDL-receptor class B 4.

LDL-receptor class A 1.

LDL-receptor class A 3.

LDL-receptor class A 3.

LDL-receptor class A 4.

LDL-receptor class A 9.

LDL-receptor class A 9.

LDL-receptor class A 9.

LDL-receptor class A 9.

LDL-receptor class A 11.

Fibronectin type-III 2.

Fibronectin type-III 3.

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  Ensembl; ENSGALG0000006598; Gallus gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia; TISSUE-Seed;
MEDLINE=95244835; PubMed=7727751;
Herzog M., Dorne A.-M., Grellet F.;
"GASA, a gibberellin-regulated gene family from Arabidopsis thaliana related to the tomato GAST1 gene.";
Plant Mol. Biol. 27:743-752(1995).
                                                                                                                                                                                                                                    Name=CASA3; OrderedLocusNames=At4g096600; ORFNames=T25P22.40; Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
    2224 QCDHQQYQDK--NGCLPCSIECNG-----CYTYGNNNCIN 2256
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                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Gibberellin-regulated protein 3 precursor.
                                                                                                                99 AA
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01-NOV-1995 (Rel. 32, Last seq
10-MAY-2005 (Rel. 47, Last anno
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-!- FUNCTION: Involved in late stages of seed maturation, or in early
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Bukaryota; Merazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibberellin-regulated protein 3. 84549B74B08A47FA CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   steps of germination.
--- SUBCELLUAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Siliques and dry seeds.
--- PTM: Six disulfide bonds may be present.
--- SIMILARITY: Belongs to the GAST1 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U11764; AAB06308.1; -; mRNA.
EMBL; AL161515; CAB78083.1; -; Genomic_DNA.
EMBL; AL161831; CAB82127.1; -; Genomic_DNA.
EMBL; AY052302; AAK96495.1; -; mRNA.
                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S60231; S60231.
InterPro; IPR003854; GASA.
Pfam; PF02704; GASA; 1.
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QBSZ58 DROME PRELIMINARY;
Q8SZ58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene family; Signal.
Nature 402:769-777(1999).
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nes 16; Conserv
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adamstides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,

Ranatides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,

Ranatides R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Ratton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., Rakendale J., Bayraktaroglu L., Beasaley B.M.,

RA Ballew R.M., Bauca A., Barkana B.P., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brokstein P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brokstein P.,

RA Borkova D., Botchan M.B., Butler H., Cadieu E., Center A., Chandra I.,

RA Booson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Gooson K., Cong F., Gorrell J.H., Gu Z., Gana P., Harris M.,

A Gooson K., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M.,

A Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

A Lasko P., Lei Y., Levitsky A.A., Li Z., Kennison J.A.,

Ran Mertei B., McIntosh T.C., Morebed M.P., McPherson D.,

Ran Merkulov G., Mallshina N.V., Mobarry C., Morris J., Moshrefi A.

Ran Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Randson D.K., Pettman G.S., Pollard J., Puri V., Reese M.G.,

Randson D.K., Remington K., Saunders R.D., Scheler F., Shen H.,

Randson D.K., Remington M.S., Sonlaers R., Shen H.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., A George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., A Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY071103; AAL48725.1; -; mRNA.

Ensembl; CG7348; Drosophila melanogaster.

R PlyBase; EBGN0036940; CG7348.

GO, GO:0005276; C:extracellular region; IEA.

GO; GO:0005061; F:chitin binding; IEA.

GO; GO:0005051; Chitin binding; IEA.

R GO: GO:0005257; Chitin bind_PerA.
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                                                                                                                                                                                                                                                                                                                                              7 QCSQNEYFDSLLHACIPCQL----RCSSNTP-----PLTCQRY--CNASVTNSVK 50
                                                                                                                                                                                                                                                                                                                 13;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Bukoptera, Endoptera, Diptera, Brachycera, Muscomorpha; Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                   DB 2; Length 353;
                                                                                                                                                                                                                                                                                                                20; Indels
                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 AA
                                                                                                                                                                                                                                                                                 21.7%; Score 61.5; D
28.1%; Pred. No. 31;
tive 8; Mismatches
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Q9VW81;
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NUCLEOTIDE SEQUENCE.
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Paciel D.J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapheton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a Whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Prise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426069; Pubmed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D. N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Wenistock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.W., Zhou W., Zhou X., Zhu S., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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353 AA; 39713 MW; 1C66916504FD130B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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nes 16; Conservative
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SEQUENCE
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NUCLEOTIDE SEQUENCE.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAIN=Rowbotham=Bradford;
PubMed=15486256; DOI=10.1126/science.1101485;
PubMed=15486256; DOI=10.1126/science.1101485;
Bradut D., Audic S., Robert C., Abergel C., Renesto P., Ogata H., La Scola B., Susan M., Claverie J.M.;
"The 1.2-Mb Genome Sequence of Mimivirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Rowbotham-Bradford;
MEDLINE=22550848; PubMed=12663918; DOI=10.1126/science.1081867;
La Scola B., Audic S., Robert C., Jungang L., de Lamballerie X.,
Drancourt M., Birtles R., Claverie J.M., Raoult D.;
A giant virus in amoebae.";
Science 299:2033-2033 (2003).
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Bukaryota, Metazoa Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                   DB 2; Length 483;
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 1.
Complete proteome; EGF-like domain; Hypothetical protein.
SEQUENCE 483 AA; 54281 MM; 4B2B7AB14BE0890E CRC64;
                                                                                                                                                                                                                                           108 CMNDGYFNHTLGRCV----CTSNWVGEHCIFRCNSGVVNKTSG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.7%; Score 61.5; DB 2; Length 4 ilarity 31.4%; Pred. No. 44; Conservative 9; Mismatches 21; Indels
                                                                                                                                                               20; Indels
                                                                                                                                                                                                                8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 306:1244-1350 (2004).
EMBL, AY653733; AAV50686.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 491 AA; 56132 MW; A3E1516CA622D31F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Mimivirus.
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                                                                                                                   21.7%; Score 61.5; DB
31.8%; Pred. No. 43;
:ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 491 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                             OSUGL4 MIMIV PRELIMINARY;
OSUGL47
01-FEB-2005 (TrEMBLrel. 29, C)
01-FEB-2005 (TrEMBLrel. 29, L)
01-FEB-2005 (TrEMBLrel. 29, L)
Hypothetical protein.
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QOVTRO;
                                                                                                         Query Match
Best Local Similarity 31.84
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nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=212035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mimivirus.
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                                                                                                                                                                                                                                                                                                                                                              DSUQL4 MIMIV
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            118 KCSVGNYFDPARRACLPVAISAAHQCSCVLPDNATLANPSDCETYFRCHSGQAELVQ 174
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The C.briggsae Sequencing Consortium;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 QCASQCEQS------CQQQCVQQQQPAAQCQTACQSSCSNS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDINE-29069613; PubMed-9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.7%; Score 61.5; DB 2; Length 4
Best Local Similarity 31.9%; Pred. No. 38;
Matches 15; Conservative 4; Mismatches 15; Indels
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InterPro; IPR009475; DUF1096.
InterPro; IPR009414; DUF1096.
InterPro; IPR009419; DUF1096.
InterPro; IPR009419; DUF1096.
InterPro; IPR06493; DUF1096; 1.
Hypothetical protein.
Rypothetical protein.
Rypothetical Arotein.
Rypothetical Protein.
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01-NOY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T12A7.2.
0RFNames=T12A7.2;
                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
45-OCT-2004 (TrEMBLrel. 28, Last annotation update)
45-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mame-CBG08690;
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                                                                                                                               432 AA
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PIR; G88846; G88846.
PIR; T24856; T24656.
HSSP; POOTS6; ITPG.
Ensembl; T12A7.2; Caenorhabditis elegans.
WormBase; WBGene00011723; T12A7.2.
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InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
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PROSITE; PS00022; EGF_1; 3.
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Q22423;
                                                                                                                                 QEILZ9 CAEBR PRELIMINARY;
Q61LZ9;
                                                                                                                                                                                                                                                                                              Caenorhabditis briggsae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
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202423
AC 02242
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DT 01-NO DT 01-NO DT 01-NO DE Hypot 00 Caeno
OC Caeno
OC CAENO
OC Rhabd
OC CAENO
OC RHABD
OC RABD
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Gaps

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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Richards S., Ashburner M., Henderson S.N.,
Bradon R.C., Rogers Y.-H.C. Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D.,
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Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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Bra Foeller C., Gabriellin J.H., Gu Z., Guan P., Harris M.,
Harrey D.A., Heiman T.J., Hernandez J.R., Houck J.,
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Brako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
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Spier E., Spradling A.C., Saunders R.D., Smith T.,
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The genome sequence of Drosophila melanogaster.",
The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22426065; PubMed=12537568; MEDLINE=22426065; PubMed=12537568; Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Peiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotum: release 3 of the Drosophila melanogaster euchromatic genome sequence."
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"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
Genome Biol. 3.RESEARCH0084.1-RESEARCH0084.20(2002).
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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J. Virol. 73:3764-3777(1999).

EMBL; AF105857; AAD27431.1; -; Genomic_RNA.

HSSP, P19549; IMEQ.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
HISTORY OF GO:0016021; C:integral to membrane; IEA.
AG:0019031; C:viral envelope; IEA.
Pfam; PF00516; GP120; 1.
AIDS: Envelope protein; Transmembrane.
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Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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MEDLINE=99214314; PubMed=10196271;
Bagnarelli P., Mazzola F., Menzo S., Montroni M., Butini L.,
                                                                                                                                                                                                                                                                                                                                EBI-166182;
EBI-172473;
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                                                                                                                                                                                                                                                                        Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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263 AA; 29480 MW; C62EBBE189C7BC96 CRC64;
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798 AA; 88442 MW; 19579B16980DF483 CRC64;
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21.6%; Score 61; DB 2; Les
Best Local Similarity 21.9%; Pred. No. 26;
Matches 14; Conservative 13; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                   263 AA
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Q9WEJ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.5
Matches 11; Conservative
                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
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SEQUENCE
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DOE Joint Genome Institute;
Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
"Comparison of two complete genome sequences of Pseudomonas syringae
pv. syringae B728a and pv. tomato DC3000.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LAGNGSSAEWWDDALPHFQQHQVVPLELFGFGNNPQPPCEDLASYADALLAATVKG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MAGQCSQNEYFDSLL----HACIPCQLRCSSNTPPLTCQ----RYCNASVTNSVKG 51
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; CAAC010000742; BGF 2.
InterPro; IPR005209; EGF 2.
InterPro; IPR005209; EGF 1:
InterPro; IPR005209; EGF 1:
INTERPRO; IPR00520; EGF 1:
INTERPRO; IPR00520; EGF 1:
INTERPRO; IPR00520; EGF 1:
INTERPRO; IPR00520; EGF 2:
INTERPRO; IPR005200; EGF 2:
INTERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.6%; Score 61; DB 2; Length 815; Best Local Similarity 30.4%; Pred. No. 85; Matches 17; Conservative 9; Mismatches 22; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feil H., Feil W.S., Lindow S.E.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000075; AAY40028.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA; 37704 MW; 2469B38E5B995B43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 815 AA; 90781 MW; 8AG38679CAF477D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG06165 (Fragment).
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QEISI8;
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                                                                NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=205918;
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                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=B728a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=B728a;
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Marcell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Marcaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
M. Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kallis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
II. Nature 411:946-957(2004).
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      132 CNSTQLFDSTWHNNGSNNTEGNDTIILPCRIKQIINMWQKVGKAMYTPPISGQIRCSSNI 191
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Edrinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OŘFNames-Psyr 5001;
Pseudomonas syringae pv. syringae B728a.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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354 AA; 39608 MW; CEBE4C670F2BDC03 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 2 SCAF15010, whole genome shotgun sequence.
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Last sequence update)
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Q4 ZLE4;
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Matches 15; Conservative
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                                                                                                                                          TGLI 195
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004 ZLE4 PSE
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21.4%; Score 60.5; DB 2; Length 339; 31.8%; Pred. No. 39; ive 5; Mismatches 20; Indels 9
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                                                                                             CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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       Query Match
Best Local Similarity 31.89
Matches 14; Conservative
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Job time : 191.8 secs

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US-11-113-202-10

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US-10-995-561-826

US-10-995-561-826

US-10-995-561-826

US-10-821-234-1081

US-11-186-284-41

US-10-95-561-956

US-11-113-826A-86

US-11-10-95-561-56

US-11-095-561-56

US-11-095-561-56

US-11-05-124-139

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US-10-821-234-128
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US-11-153-880-2
US-11-064-774A-22
US-11-147-047-50
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                                                                                                          December 21, 2005, 16:11:46; Search time 5.6 Seconds (without alignments) 43.302 Million cell updates/sec
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Sequence 1
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1_CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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US-10-742-634-9
US-10-967-527A-8
US-10-967-527A-10
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US-10-967-527A-19
US-11-137-465-35
US-11-137-465-35
US-11-108-172-1116
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S-10-967-527A-14
S-10-995-561-1033
S-10-995-561-1034
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Maximum Match 100%
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US-11-109-157A-2

US-11-108-528-84

US-11-109-157A-1

US-11-11-101-26

US-10-131-826A-484

US-10-821-234-1403

US-10-821-207-3

US-11-102-621-69

US-11-102-621-69

US-11-102-621-13

US-11-06-821-13

US-11-102-621-113

US-11-102-621-113
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US-11-102-621-134
US-10-763-712A-69
US-10-763-712A-112
US-10-821-234-1636
US-10-878-556A-150
US-11-045-802-34
US-11-055-822-460
US-11-055-822-702
US-10-995-561-659
US-11-051-14
US-11-132-285-2
US-10-947-8
US-11-055-822-100
US-11-137-751-46
US-11-113-751-48
US-11-1186-284-203
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RESULT 1

US-10-967-527A-9

; Sequence 9, Application US/10967527A

; Publication No. US20050256041A1

; GENERAL INFORMATION:
; APPLICANT: Brian A.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17

; FILE REFERENCE: 03-17

; CURRENT APPLICATION NUMBER: US/10/967,527A
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Sequence 9, Application US/10742634;
Sequence 9, Application US/10742634;
Sequence 9, Application No. US20060249671A9
GENERAL INFORMATION:
APPLICANT: Parmaelee, David
APPLICANT: Galperina, Olga
APPLICANT: Galperina, Olga
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses The
TITLE OF INVENTION: NUMBER: US 60/435,262
CURRENT FILING DATE: 2003-12-22
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/467,198
PRIOR FILING DATE: 2003-05-02
PRIOR FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
LENGTH. 18A
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                                                                                                                                                                                                                                                                                                                                   100.0%; Score 201; DB 6; Length 40; 100.0%; Pred. No. 3e-20; tive 0; Mismatches 0; Indel8
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Sequence 8, Application US/10967527A
Publication No. US20050256041A1
SEREMAL INFORMATION:
APPLICANT: Fox, Brian A.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Receptor
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT APPLICANT NUMBER: US/10/967,527A
CURRENT FILIG DATE: 2004-10-18
PRIOR APPLICATION NUMBER: 60/511,698
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100.0%; Score 201; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 34; Conservative 0; Mismatches 0;
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                PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 40
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAMME/KEY: DOMAIN
NOARF/KEY: DOMAIN
USCATION: (1)...(40)
US-10-967-527A-9
CURRENT FILING DATE: 2004-10-18
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Matches 34; Conservative
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CRGANISM: Homo sapiens
US-10-742-634-9
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US-10-742-634-9
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Query Match 35.6%; Score 71.5; DB 6; Length 249; Best Local Similarity 35.3%; Pred. No. 0.0084; Matches 12; Conservative 8; Mismatches 13; Indels
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33.1%; Score 66.5; DB 6; Length 2
Best Local Similarity 32.4%; Pred. No. 0.043;
Matches 11; Conservative 8; Mismatches 14; IndelB
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US-10-967-527A-19
is Sequence 19, Application US/10967527A
sequence 19, Application US/10967527A
sublication No. US20050256041A1
sequence 19, Application:
APPLICANT: Pox, Brian A.
TITLE OF INVENTION: Zenfr14, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
PRIOR FILING DATE: 2003-10-16
SEQ ID NO 19
SEQ ID NO 19
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FOX, Brian A.
APPLICANT: HOLloway, James L.
APPLICANT: HOLloway, James L.
APPLICANT: HOLloway, James L.
APPLICANT: HOLloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zrnfr14, A Tumor Necrosis Factor;
TITLE OF INVENTION: Receptor;
FILE REFERENCE: 03-10
CURRENT FILING DATE: 2004-10-18
FRIOR APPLICATION NUMBER: 60/511,698
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 48
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; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
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FEATURE:
NAME/KRY: DOMAIN
LOCATION: (1)...(48)
OTHER INFORMATION: cysteine rich
US-10-967-527A-20
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ORGANISM: homo sapiens
US-10-967-527A-19
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US-10-967-527A-21

Sequence 21, Application US/10967527A

Sequence 21, Application US/10967527A

Sequence 21, Application US/10967527A

Sequence 21, Application US/10967527A

SEQUENT: NOW. Brian A.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: Zrhfr14, A Tumor Necrosis Factor

TITLE OF INVENTION: Zrhfr14, A Tumor Necrosis Factor

TITLE OF INVENTION: Zchfr14, A Tumor Necrosis Factor

TITLE OF INVENTION: 203-17

CURRENT APPLICATION NUMBER: US/10/967,527A

CURRENT APPLICATION NUMBER: 60/511,698

PRIOR PILING DATE: 2003-10-16

NUMBER OF SEQ ID NOS: $1

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

LENGTH: 249

TYPE: PRT

OCCUPATION MUMBER: CONSIDER 2003-10-16

NUMBER OF SEQ ID NOS: $1

SEQ ID NO 21

SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Holloway, James L.
APPLICANT: Holloway, James L.
APPLICANT: Holloway, James L.
APPLICANT: Brepard, Paul O.
TITLE OF INVENTION: Zenfri4, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR FILING DATE: 2004-10-18
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication No. US20050256041A1
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 34, Conservative
                                                                                                SEQ ID NO 8
LENGTH: 184
TYPE: PRT
ORGANISM: homo sapiens
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LENGTH: 185
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                               9; Indels
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Sequence 7, Application US/10967527A

Publication No. US20050256041A1

GENERAL INFORMATION:

APPLICANT: Fox, Brian A.

APPLICANT: Holloway James L.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: Zhff14, A Tumor Necrosis Factor

TITLE OF INVENTION: Zhef14, A Tumor Necrosis Factor

TITLE OF INVENTION: Receptor

FILE REFERENCE: 03-17

CURRENT APPLICATION NUMBER: US/10/967,527A

CURRENT APPLICATION NUMBER: 60/511,698

PRIOR FILING DATE: 2003-10-16

PRIOR FILING DATE: 2003-10-6

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7
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                                                                                    1 CSONEYFDSLLHACIPCQL-----RCSSNT 25
28.9%; Pred. No. 0.91; tive 5; Mismatches
                                                                                                                                                                                                                                                                                   Sequence 36. Application US/11137465
PUBLICATION NO. US2005025558A1
GENERAL INFORMATION
APPLICANT: Agarwal, Pankaj
APPLICANT: Mizvi, Saffa, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Kabnick, Karen
TTILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/237,465
CURRENT APPLICATION NUMBER: US/10/239,663
PRIOR PILING DATE: 2002-09-24
PRIOR PILING DATE: 2001-03-22
PRIOR PILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.6%;
Best Local Similarity 28.9%;
Matches 11; Conservative 5
   Best Local Similarity 28.9% Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens US-11-137-465-36
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ORGANISM: mus musculus
US-10-967-527A-7
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Sequence 7, Application US/10742634

Sequence 7, Application No. US20050249671A9

Jebulication No. US20050249671A9

GENERAL INFORMATION:
APPLICANT: Parmelee Pavid
APPLICANT: Parmelee Pavid
APPLICANT: Galperina, Olga
APPLICANT: Hilbert, David
APPLICANT: Galperina, Olga
APPLICANT: Hilbert, David
APPLICANT: Rosen, Craig A,
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses Th
FILE REFERENCE: 1488.1810002
CURRENT APPLICATION NUMBER: US/10/742,634
CURRENT FILING DATE: 2003-12-22
PRIOR PLILING DATE: 2002-12-22
PRIOR PLILING DATE: 2003-05-02

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 7

LENGTH: 293

LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 33.1%; Score 66.5; DB 6; Length 293; 1 Similarity 32.4%; Pred. No. 0.043; 11; Conservative 8; Mismatches 14; Indels
         | : : | : | | | | : | : | : | 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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Sequence 35, Application US/11137465

Publication No. US2005025558A1

GENERAL INFORMATION:

APPLICANT: Agarwal, Pankaj

APPLICANT: Miradoch, Paul R.

APPLICANT: Smith, Randall, F.

APPLICANT: Smith, Randall, F.

APPLICANT: Xiang, Zhaoying

APPLICANT: Xiang, Zhaoying

APPLICANT: Xiang, Zhaoying

APPLICANT: Wabnick, Raren

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GPS0018

CURRENT APPLICATION UNMBER: US/10/239,663

PRIOR FILING DATE: 2002-09-24

PRIOR FILING DATE: 2001-03-22

PRIOR FILING DATE: 2001-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 35

LENGTH, 897
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ORGANISM: Homo sapiens
US-11-137-465-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-742-634-7
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DB 7; Length 897;

29.6%; Score 59.5;

Query Match

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APPLICANT: Fisher F., Eric
APPLICANT: Edwards K., Carl
APPLICANT: Edwards K., Carl
APPLICANT: Kieft L., Gary
TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
TITLE OF INVENTION: Type-II Receptors
FILE REFERENCE: 02-006-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50; DB 7; Length 455; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
24.9%; Score 50; DB 7; Length 161;
Best Local Similarity 35.3%; Pred. No. 3.5;
Matches 12; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-182-946-3
Sequence 3, Application US/11182946
Sequence 3, Application US/11182946
Publication No. US20050255100A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Ying-Fei
APPLICANT: Gentz, Reven
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1468-1280004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSONE---YFDSLLHACIPCOLRCSSNTPPLTCO 31
                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 02-006-A
CURRENT APPLICATION NUMBER: US/11/126,126
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: 09/882,735
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 1097-07-09
PRIOR PELING DATE: 1997-07-09
PRIOR PELING DATE: 1997-07-09
PRIOR PILING DATE: 1997-07-09
PRIOR APPLICATION NUMBER: 60/039,792
PRIOR FILING DATE: 1997-02-07
PRIOR FILING DATE: 1997-01-3
PRIOR FILING DATE: 1996-07-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATCHING VATE: 1996-07-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATCHIN VET: 2.0
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CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US/10/186,643
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US/09/573,986
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 3
LENGTH: 455
                            US-11-126-126-2
; Sequence 2, Application US/11126126
; Publication No. US20050250696A1
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ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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PRIOR FILING DATE: 2001-12-19
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 09/649,811
PRIOR APPLICATION NUMBER: US 09/609,448
PRIOR APPLICATION NUMBER: US 09/609,488
PRIOR APPLICATION NUMBER: US 09/609,889
PRIOR APPLICATION NUMBER: US 09/575,251
PRIOR APPLICATION NUMBER: US 09/519,444
PRIOR PILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/480,321
PRIOR APPLICATION NUMBER: US 09/480,321
PRIOR APPLICATION NUMBER: US 09/476,296
PRIOR FILING DATE: 2000-01-0
PRIOR FILING DATE: 2000-01-0
PRIOR PILING DATE: 2000-01-0
PRIOR APPLICATION NUMBER: US 09/476,296
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TITLE REFERENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11/108,172
CURRENT FILING DATE: 2005-04-15
Score 58; DB 6; Length 175;
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
                                                            6; Indels
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26.6%; Score 53.5; Di
Best Local Similarity 34.3%; Pred. No. 26;
Matches 12; Conservative 5; Mismatches
                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                      Sequence 1116, Application US/11108172
Publication No. US20050260177A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lodes, Michael J.
Secrist, Heather
Benson, Darin R.
Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
                                                                                                                         1 CSONEYFDSLLHACIPCOL 19
                                                                                                                                                               22 CNQTECFDPLVRNCVSCEL 40
Query Match 28.9%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Jiangchun
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US-11-108-172-1116
                                                                                                                                                                                                                                                                            RESULT 12
US-11-108-172-1116
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LENGTH: 5405
TYPE: PRT
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TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
FILE REFERENCE: PF511P1
CURRENT APPLICATION NUMBER: US/11/132,285
CURRENT FILING DATE: 2005-05-19
PRIOR APPLICATION NUMBER: US/10/046,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
TITLE OF INVENTION: Receptor
GURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            752 CSPGHFYNTTTHRCIRCPLGTYQPEFGKNNCVSCPGNT 789
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Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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                                          PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR PILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/10967527A Publication No. US20050256041A1
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; Sequence 61, Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
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26.3%;
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Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: homo sapiens
US-10-967-527A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                           APPLICATION N
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-10-967-527A-18
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   4; Gaps
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US-11-113-424-37
; Sequence 37, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR APPLICATION NUMBER: 60/257,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7; Length 909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen, Craig A
APPLICANT: Pan, James G
APPLICANT: Gentz, Reiner L
APPLICANT: Dixit, Vishva M
TITLE OF INVENTION: Death Domain Containing Receptor-4
FILE REFERENCE: PF355P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.9%; Score 50; DB 7; Le:
35.3%; Pred. No. 16;
tive 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 CRKNQYRHYWSENLFQCFNCSL-CLNGTVHLSCQ 157
                                                                                                                 127 CRKNOYRHYWSENLFQCFNCSL-CLNGTVHLSCQ 159
                                                          31
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                                                          1 CSONE --- YFDSLLHACIPCOLRCSSNTPPLTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PF355P3
CURRENT APPLICATION NUMBER: US/11/076,187
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: 60/035,722
PRIOR FILING DATE: 1997-01-28
PRIOR FILING DATE: 1997-01-29
PRIOR FILING DATE: 1998-01-27
PRIOR PRIOR PELIOR DATE: 1998-01-27
PRIOR PRIOR DATE: 1998-01-27
PRIOR PLING DATE: 1999-01-27
PRIOR PLING DATE: 1999-06-06
PRIOR PLING DATE: 1999-06-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2002-08-06
PRIOR PLING DATE: 2002-08-30
PRIOR PLING DATE: 2002-08-37
PRIOR PLING DATE: 2004-03-11
                                                                                                                                                                                                      RESULT 15
US-11-076-187-4
is Sequence 4, Application US/11076187
is Publication No. US20050244857A1
igeneral information:
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Best Local Similarity 35.3
Matches 12; Conservative
   12; Conservative
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ORGANISM: Homo sapiens
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| Publication Wo. US20050272054A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: CARDILL, Michele et al. |
| TITLE OF INVENTION: CARDILL, MICHELE POLYMORERS AND DRUG RESPONSE, METHODS OF ITTLE OF INVENTION: DETECTION AND USES THEREOF |
| FILE REPERRENCE: CLOO1559 |
| CURRENT APPLICATION NUMBER: US/10/995,561 |
| NUMBER OF SEQ ID NOS: 85702 |
| SOFTHARE: FRATSEQ for Windows Version 4.0 |
| SEQ ID NO 1033 |
| LENGTH: 1798 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.9%; Score 48; DB 6; Length 49; Best Local Similarity 30.0%; Pred. No. 2.3; Matches 9; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
US-10-967-527A-14

| Sequence 14, Application US/10967527A
| Publication No. US20050256041A1
| GENERAL INFORMATION:
| APPLICANT: Fox, Brian A. APPLICANT: Fox, Brian A. APPLICANT: Fox, Brian A. APPLICANT: Sheppard, Paul O. ITLE OF INVENTION: Receptor TITLE OF INVENTION: Receptor FILE REFERENCE: 03-17
| CURRENT APPLICATION NUMBER: US/10/967,527A |
| CURRENT FILING DATE: 2004-10-18 |
| PRIOR APPLICATION NUMBER: 60/511,698 |
| NUMBER OF SEQ ID NOS: 51 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| IRMATION: A.A. |
| IRMATICATION: A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CGENEYYNQTTGLCQECPPCGPGEEPYLSC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSONEYFDSLLHACIPCOLRCSSNTPPLTC 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSONEYFDSLLHACIPCOLRCSSNTPPLTC 30
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: DOMAIN
COTATION: (1)...(49)
COTHER INFORMATION: cysteine rich
US-10-967-527A-15
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ORGANISM: homo sapiens
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ORGANISM: homo sapiens
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US-10-995-561-1033
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APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zanfil4, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 297
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US-10-967-227A-15

Sequence 15, Application US/10967527A

Publication No. US20050256041A1

GENERAL INFORMATION:

APPLICANT: Fox, Brian A.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: Zenff14, A Tumor Necrosis Factor

TITLE OF INVENTION:

FILE REPERENCE: 03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

24.4%; Score 49; DB
Best Local Similarity 47.6%; Pred. No. 6.5;
Matches 10; Conservative 3; Mismatches
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   PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/261,960
PRIOR PILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR PLING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 60/149,450
PRIOR APPLICATION NUMBER: 60/149,712
PRIOR APPLICATION NUMBER: 60/149,712
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 61
LENGTH: 231
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3 CQENEYWDQ-WGRCVTCQ-RC 21
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Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-132-285-61
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75 SRNNH----LPACLSCNGRCNSN 93
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US-10-995-561-1016
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                              25;
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                                                                                   Length 1798;
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                                                                                                                              10; Indels
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US-11-182-946-13

Sequence 13, Application US/11182946

Publication No. US20050255100A1

GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.128004
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US/11/182,946
CURRENT FILING DATE: 2005-07-02
PRIOR PILING DATE: 2005-07-02
PRIOR PILING DATE: 2000-05-18

PRIOR PILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 13

LENDARL 2013
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                                                                                   Query Match
23.6%; Score 47.5; D:
Best Local Similarity 26.4%; Pred. No. 60;
Matches 14; Conservative 4; Mismatches
                                                                                                                                                                        1 CSONEYFDSLL-------HACIP--
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; Sequence 1034, Application US/10995561
; Palbication No. WS20050272054A1
; GENERAL INFORMATION:
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Best Local Similarity 26.4
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-1034
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ORGANISM: Homo sapiens
    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1033
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2 SQNEYFDSLLHACIPCOLRCSSN 24

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Sequence 1016, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION UNMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1016
LENGTH: 3690
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NOS: 85702
SEQ ID NO 1015
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"Sequence 1076, Application US/10821234
"Sequence 1076, US20050255114A1
"Sequence 1076, US20050255114A1
"SUBJICATION NO. US20050255114A1
"APPLICANT: Stache-Crain, Birgit
"APPLICANT: APPLICANT: Application: Susan
"APPLICANT: Tang, Y. Tom
"APPLICANT: Tang, Y. Tom
"STILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia; FILE REFERENCE: 821A
"CURRENT APPLICATION NUMBER: US/10/821,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 6; Length 3714;
Pred. No. 1.3e+02;
4; Mismatches 15; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSQNEYFD---SLLHACIPCQ-----LRCSSNTPPLTCQR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .-----LRCSSNTPPLTCQR 32
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23.4%; Score 47; DB 6; Length 3690;
Best Local Similarity 26.0%; Pred. No. 1.38+02;
Matches 13; Conservative 4; Mismatches 15; Indels
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Best Local Similarity 26.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CRGANISM: Homo sapiens US-10-995-561-1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens US-10-995-561-1015
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/219,442
FILING DATE: 23-DEC-1998
                                                                                                                                                                      US-11-064-769-2
; Sequence 2, Application US/11064769
; Publication No. US20050256075A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.1%;
Best Local Similarity 33.3%;
Matches 12; Conservative :
        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WASHINGTON
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STATE: DC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 419
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          Matches
                                                                                      셤
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                                                                                                                                                                                                                                                                              Gaps
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Publication No. US200502560501

GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 350;
                                                                                                                                                                                                                                   Length 3717;
                                                                                                                                                                                                                                                      .3e+02;
les 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/153,880
FILNG DATE: 16-jun-2005
CLASSIFICATION 16-jun-2005
FILNG APPLICATION DATA:
APPLICATION NUMBER: US/09/219,442
FILING DATE: 23-DEC-1998
CLASSIFICATION:
APPLICATION NUMBER: 08/999,811
FILING DATE: EN CASSIFICATION NUMBER: 08/999,811
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REGISTRATION NUMBER: 36,351
REGISTRATION NUMBER: 36,351
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488:100004
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                   Query Match 23.4%; Score 47; DB 6; Best Local Similarity 26.0%; Pred. No. 1.3e+02 Matches 13; Conservative 4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46.5; 1
Pred. No. 20;
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PL SEQ genes Version 1.0
SEQ ID NO 1076
LENGTH: 3717
                                                                                                                                                                                                                                                                                                                       1 CSQNEYFD---SLLHACIPCQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.1%;
33.3%;
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-11-153-880-4
                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1076
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D
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US-11-153-880-4
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APPLICANT: Alfertuala, Seppo
APPLICANT: Hiltunen, Mikko O
APPLICANT: Jellech, Marku M
APPLICANT: Jellech, Marku M
APPLICANT: Jellech, Marc G
APPLICANT: Jellech, Marc G
TITLE OF INVENTION: Use of VEGF-C or VEGF-D Gene or Protein to Prevent Restenosis
FILE REFERENCE: 2896/735601A
CURRENT APPLICATION NUMBER: US/11/064,769
CURRENT FILING DATE: 1999-10-26
PRIOR PILING DATE: 1999-10-26
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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3
Gaps
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US-11-123-800-2
US-211-123-800-2
Sequence 2, Application US/11153880
Fublication No. US20050256050A1
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
CARESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46.5; DB 7; Length 4
Pred. No. 23;
2; Mismatches 19; Indels
2; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/153,880
CLASCIFTAATION:
                                                                                                259 CGANREFDENTCQCV-CKRTCPRNQPLNPGKCACEC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 CGANREPDENTCQCV-CKRTCPRNOPLNPGKCACEC 362
                                                 1 CSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYC 34
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APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PACENTIN VERBION 3.2
SOFTWARE: PACENTIN VERBION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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US-11-113-424-35
US-11-113-424-35
Sequence 35, Application US/11113424
Sequence 35, Application No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same; FILE REPERENCE: 21402-225
CURRENT APPLICATION WHORE: US/11/113,424
CURRENT FILING DATE: 2005-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 CSPGHHYNTTTHRCIRCPVGTYQPEFGQNHCITCPGNT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPCQ-----LRCSSNT 25
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Best Local Similarity 30.3%; Pred. No. 44;
Matches 10; Conservative 3; Mismatches
                       FILE REFERENCE: GPS0016
CURRENT APPLICATION WUMBER: US/11/147,047
PRIOR APPLICATION WUMBER: US/10/221,097
PRIOR FILING DATE: 2005-06-07
PRIOR FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-05
PRIOR FILING DATE: 2000-03-05
PRIOR PILING DATE: 2000-03-05
PRIOR PILING DATE: 2000-03-05
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/10770726; Publication No. US20050266409A1; GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.1%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.74
Conservative
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US-10-770-726-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-147-047-50
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Sequence 22, Application US/11064774A

Sequence 22, Application US/11064774A

Sequence 22, Application US/11064774A

PUBLICATION NO. US20050267024A1

SERBRAL INFORMATION:

APPLICANT: Alitalo et al.

TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWT

TITLE OF INVENTION: FACTOR DAS AND PROTEINS

FILE REFERENCE: 28967/3597782

CURRENT APPLICATION NUMBER: 08/11/064,774A

CURRENT APPLICATION NUMBER: 08/11/064,774A

PRIOR APPLICATION NUMBER: 08/0/205,331

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 1212

SSOTUMARE: Patentin Ver. 3.2

SSOTUMARE: Patentin Ver. 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 CGANREFDENTCQCV-CKRTCPRNQPLNPGKCACEC 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; Score 46.5; DB 33.3%; Pred. No. 23; tive 2; Mismatches
                                                         PLILING JABE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: MARKOWICZ, KAREN R.

REGISTRATION NUMBER: 36,351
REFRERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELEFAX: (202)371-260
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/11147047
Publication No. US20050260668A1
GENERAL INPORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdock, Paul R.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
      APPLICATION NUMBER: 08/999,811 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.1%
Best Local Similarity 33.3%
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein US-11-153-880-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-11-064-774A-22
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Query Match
Best Local Similarity 23.7
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-11-113-424-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 47;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 23.1%; Score 46.5; DB 7; Length 9 Best Local Similarity 23.7%; Pred. No. 47; Matches 9; Conservative 5; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46.5;
Pred. No. 47
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-12-0
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR FILING DATE: 2001-09-14
PRIOR PRILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-05-14
PRIOR PLILING DATE: 2001-05-19
PRIOR PLILING DATE: 2001-05-19
PRIOR PLILING DATE: 2001-05-05
PRIOR PLILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-05-05
PRIOR PLILING DATE: 2001-05-05
PRIOR PLILING DATE: 2001-05-05
PRIOR PLING DATE: 2001-05-05
PRIOR PLING DATE: 2001-05-02
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23.1%;
Best Local Similarity 23.7%;
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-11-137-465-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus
US-11-113-424-35
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1 CSQNEYFDSLLHACIPCQ------LRCSSNT 25

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GENERAL INFORMATION,
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: TIGAL, TAMARA
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
TITLE OF INVENTION: COMPSISING NOTCH LIGAND PROTEINS
TITLE OF INVENTION NUMBER: US/11/078,735
CURRENT TAILING DATE: 2003-03-09
PRIOR PILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-09-10
PRIOR FILING DATE: 2002-09-10
PRIOR PILING DATE: 2002-09-10
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Pred. No. 48;
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Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches
PRIOR FILING DATE: 2001-09-14
PRIOR PLING DATE: 2001-05-29
PRIOR PLING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/284,153
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SEQ ID NO 36
LENGTH: 999
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; Sequence 13, Application US/11078735
; Publication No. US20050261477A1
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Publication No. US20050261477A1
                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.1%;
Best Local Similarity 23.7%;
Matches 9; Conservative
                                                                                                                                                                                                                                                         TYPE: PRT;
CRGANISM: Homo sapiens
US-11-113-424-36
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Fublication No. US2005026071341

GENERAL INFORMATION:

APPLICATY: Gangolli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/11/113,424

FRIOR APPLICATION NUMBER: 60/256,704

PRIOR APPLICATION NUMBER: 60/316,59

PRIOR PLING DATE: 2000-12-19

PRIOR FILING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/31,613

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-08-29
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                                                                                                                                                                                                                                                                                                   Score 46.5; DB 7; Length 96 Pred. No. 47; 5; Mismatches 11; Indels
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23.7%; Pred. No. 48;
tive 5; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHACIPCQ------LRCSSNT 25
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 965
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FILING DATE: 2001-07-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-080-991-50
, Sequence 50, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
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Best Local Similarity 23.7%;
Matches 9; Conservative
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Best Local Similarity 23.74
The Strong Strongervative
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ORGANISM: Homo sapiens
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-11-147-047-51
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12 HLELQIRVRCDENYYSATCNKFC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/11078735
Publication No. US20050261477A1
                                                                                                                      ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-078-735-14
                         SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 14
LENGTH: 63
NUMBER OF SEQ ID NOS: 51
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ORGANISM: Homo sapiens
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            APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: MCKENZIE, GRAHAME JAMES
APPLICANT: TUGAL, TAMARA
APPLICANT: TUGAL, TAMARA
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
TILLS OF INVENTION: COMPRISE: US/11/078,735
CURRENT FILING DATE: 2005-03-10
PRIOR FILING DATE: 2003-09-09
PRIOR FILING DATE: 2003-04-04
PRIOR PELICATION NUMBER: PCT/GB03/03285
PRIOR APPLICATION NUMBER: PCT/GB03/0525
PRIOR PELICATION NUMBER: PCT/GB02/05137
PRIOR PELICATION NUMBER: PCT/GB02/05137
PRIOR PELICATION NUMBER: PCT/GB02/05137
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR PELICATION NUMBER: GB 0220912.0
PRIOR PELICATION NUMBER: GB 0220913.8
PRIOR PELICATION NUMBER: GB 0220913.8
PRIOR FILING DATE: 2002-09-10
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Publication No. US200S0261477A1

GENERAL INCPRAITON.

APPLICANT: CHAMION, BRIAN ROBERT

APPLICANT: CHAMION, BRIAN ROBERT

APPLICANT: LENNARD, ANDREW CHRISTOPHER

APPLICANT: TUGAL, TAWARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS

TITLE OF INVENTION: COMPRESSING NOTCH LIGAND PROTEINS

FILE REFERENCE: 674525-2019

PRIOR APPLICATION NUMBER: PCT/GB03/03285

PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: PCT/GB03/05137

PRIOR APPLICATION NUMBER: PCT/GB02/05137

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2002-01-13

PRIOR FILING DATE: 2002-01-13

PRIOR FILING DATE: 2002-01-13

PRIOR FILING DATE: 2002-01-13

PRIOR FILING DATE: 2002-01-10

PRIOR FILING DATE: 2002-01-10

PRIOR FILING DATE: 2002-09-10

PRIOR FILING DATE: 2002-09-10
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12 HLELQIRVRCDENYYSATCNKFC 34
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US-11-078-735-14
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APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: MCKEWIZEL, GRAHAME JAMES
APPLICANT: TUGAL, TAWARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
TITLE OF INVENTION PROPER: US/11/078,735
CURRENT APPLICATION NUMBER: PCT/GB03/03908
PRIOR APPLICATION NUMBER: PCT/GB03/03285
PRIOR APPLICATION NUMBER: PCT/GB03/03285
PRIOR PLING DATE: 2003-08-01
PRIOR PLING DATE: 2003-01-07
PRIOR PLING DATE: 2003-01-07
PRIOR PLING DATE: 2003-01-07
PRIOR PLING DATE: 2002-11-13
PRIOR PLING DATE: 2002-11-13
PRIOR PLING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: PCT/GB02/05137
PRIOR PLING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: PCT/GB02/05137
PRIOR APPLICATION NUMBER: PCT/GB02/05137
PRIOR PLING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0220912.0
PRIOR PRILING DATE: 2002-09-10
PRIOR PLING DATE: 2002-09-10
PRIOR PRILING DATE: 2002-09-10
PRIOR PLING DATE: 2002-09-10
PRIOR PLING DATE: 2002-09-10
PRIOR PRILING DATE: 2002-09-10
PRIOR PRIOR PRILING DATE: 2002-09-10
PRIOR PRILING DATE: 2
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; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION:
; FILE REFERENCE: PF511P1
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Ouery Match 22.9%; Score 46; DB 7; Length 63; Best Local Similarity 30.4%; Pred. No. 5.2; Matches 7; Conservative 5; Mismatches 11; Indels
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US-LI-O78-735-21.

US-LI-O78-735-21.

US-LI-O78-735-21.

Sequence 21, Application US/11078735

Publication No. US20050261477A1

GENERAL INCOMATION:

APPLICANT: CHANFION:

APPLICANT: CHANFION:

APPLICANT: MCKENZIE, GRAHAME JAMES

APPLICANT: MCKENZIE, GRAHAME JAMES

APPLICANT: MCKENZIE, GRAHAME JAMES

APPLICANT: MCKENZIE, GRAHAME JAMES

APPLICANT: TILORAL, TAMARA

TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS

FILE REFERENCE: 67425-2019

CURRENT FILING DATE: 2005-03-10

FRIOR PLICATION NUMBER: PCT/GB03/0306

PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-04-04

PRIOR PLICATION NUMBER: PCT/GB03/01525

PRIOR PLICATION NUMBER: PCT/GB02/05137

PRIOR PLICATION NUMBER: PCT/GB02/05137

PRIOR PLING DATE: 2003-01-07

PRIOR PLING DATE: 2003-01-07

PRIOR FILING DATE: 2002-01-113

PRIOR PLING DATE: 2002-01-113

PRIOR PLING DATE: 2002-01-13

PRIOR PLING DATE: 2002-01-13

PRIOR PLING DATE: 2002-01-13

PRIOR PLING DATE: 2002-01-13

PRIOR PLING DATE: 2002-09-10

PRIOR FILING DATE: PARE CALL TAME CALL TAME
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22.9%; Score 46; DB 7; Length 1062;
Best Local Similarity 36.4%; Pred. No. 59;
Matches 8; Conservative 3; Mismatches 7; Indels
APPLICANT: Rizvi, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Sanith, Randall, F.
APPLICANT: Stang, Shaoying
APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPSOO18
CURRENT FILING DATE: 2005-05-25
CURRENT FILING DATE: 2005-06-25
PRIOR APPLICATION NUMBER: US/11/137,465
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: ECT/USO1/09226
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 43
LENGTH: 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-137-465-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
22.9%; Score 46; DB 7; Length 350;
Best Local Similarity 43.5%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 45
US-11-182-946-14
IS Sequence 14, Application US/11182946
Sequence 14, Application US/11182946
Publication No. US20050255100A1
GRUERAL INFORMATION:
APPLICANT: Wi, Ying-Fei
APPLICANT: Wi, Jian
APPLICANT: Wi, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
CURRENT FILING DATE: 2005-07-18
FRIOR APPLICATION NUMBER: US/11/182,946
PRIOR APPLICATION NUMBER: US/11/186,643
FRIOR APPLICATION NUMBER: US/09/573,986
FRIOR APPLICATION NUMBER: 2002-07-02
FRIOR APPLICATION NUMBER: 2002-07-02
FRIOR APPLICATION NUMBER: 2002-07-05
FRIOR APPLICATION NUMBER: 2002-07-05
FRIOR APPLICATION NUMBER: 2002-07-05
FRIOR PELING DATE: 2002-07-05
FRIOR PELING DATE: 2002-07-05
FRIOR PELING DATE: 2002-07-05
FRIOR PELING DATE: 2002-07-05
FRIOR APPLICATION NUMBER: 27
           CURRENT FILING DATE: 2005-05-19
PRIOR PILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR PRILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SONEYFDSLLHACIPCOLRCSSN 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-11-182-946-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 350
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ORGANISM: Homo sapiens US-11-078-735-21

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US-10-763-712A-76
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE

LOCATION: (180)

CHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-986-501-120
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
FRIOR PELING DATE: 2001-10-06
FRIOR PELING DATE: 2001-10-06
FRIOR APPLICATION NUMBER: 09/774,639
FRIOR PELING DATE: 2000-10-06
FRIOR PELING DATE: 2000-10-06
FRIOR PELING DATE: 1099-02-04
FRIOR FILING DATE: 1999-02-04
FRIOR PELING DATE: 1999-02-04
FRIOR PILING DATE: 1999-02-04
FRIOR PELING DATE: 1999-08-19
FRIOR PELING DATE: 1997-08-19
                                                                           Gaps
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Query Match 22.9%; Score 46; DB 7; Length 1238; Best Local Similarity 30.4%; Pred. No. 68; Matches 7; Conservative 5; Mismatches 11; Indels
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                                                                                                                                                                                   189 HLELQIRVRCDENYYSATCNKFC 211
                                                                                                                                            12 HACIPCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 120, Application US/10986501; Publication No. US20050244845A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                 RESULT 48
US-10-986-501-120
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LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
22.4%; Score 45; DB 6; Length 450;
Best Local Similarity 29.6%; Pred. No. 38;
Matches 8; Conservative 4; Mismatches 15; Indels
RESULT 49
US-10-967-527A-16

Sequence 16, Application US/10967527A

Sequence 16, Application US/10967527A

Sequence 16, Application US/10967527A

SEQUENCE 16, Application US/10967527A

SEQUENCENT: Polloway, James L.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: ZLAFE14, A Tumor Necrosis Factor

TITLE OF INVENTION: ZLAFE14, A Tumor Necrosis FLIE REPERENCE: 03-17

CURRENT APPLICATION NUMBER: US/10/967,527A

CURRENT APPLICATION NUMBER: 60/511,698

PRIOR FILING DATE: 2003-10-16

PRIOR FILING DATE: 2003-10-16

SEQ ID NO 16

SERVING MARKER: PART ARB

TYPE: PRT

ORGANISM: mus musculus

US-10-967-527A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 : | | : | | : | | : | 31 CGENEYHNQTTGLCQQCPPCR---PGEEPYMSC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFD---SLLHACIPCQLRCSSNTPPLTC 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 51
US-11-054-385-12
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Gaps

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8; Indels

Length 272;

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APPLICANT: Tunaabe, Colin K
APPLICANT: Watenabe, Colin K
APPLICANT: Wood, William
APPLICANT: Aloady Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 19330RIC128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT APPLICATION NUMBER: 06/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-19
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                                                Sequence 272, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 937, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION: APPLICANT: Labat, Ivan APPLICANT: Stache-Crain, Birgit APPLICANT: Andarmani, Susan APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                                                                               Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                       Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                              Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-272
                                 JS-10-131-826A-272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-821-234-937
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Sequence 166, Application US/10689742

Publication No. US20050250180A1

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward R
APPLICANT: Racie, Lisa A
APPLICANT: Spaniding, Vikki
APPLICANT: Spaniding, Vikki
APPLICANT: Treacy, Maurice
APPLICANT: Spaniding, Vikki
CURRENT FILING DATE: 200091.10
CURRENT APPLICATION NUMBER: US/10/689,742
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 231

SOFTWARE: PatentIn version 3.2

SEQ ID NO 186

LENGTH: 220
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                                                                           SPELICANT: MIZUTANI,

APPLICANT: MIZUTANI,

APPLICANT: TANAKA, Yoshikazu

APPLICANT: KUSUMI, Takaaki

APPLICANT: SAITO, Kazuki

APPLICANT: SAITO, Kazuki

APPLICANT: ZHIZHONG, Gong

TITLE OF INVENTION: GENES ENCODING PROTEINS HAVING TRANSGLYCOSYLATION

FILE REFERENCE: 001560-356

CURRENT PALLOATION NUMBER: US/09/147,955

PRIOR APPLICATION NUMBER: DS/09/03-94

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1997-07-25

NUMBER OF SEQ ID NOS: 12.0
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22.1%; Score 44.5; DB 6; Length 320;
Best Local Similarity 33.3%; Pred. No. 33;
Matches 13; Conservative 1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 7; Length 468;
Pred. No. 39;
1; Mismatches 6; Indels
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36 EAFDSVLGDTASCHRACQLTYPLHTYPKEEELYACQRGC 74
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Sequence 12, Application US/11054385 Publication No. US20050257291A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.3.
Then 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Petunia hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-186
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US-10-689-742-186
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LENGTH: 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
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US-11-186-284-228
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
PRIOR FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                            Score 44.5; DB 6; Length 332;
Pred. No. 34;
1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 21.9%; Score 44; DB 6; Length 304; Local Similarity 28.9%; Pred. No. 37; les 11; Conservative 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                 5 EYFDSLLHACIPCQLRCSSNTPPLT------CQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                         44 EAFDSVLGDTASCHRACQLTYPLHTYPKEEELYACQRGC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 CRANENRFYYNSVIGKCRPFKYSGCGGNENNFTSKQEC 263
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               FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PL_SEQ_genes Version 1.0
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 466, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1540, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION:
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SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1540
LENGTH: 304
                                                                                                                                                                                                                                                                                              Query Match
22.1%;
Best Local Similarity 33.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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DeForge, Laura
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Gurney, Austin L
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Smith, Victoria
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US-10-821-234-1540
                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-10-821-234-937
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US-10-821-234-1540
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US-10-131-826A-466
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Best Local S
Matches 11
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APPLICANT:
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APPLICANT:
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APPLICANT: Zhang, MILITANI
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT FILING DATE: 202-04-24
FRICH PAPLICATION NUMBER: 06/049911
PRIOR PELING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059116
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR APPLICATION NUMBER: 60/059588
PRIOR PLING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
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Similarity 42.1%; Score 44; DB 6; Length 437;
8; Conservative 3; Mismatches o ---
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, ITLILE OF INVENTION: METHODS FOR IDENTIFICATION.
TITLE OF INVENTION: THERAPY OF COLON CANCER FILE EPPERBUCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/11/301,822
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-01-05
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
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APPLICANT: Zhang, Zemin ACIDS ENCODING THE SAME TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT PILING DATE: 1997-06-18
PRIOR PAPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-19
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SEQ ID NO 142
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21.9%; Score 44; DB 6; Length 1036;
Best Local Similarity 44.0%; Pred. No. 1.1e+02;
Matches. 11; Conservative 3; Mismatches 9; Indels
                       Indels
                     6
Best Local Similarity 44.0%; Pred. No. 1e+02; Matches 11; Conservative 3; Mismatches
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                                                                                                        826 DSCTHCYCLQGQTLCSTVSCPPLPC 850
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                                                                     8 DSLLHA-CIPCQLRCSS-NTPPLTC 30
                                                                                                                                                                                                                        Sequence 142, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
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Gurney, Austin L.
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Smith, Victoria
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Filvaroff, Ellen
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APPLICANT:
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; Sequence 1412. Application US/2005025114A1
; Sequence 1412.
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Labat, Ivan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Andarmani, Susan
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REPRENCE: 821A
; CURRENT FILING DATE: 2004-04-07
; PRIOR PILING DATE: 2003-04-07
; PRIOR PILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NO 1412
; SEQ ID NO 1412
; LENGTH: 703
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                                                                                                                                                                                     Query Match

21.9%; Score 44; DB 7; Length 514;
Best Local Similarity 42.1%; Pred. No. 57;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 6; Length 703;
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.9%; Score **, 27.3%; Pred. No. 75; **ive 2; Mismatches 12; Indels
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US-11-067-121-7
Sequence 7, Application US/11067121
PUblication No. US20050261185A1
GENERAL INFORMATION:
APPLICANT: Martin, Cecile
APPLICANT: Martin, Cecile
CURRENT: RONGANI, Lena
TITLE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 1890-9002001
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR FILING DATE: 2004-06-02
PRIOR FILING DATE: 2004-06-02
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 7
LENGTH: 1028
TYPE: FRALESQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1028
TYPE: PRI
US-11-067-121-7
         NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 228
LENGTH: 514
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                                                                                                                                                                                                                                                                                  12 HACIPCOL--RCSSNTPPL 28
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; ORGANISM: Homo Sapiens
US-11-186-284-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-821-234-1412
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21.9%; Score 44; DB 7; Length 1028;

Query Match

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US-10-995-561-827
; Sequence 827, Application US/10995561
; Publication No. US20050272054A1
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENERAL SASOCIATED WITH
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REPREBENCE: CLO01559
; CURRENT APPLICATION UNMER: US/10/995,561
; CURRENT PILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SEQ ID NO 827
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TITLE OF INVENTION: GENETIC POLYMORHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOOISS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FEALSEQ for Windows Version 4.0
SEQ ID NO 825
LENGTH: 2480
TYPE: PRI
CRAMISM: Homo sapiens
US-10-995-561-825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 6; Length 2480; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.9%; Score 44; DB 7; Length 1255; Best Local Similarity 35.3%; Pred. No. 1.2e+02; Matches 6; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                867 CNDNLDFSIPGSCDSLSGSCLICK-----PGTTGRYC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSQNEYF-----DSLLHACIPCQLRCSSNTPPLTCQRYC 34
CURRENT FILING DATE: 2005-04-22

PRIOR APPLICATION NUMBER: US 60/590,473

PRIOR FILING DATE: 2004-07-23

PRIOR APPLICATION NUMBER: US 60/564,893

PRIOR FILING DATE: 2004-04-22

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 10

LENGTH: 1255
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Publication No. US20050272054A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          560 CLPCHPECQPQNGSVTC 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 CIPCOLRCSSNTPPLTC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.9%;
32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-10-995-561-827
                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-113-202-10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 64
US-10-995-561-827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-995-561-825
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
TILL CANT: Brown, COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MODULATING SIGNALING BY IGF-1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: ACTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DFA-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT PILING DATE: 2004-12-22
PRIOR FILING DATE: 2003-06-27
PRIOR FILING DATE: 2003-06-27
PRIOR FILING DATE: 2003-06-27
WHICH APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.9%; Score 44; DB 6; Length 1255; Best Local Similarity 35.3%; Pred. No. 1.2e+02; Matches 6; Conservative 2; Mismatches 9; Indels
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US-11-113-202-10
i Sequence 10, Application US/11113202
i Sequence 10, Application US/11113202
i Bublication No. US20050272637A1
i GENERAL INFORMATION:
i APPLICANT: Clinton, Gail M.
i APPLICANT: Shamieh, Lara
i TITLE OF INVENTION: RECEPTOR AND ERBB RECEPTORS
i TITLE OF 10071201
i TITLE OF 100712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 62
US-11-022-562-213
Sequence 213, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
   US-10-770-726-62
; Sequence 62, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 CLPCHPECQPQNGSVTC 576
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Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 213
LENGTH: 1255
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LENGTH: 1255
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DB 7; Length 757;

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21.6%; Score 43.5; L
35.0%; Pred. No. 93;
tive 5; Mismatches
          APPLICANT: Rondall, Lena
TITLE OF INVENTION: THERAPETTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION NUMBER: US/11/067,121
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR PILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
PRIOR FILING DATE: 2004-06-02
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 757
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Best Local Similarity 35.07
Matches 7; Conservative
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ORGANISM: Homo sapiens
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; Sequence 1081, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Andarmani, Susan
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1081
LENTH: 347
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Sequence 826, Application US/10995561

Sequence 826, Application US/10995561

Publication No. US20050272054A1

SEGNERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLO01559

CURRENT PELICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOCTWARE: FRRESEQ for Windows Version 4.0
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.9%; Score 44; DB 6; Length 3116; Best Local Similarity 32.5%; Pred. No. 2.7e+02; Matches 13; Conservative 4; Mismatches 9; Indels 1
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                                                                                          867 CNDWLDFSIPGSCDSLSGSCLICK-----PGTTGRYC 898
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                                             1 CSQNEYF-----DSLLHACIPCQLRCSSNTPPLTCQRYC 34
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/11067121
Publication No. US20050261185A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.6
Best Local Similarity 30.2
Matches 13; Conservative
  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-11-067-121-16
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     Matches
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APPLICANT: PILIENTIAN FARMANCE COLOURS, APPLICANT: PAPLICANT: Guillemette, Tracy L. APPLICANT: Guillemette, Tracy L. APPLICANT: Guillemette, Tracy L. APPLICANT: Sanakar, Shubhangi APPLICANT: Schlegel, Robert B. APPLICANT: Schlegel, Robert B. APPLICANT: Thibodeau, Stephen N. APPLICANT: Thibodeau, Stephen N. TITLE OF INVENTION: MUTHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: MUTHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF COLON CANCER FILE REFERENCE: MPMO1-029P2RNM FILE OF INVENTION: THERAPY OF COLON CANCER FILE OF INVENTION: MPMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR PLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-03-05
PRIOR PLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-05
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 757
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Best Local Similarity 35.0%; Pred. No. 93;
Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                  Sequence 41, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | :: | | : : | |: 134 HPCFP-RVRCINTSPGFRCE 152
| | | ::|| : :| |:
134 HPCFP-RVRCINTSPGFRCE 152
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RESULT 70 US-10-131-826A-86

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Gaps

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Sequence 184, Application US/11113424

Publication No. US200S0260713A1

GENERAL INFORMATION:

APPLICANT: Gangolli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same File REPERBNCE: 21402-225

CURRENT FILING DATE: 2005-04-21

PRIOR APPLICATION NUMBER: US/11/113,424

CURRENT FILING DATE: 2000-12-19

PRIOR PLING DATE: 2000-12-19

PRIOR PLING DATE: 2001-10-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: 60/315,617

PRIOR PLING DATE: 2001-09-24

PRIOR PLING DATE: 2001-07-24

PRIOR PLING DATE: 2001-09-14
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                                                                                                                                                                                                                                                                                                              Length 2214;
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                                                                                                                                                                                                                                                                                                           Score 43; DB 7;
Pred. No. 2.7e+02;
5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US/10/176,847
PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94
LENGTH: 2214
TYPE: PRT
ORGANISM: Homo sapiens
US-11-080-991-94
                                                                                                                                                                                                                                                                                                                                                                                                                       14 CIPCOLRCSSNT-----PPLTCQRYC 34
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US-10-995-561-556
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US-11-080-991-94

US-11-080-991-94

Sequence 94, Application US/11080991

Publication No. US20050266437A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST

TITLE OF INVENTION:

TITLE OF INVENTION: AND OVARIAN CANCER

FILE REFERENCE: MRI-039

CURRENT APPLICATION NUMBER: US/11/080,991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TILLE OF INVENTION: ACIDS ENCODING THE SAME

CURRENT FILING DATE: 203-04-24

PRIOR PELICATION NUMBER: 60/05911

PRIOR APPLICATION NUMBER: 60/05911

PRIOR APPLICATION NUMBER: 60/059113

PRIOR PILING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-17

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-09-19

PRIOR PLING DATE: 1997-09-19
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  Sequence 86, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe, Colin K
                                                                                                                    Beresini, Maureen
DeForge, Laura
                                                                                                                                                                                                                           Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                                        Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                           Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                 Sherwood, Steven
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ORGANISM: Homo Sapien
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Sequence 10, Application No. US20050257285A1

Publication No. US20050257285A1

SERENAL INFORMATION:
APPLICANT: LOS Alamos National Laboratory
APPLICANT: Gupta, Goutam
TITLE OF INVENTION: Compositions and Methods for the Treatment of Pierce's Disease
TITLE REFERENCE: S.102.340

FILE REFERENCE: 2.102.340

CURRENT PILING DATE: 2004-05-14

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.2

SEQ ID NO 10

LENGTH: 160
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Sequence 1504, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom and Treatment of Preeclampsia
TITLE OF INFORMITION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR PILING DATE: 2003-04-07

PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTMARE: pt_SEQ_genes Version 1.0

SEQ ID NO 1504

LENGTH: 419
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21.1%; Score 42.5; DB 7; Length 126;
Best Local Similarity 45.0%; Pred. No. 27;
Matches 9; Conservative 2; Mismatches 4; Indels
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR FILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 184
LENGTH: 126
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OTHER INFORMATION: Chimeric protein US-10-846-172A-10
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-855-158-11

US-10-216-074-17

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US-09-855-158-10

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			Sequence 1, Appliance 2 sequence 18, Appliance 2 sequence 35, Appliance 2 sequence 35, Appliance 2 sequence 1, Appliance 2 sequence 60022, A sequence 62860, A sequence 253740, Sequence 110099, A sequence 11325, A sequence 1552, Appliance 1553, Appliance 150, Appliance 15	
1-097-143-41457 Sequence 9-886-429-2 Sequence 9-162-435-21 Sequence 9-860-779-21 Sequence 9-898-570-10 Sequence 9-839-446-12 Sequence 9-339-663-35 Sequence	0-470-390A-12 Sequence 0-450-763-3668 Sequence 0-450-773-6 Sequence 0-480-172-2 Sequence 0-899-570-14 Sequence 0-108-260A-2874 Sequence 0-29-663-36 Sequence 0-406-073-8 Sequence 0-406-073-8 Sequence 0-406-073-15 Sequence	930-512-18 Sequence -898-570-16 Sequence -989-446-16 Sequence -980-172-20 Sequence -986-1049-49 Sequence -021-874-49 Sequence -021-874-14 Sequence -026-914-14 Sequence -021-874-53 Sequence -021-874-53 Sequence -021-874-53 Sequence -021-874-53 Sequence -021-874-53 Sequence -021-874-14 Sequence -021-874-14 Sequence -021-874-14 Sequence -021-874-14 Sequence	Sequence Seq	-218-1102-420 Sequence -399-456-15 Sequence -0.094-749-2573 Sequence -0.29-386-27641 Sequence -0.296-774-816 Sequence -296-774-810 Sequence -296-774-810 Sequence -0.21-874-150 Sequence -0.21-874-150 Sequence -0.21-874-151 Sequence -0.21-874-151 Sequence -0.21-874-151 Sequence -0.380-703-18 Sequence -380-703-18 Sequence -380-703-18 Sequence -380-703-18 Sequence -36-683-1590 Sequence -764-881-4135 Sequence -764-881-4135 Sequence
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Length 34;

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Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7
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Parent No. US20020081296A1

GENERAL INFORMATION:
APPLICANT: THELLL, LARS EYDE
APPLICANT: THELLL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
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-10-424-599-191216
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RESULT 2
US-09-855-158-7
Sequence 7, Application US/09855158
Sequence 7, Application No. US2002086018A1
Sequence 7, Application No. US2002086018A1
Sequence 7, Application No. US20020086018A1
Sequence 7, Application No. US20020086018A1
SETILE REPERENCE: APPLICATION: AMOUNT TITLE OF INVENTION: 3, AND TACI
TITLE OF INVENTION: 3, AND TACI
STILE REPERENCE: A-646A
CURRENT APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
SETING DATE: 2000-05-12
NUMBER OF SECIEN VERSION 3.1
SEQUENCE: APPLICATION NUMBER: US 60/204,039
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; Sequence 6, Application US/09854864
; Sequence 6, Application US/09854864
; GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT PILLIG DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: SI
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Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 34; Conservative 0; Mismatches 0;
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL)
TITLE OF INVENTION: MAD TACI
FILE REFERENCE: A-606A
CURRENY APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2001-09-11
PRIOR PLING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PLING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTI OF SEQ ID NOS: 30
SOFTWARE: PATENTI OF SEQ ID NOS: 30
LENGTH: 50
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Sequence 13. Application US/09854864

Sequence No. US20020081296A1

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLX5/AGP-3, AND TACI

TITLE OF INVENTION: BLX5/AGP-3, AND TACI

FILE REFERENCE: A-668

CURRENT FILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 13

LENGTH B1

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US-09-855-158-13
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; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR APPLICATION NUMBER: US 60/214,591
; RIUMBER OF SEQ ID NOS: 31
; SEQ ID NO 2:
LENGTH: 58
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Publication No. US2002086018A1
GENERAL INFORMATION: LARS EVDE
APPLICANT: THELL, LARS EVDE
APPLICANT: TU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-12
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                                                             Ouery Match 100.0%; Score 201; DB 3; Length 51; Best Local Similarity 100.0%; Pred. No. 3.1e-17; Matches 34; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 34; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin version 3.1
SEQ ID NO LENGTH: 51
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US-09-855-158-6
; ORGANISM: Homo sapiens
US-09-854-864-6
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US-09-854-864-21
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US-09-855-158-6
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Best Local Similarity 100.0%; Pred. No. 1.16-16;
Matches 34; Conservative 0; Mismatches 0; Indels
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Olest Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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APPLICANT: MacKay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tachopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Schneider, Pascal
APPLICANT: Blogen, Inc.
APPLICANT: Blogen, Inc.
APPLICANT: Morech RED S.A.
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077, 438
CURRENT FILING DATE: 2002-02-18
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
                  CURRENT APPLICATION NUMBER: US/09/055,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-27
PRIOR PLING DATE: 2000-06-27
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SEQ ID NO S: SQ ID NOS: 31
SEQ ID NO S: LENGTH: 181
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APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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ORGANISM: homo sapien
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US-10-077-438-1
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Sequence 13, Application US/09855158
Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
TILLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
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Sequence 5, Application US/09855158

Sequence 5, Application No. US2002086018A1

SERVERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: YU, GAN.

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, I TITLE OF INVENTION: 3, AND TACI
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Sequence 5, Application US/09854864

Sequence 5, Application US/09854864

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BCYS/AGP-3, AND TACI

TITLE OF ILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR PELLING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR PILLING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 34; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Consensus
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LENGTH: 81
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; ORGANISM: Homo sapiens
US-10-068-725-2
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ORGANISM: homo sapien
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100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels
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APPLICANT: Ambrose, Christine
APPLICANT: Techopy, Juse
APPLICANT: Techopy, Juse
APPLICANT: Techopy, Juse
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
ITLE OF INVENTION: Baff Receptor (BCMA), An
FILE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION: 1990-CT
CURRENT APPLICATION NUMBER: 60/149,378
FRIOR FILING DATE: 1999-08-17
FRIOR FILING DATE: 2000-02-11
FRIOR APPLICATION NUMBER: 60/149,378
FRIOR FILING DATE: 2000-02-11
FRIOR APPLICATION NUMBER: 60/183,536
FRIOR FILING DATE: 2000-02-18
FRIOR FILING DATE: 2000-0
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
Title OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
                                                                                                                                                                                                                                              CURRENT APPLICATION:
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT PILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR PAPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRAEEG for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/10077137; Publication No. US20020172674A1; GENERAL INFORMATION: APPLICANT: MacKey, Fabienne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 184
TYPE: PRT
ORGANISM: homo sapien
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ORGANISM: homo sapien
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Best Local Similarity
Matches 34; Conserv
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US-20-068-725-2

US-20-068-725-2

US-20-068-725-3

US-20-068-725-3

US-20-08-3-1

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100.0%; Score 201; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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Sequence 7, Application US/10077137
Publication No. US20020172674A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Browning, Jeffrey
APPLICANT: Tschopp, Jurge
APPLICANT: Tschopp, Jurge
APPLICANT: Thompson, Jeffrey
APPLICANT: Hompson, Jeffrey
APPLICANT: Description Information Applicant
FILE REFERENCE: ABORDET
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT APPLICATION NUMBER: 60/193,78
PRIOR FILING DATE: 1999-08-17
PRIOR PILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-
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CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
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US-10-152-363A-27
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FILE REFERENCE: 00-103
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US-10-152-363A-27
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                     WS-10-151-882-47

WS-10-151-882-47

Bublication No. US20030059862A1

Bublication No. US20030059862A1

Bublication No. US20030059862A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

CURRENT APPLICATION NUMBER: US/10/151,882

CURRENT FILING DATE: 2002-05-22

RRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.0

SEQ ID NO 47

LENGTH: 184

TYPE: PRT
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CHARLE INCOGRATION:
APPLICANT: Apotech Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof;
FILE REPRENCE: A003 PCT
CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/21568
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/181807
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/157933
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 12
SEQ ID NOS: 12
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; Publication No. US20030092164A1
; GENERAL INFORMATION:
    APPLICANT: Genes, Jane A.
    APPLICANT: APPLICANT: Menfeng
    APPLICANT: Henne, Randal M.
    APPLICANT: APPLICANT: Henne, Randal M.
    APPLICANT: Grant, Francis, J.
    TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 201; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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Sequence 11. Application US/10216074
| Sequence 11. Application US/10216074
| Publication No. US20030148445A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TILL OF INVENTION: METHODS OF USE THEREOF
| TILLE OF INVENTION: MUMBER: US/10/216,074
| TILLE OF INVENTION NUMBER: US/09/565,423
| PRIOR FILING DATE: 2000-05-05
| PRIOR FILING DATE: 2000-05-01
| PRIOR FILING DATE: 1999-05-06
| NUMBER OF SEQ ID NOS: 17
| SEQ ID NO 11
| SEQ ID NO 11
| TENEUTH: 184
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           Length 184;
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| Sequence 27, Application No. US20030103986A1 |
| Sepublication No. US20030103986A1 |
| GENERAL INFORMATION: |
| APPLICANT: Rixon, Mark W. |
| TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins FILE REFRENCE: 01-20 |
| FILE REFRENCE: 01-20 |
| CURRENT APPLICATION NUMBER: US/10/152,363A |
| CURRENT FILING DATE: 2002-05-20 |
| PRIOR FILING DATE: 2001-05-24 |
| NUMBER OF SEQ ID NOS: 70 |
| SEQ ID NOS: 70 |
| SEQ ID NOS: 70 |
| TYPE: PRI |
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Query Match
100.0%; Score 201; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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SEQUENCE 6, Application US/10485489

PUBLICALINORMATION:
APPLICANT: Dixit, Vishva
APPLICANT: Ridgway, John
APPLICANT: Ridgway, John
APPLICANT: Ridgway, John
APPLICANT: Ridgway, John
CURRENT APPLICATION NUMBER: US/10/485,489
CURRENT APPLICATION NUMBER: PCT/US02/23487
PRIOR APPLICATION NUMBER: PCT/US02/23487
PRIOR FILING DATE: 2002-07-24
PRIOR FILING DATE: 2002-07-24
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 19
SEQ ID NOS: 19
SEQ ID NOS: 19
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100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                           Indels
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CURRENT APPLICATION UNMBER: US/10/626,914
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/398,530
PRIOR PILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 6
                                                                                                                                                Score 201; DB 4;
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                        8 CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
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                                                                                                                                                100.0%;
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APPLICANT: CHUNTHARAPAL, ANAN
APPLICANT: GREWAL, IQBAL
APPLICANT: KIM, KYUNG JIN
APPLICANT: YAN, MINHONG
                                                                                                                                                Ouery Match
Best Local Similarity 100.
Matches 34; Conservative
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
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US-10-087-080-39
i Sequence 39, Application US/10087080
j Publication No. US2003023820A1
i GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: ARCENTED TO US20030235820A1
APPLICANT: Eas Western Reserve University
APPLICANT: Case Western Reserve University
TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer,
CURRENT FILING DATE: 2006-10-25
FRIOR FILING DATE: 2001-02-27
FRIOR APPLICATION NUMBER: US 60/281,149
FRIOR FILING DATE: 2001-04-02
FRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 39
FRIOR FILING DATE: 2001-04-17
SEQ ID NO 39
FRIOR FILING DATE: 2001-04-17
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APPLICANT: Parmelee, David
APPLICANT: Parmelee, David
APPLICANT: Galperina, Olga
APPLICANT: Galperina, Olga
APPLICANT: Galperina, Olga
APPLICANT: Hibbert, David
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses TH
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses TH
TITLE OF INVENTION: Number: US/10/742,634
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US 60/457,198
PRIOR FILING DATE: 2003-05-02
PRIOR FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 17
SOFWARE: Patentin Version 3.1
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                                                                                                                     Gaps
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US-10-087-080-39
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                                                          Length 184;
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                                                    Query Match
100.0%; Score 201; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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100.0%; Score 201; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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Publication No. US20040208824A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-216-074-11
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Sequence 9, Application US/09854864

Sequence 9, Application US/09854864

Sequence 10. US20020081296A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EXDE

APPLICANT: TYU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: METS/AGP-3, AND TACI

FILE REFERENCE: A-68684

CURRENT FILING DATE: 2001-09-11

PRIOR PPLICATION NUMBER: US 60/204,039

PRIOR PPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

SEQUENCE: ACCOUNCE-12

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 9.
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APPLICANT: ADIACEW Chan
APPLICANT: Oian Gong
APPLICANT: Oian Gong
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040R1P1
CURRENT APPLICATION NUMBER: US/11/021,874
CURRENT PILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR PELING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR PELING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR APPLICATION NUMBER: US 60/476,114

PRIOR APPLICATION NUMBER: US 60/476,114

PRIOR APPLICATION NUMBER: US 60/476,114

PRIOR APPLICATION NUMBER: US 60/476,114
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100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels (
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100.0%; Pred. No. 1.6e-16;
tive 0; Mismatches 0;
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                                           8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
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               1 CSONEYFDSLLHACIPCOLRCSSNTPPLICORYC 34
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Publication No. US20050163775A1
GENERAL INFORMATION:
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Matches 34; Conservative
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US-09-854-864-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-11-021-874-27
                                                                                                                                                              US-11-021-874-27
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US-09-854-864-9
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Publication No. US20050238650A1

GENERAL INFORMATION:

APPLICANT: Growley, Craig

APPLICANT: Crowley, Craig

APPLICANT: De Savvage, Frederic J.

APPLICANT: Bens, Allen

APPLICANT: Bens, Allen

APPLICANT: Follon, Andrew

APPLICANT: Smith, Victoria

TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of

TITLE OF INVENTION: Hematopoietic Origin

FILE REFERENCE: P5105R1US

CURRENT FILING DATE: 2004-11-16

PRIOR APPLICATION NUMBER: US 60/520,842

PRIOR APPLICATION NUMBER: US 60/532,426

PRIOR PILING DATE: 2003-11-17

PRIOR FILING DATE: 2003-11-14

SEQ ID NO 46

LENGTH: 184

TUDENCH: 184

LENGTH: 184

TUDENCH: 184
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Publication No. US20050095243A1

GENERAL INFORMATION:

APPLICANT: Addrew Chan

APPLICANT: Alavius Martin

TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

CURRENT APPLICATION NUMBER: US/10/861,049

CURRENT FILING DATE: 2004-06-04

PRIOR FILING DATE: 2003-06-05

PRIOR PAPLICATION NUMBER: US 60/476,481

PRIOR FILING DATE: 2003-06-05

PRIOR FILING DATE: 2003-06-05

PRIOR FILING DATE: 2003-06-05

NUMBER OF SEQ ID NOS: 145

SEQ ID NO 27
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                    Indels
100.0%; Pred. No. 1.1e-16; tive 0; Mismatches 0;
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                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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Best Local Similarity 100.
Matches 34; Conservative
Best Local Similarity 100. Matches 34; Conservative
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, ORGANISM: Homo sapiens
US-10-861-049-27
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ORGANISM: Homo sapiens
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US-10-989-826-46
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GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Ambrose, Christine
APPLICANT: Ambrose, Christine
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENOTH: 207
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APPLICANT: Machony, Jeffrey
APPLICANT: Tachopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Bogen, Inc.
APPLICANT: Bagen, Inc.
APPLICANT: Bagen, Inc.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: UNMBER: 60/149,378
FRIOR FILING DATE: 2000-02-11
FRIOR APPLICATION NUMBER: 60/181,684
FRIOR APPLICATION NUMBER: 60/181,536
FRIOR PILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 207
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Publication No. US20020172674A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MacKay, Fabienne APPLICANT: Browning, Jeffre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homo sapien
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                                                                                            Sequence 9, Application US/09855158

| Sequence 9, Application US/09855158
| Publication No. US20020086018A1
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: THEILL, LARS EYDE
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
| TITLE OF INVENTION: 3, AND TACI
| TITLE OF INVENTION: 3, AND TACI
| TITLE OF INVENTION: 3, AND TACI
| FILE REFERENCE: A-686A
| CURRENT APPLICATION NUMBER: US 60/214,591
| PRIOR PILING DATE: 2000-06-27
| PRIOR PILING DATE: 2000-06-12
| PRIOR APPLICATION NUMBER: US 60/204,039
| PRIOR APPLICATION NUMBER: US 60/204,039
| PRIOR PELING DATE: 2000-05-12
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US-10-115-192-12

Sequence 12, Application US/10115192

Publication No. US20030082175A1

GENERAL INFORMATION:

APPLICANT: Apotech R & D S.A.

APPLICANT: Blogen, Inc.

TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof

FILE REFERENCE: A083PCT

CURRENT APPLICATION NUMBER: US/10/115,192

CURRENT FILING DATE: 2002-04-02

PRIOR APPLICATION NUMBER: 60/181807

PRIOR PLING DATE: 2000-06-30

PRIOR PLING DATE: 2000-06-30

PRIOR PLING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FBSELSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 283;
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100.0%; Score 201; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 34; Conservative 0; Mismatches 0;
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US-10-077-438-3
Sequence 3, Application US/10077438
; Publication No. US20020165156A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: homo sapiens
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Sequence 10, Application US/09854864

j Sequence 10, Application US/09854864

j Batent No. US20020081296A1

GENERAL INFORMATION:

APPLICANT: THEILL,

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REPERENCE: A-6686B

CURRENT FILING DATE: 2001-09-11

PRIOR PAPLICATION NUMBER: US 60/204,039

PRIOR PAPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

SPIOR APPLICATION NUMBER: US 60/214,591
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Sequence 17, Application US/10216074

Publication No. US20330148445A1

GENERAL INFORMATION:

APPLICATH: Shu, Hong-Bing

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: METHODS OF USE THEREOF

PILE REFERENCE: 2879-7-7

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT FILING DATE: 2000-05-05

PRIOR PELING DATE: 2000-05-05

PRIOR PILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: UNKNOWN

PRIOR APPLICATION NUMBER: 60/132,892

PRIOR APPLICATION NUMBER: 60/132,892

PRIOR PILING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 17

LENGTH 185
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Pred, No. 9.5e-09;
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Best Local Similarity 70.6%;
Matches 24; Conservative 2
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Best Local Similarity 70.6*
Matches 24; Conservative
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US-09-854-864-10
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US-09-855-158-10
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-06-27
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARES PARENT IN VERSION 3.1
SEQ ID NO 11
LENGTH: 185
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                                                                46 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCLHACIPCQLRCSSNTPPLTCQRYC 99
                           -- LHACI PCOLRCSSNTPPLTCORYC 34
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67.7%; Score 136; DB 3; 1

Best Local Similarity 70.6%; Pred, No. 9.5e-09;

Matches 24; Conservative 2; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
, ORGANISM: Murine
US-09-855-158-11
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US-09-854-864-11
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US-10-216-074-17
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US-09-854-864-11
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US-09-892-158-178-178
US-09-892-158-178-178
US-09-892-158-178-178
Publication No. US20020086018A1
FURBLIANTON: US20020086018A1
FURBLIANTION: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL)
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT FALING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
FRIOR PRIOR SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 17
TYPE: PRT
ORGANISM: human-murine Consensus
US-09-855-158-12
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                                                                                                                                                                    ch 46.5%; Score 93.5; DB 3; Length 117; 1 Similarity 69.7%; Pred. No. 0.00096; 23; Conservative 1; Mismatches 2; Indels '
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Fublication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MOTEL ON:
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: ACANCR
FILE REFERENCE: 52945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/07/192
FRIOR PRILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
SOFTHAME: FastSEQ for Windows Version 4.0
SOFTHAME: PageSEQ for Windows Version 4.0
SEQ ID NO 1647
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                                                                                                                                                                                                                                                                      2 SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                       2 AOCEYFDSLLHAC-PC-LRCS----PPTCQ-YC 27
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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12
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US-10-087-192-1647
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US-10-087-192-1647
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Best Local S:
Matches 23
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Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION:
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
FRIOR APPLICATION NUMBER: US 60/204,039
FRIOR FILING DATE: 2000-05-12
FRIOR FILING DATE: 2000-06-12
FRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 31
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APPLICANT: SIONG, FEI
TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
FILE REFERENCE: A-743
CURRENT APPLICATION NUMBER: US/10/145,206
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/290,196
PRIOR FILING DATE: 2001-05-11
SOFTWARE: PATENT NOS: 197
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Pred. No. 6.8e-08;
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100.0%; Pred. No. ...
0; Mismatches
                    FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3:1
SOFTWARE: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 197, Application US/10145206; Publication No. US20030195156A1 GENERAL INPORMATION: APPLICANT: MIN, HOSUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 CSQNEYFDSLLHACIPCQLRC 42
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  3, AND TACI
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                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
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Best Local Similarity
Matches 21; Conserval
     TITLE OF INVENTION:
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US-10-145-206-197
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US-09-854-864-12
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Query Match 35.6%; Score 71.5; DB 4; Length 249; Best Local Similarity 35.3%; Pred. No. 0.97; Matches 12; Conservative 8; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
33.6%; Score 67.5; DB 4; Length 1
Best Local Similarity 37.8%; Pred. No. 17;
Matches 14; Conservative 4; Mismatches 14; Indels
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8; Mismatches 14;
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: A 570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 45
LENGTH: 37
                                                                                6 CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                             1 CSONEYFDSLLHACIPCOLRCSSNTPPLICORYC 34
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33.1%; Score 66.5;
Best Local Similarity 32.4%; Pred. No. 0.6
Matches 11; Conservative 8; Mismatches
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ORGANISM: Mus Musculus
US-10-180-903-2
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CRGANISM: Homo sapiens
US-09-779-050A-45
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US-09-854-864-20

RESULT 44

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; Sequence 20, Application US/09854864;
; Patent No. US20020081296A1
; GENERAL INFORMATION:
    APPLICANT: THEILL, LARS EYDE
    APPLICANT: THEILL, LARS EYDE
; APPLICANT: TU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
    TITLE OF INVENTION: BLXS/AGP-3, AND TACI
; FILE REFERENCE: A-6868
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT PILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-05-12
; PRIOR PILING DATE: 2000-06-12
; PRIOR PILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 20
; LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09855158

Sequence 20, Application US/09855158

Publication No. US20020086018A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EXDE

APPLICANT: TV, GANG

TITLE OF INVENTION: 3, AND TACI

TITLE OF INVENTION: WHORER: US/09/855,158

CURRENT FILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-06-21

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

LENGHH: 59
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Factor No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS EXDE
THEILL, THEILL, THEILL, THEILL,
THILL THEILL, THEILL,
THILE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGF-3, AND TACI
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; ORGANISM: Homo sapiens
US-09-855-158-20
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US-09-854-864-20
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US-09-854-864-16
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US-09-855-158-20
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Thu Dec 22 14:13:30 2005

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Sequence 15, Application US/09855158

Sequence 15, Application US/09855158

Sequence 15, Application No. US20020086018A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

ITLE OF INVENTION:

ITLE OF INVENTION:

FILE REPERBACE: A-686A

CURRENT APPLICATION NUMBER: US/09/855,158

CURRENT PILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-06-27

PRIOR PILING DATE: 2000-06-12

PRIOR PILING DATE: 2000-06-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGHI: 166
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Sequence 6, Application US/10293816

Publication No. US20030082173A1

GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: ALWHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
TILL REFERENCE: 44158/254623
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR PILING DATE: 1999-04-12
PRIOR PILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.1%; Score 66.5; DB 3; Length 166; Best Local Similarity 32.4%; Pred. No. 2.7; Matches 11; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                               DB 3; Length 166;
                                                                                                                                                                                            Score 66.5; DB 3; Length 1
Pred. No. 2.7;
8; Mismatches 14; Indels
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       NUMBER OF SEQ ID NOS: 31
SOFWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 166
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Best Local Similarity 32.4%;
Matches 11; Conservative
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ORGANISM: Homo sapiens
                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                 US-09-854-864-15
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Publication No. US20020086018A1
GENERAL INFORMATION:
BAPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: 3, AND TACI
FILE REPERENCE: A-686A
CURRENT FILING DATE: 2001-09-11
FRICA APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PACENTIN VERSION 3.1
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US-09-854-864-15

Sequence 15, Application US/09854864

Patent No. US20020081296A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILLE REFRENCE: A-668B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR PILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-06-27
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33.1%; Score 66.5; DB 3;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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33.1%; Score 66.5; Di
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-16
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US-09-855-158-16
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APPLICANT: Dixit, Vishva
APPLICANT: Grewal, Igbal
APPLICANT: Ridgway, John
APPLICANT: Ridgway, John
APPLICANT: Ridgway, John
TITLE OF INVENTION: TACIB and BR3 Polypeptides and Uses Thereof
FILE REFRENCE: 11669.175USWO
CURRENT APPLICATION NUMBER: US/10/485,489
CURRENT FILING DATE: 2002-01-30
PRIOR FILING DATE: 2002-01-34
PRIOR PELING DATE: 2002-07-24
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 19
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33.1%; Score 66.5; DB 5; Length 265;
Best Local Similarity 32.4%; Pred. No. 4.2;
Matches 11; Conservative 8; Mismatches 14; Indels
             DB 5; Length 171;
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APPLICANT: CHUNTHARAPAI, ANAN
APPLICANT: CHUNTHARAPAI, ANAN
APPLICANT: KIM, KYUNG JIN
APPLICANT: YAN, MINHONG
TITLE OF INVENTION: TACI Antibodies and Uses Thereof
FILE REFERENCE: P1942R1
CURRENT APPLICATION NUMBER: US/10/626,914
CURRENT APPLICATION NUMBER: US 60/398,530
PRIOR FILING DATE: 2003-07-25
PRIOR FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
LENGTH: 265
             Score 66.5; DB 5; 1
Pred. No. 2.8;
8; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/10626914 Publication No. US20050043516A1 GENERAL INFORMATION:
                Query Match
Best Local Similarity 32.4%;
Matches 11; Conservative
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CORGANISM: Homo sapiens
US-10-485-489-19
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; Sequence 6, Application US/11079418
; Publication No. US20050183148A1
; GENERAL INFORMATION:
APPLICANT: Brain, Richard J.
APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CURRENT APPLICANTON NUMBER: US/11/079,418
CURRENT APPLICATION NUMBER: US/293,816
FRIOR FILING DATE: 2002-01-14
FRIOR FILING DATE: 1999-04-12
FRIOR FILING DATE: 1997-03-03
FRIOR FILING DATE: 1999-04-12
FRIOR FILING DATE: 1999-04-13
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                                                                                 Score 66.5; DB 4; Length 166;
Pred. No. 2.7;
8; Mismatches 14; Indels
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Sequence 18, Application US/10684149

Publication No. US20050009149A1

GENERAL INFORMATION:

APPLICANT: West, James W.

TITLE OF INVENTION: Production of Homotrimeric Fusion

TITLE OF INVENTION: Proteins

FILE REFERENCE: 02-17

CURRENT APPLICATION NUMBER: US/10/684,149

CURRENT APPLICATION NUMBER: 60/417,801

PRIOR APPLICATION NUMBER: 60/417,801

PRIOR PILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 22

SOFTWARE FRASESE for Windows Version 3.0

LENGTH: 171
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Pred. No. 2.7;
8; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 33.1%;
Local Similarity 32.4%;
les 11; Conservative
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                                                                                    Query Match 33.1%;
Best Local Similarity 32.4%;
Matches 11; Conservative
; ORGANISM: Homo sapiens
US-10-293-816-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-11-079-418-6
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Best Local &
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Sequence 22, Application US/09879919
; Sequence 22, Application US/09879919
; Patent No. US2002064829A1
; GENERAL INFORMATION:
; APPLICATNT: YL Guo-Liang, et al.
; TTTLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon FILE REFERENCE: PF253P1
; CURRENT RELING DATE: 2001-06-14
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/277, 978
; PRIOR FILING DATE: 2001-03-23
; PRIOR FILING DATE: 2001-03-23
; PRIOR FILING DATE: 2001-03-23
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/211,952
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-16
; PRIOR PILING DATE: 2000-06-16
; PRIOR PELING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR APPLICATION NUMBER: 60/016,812
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33.1%; Score 66.5; DB 3; Length 291;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels
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                                                                        Sequence 43, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43
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ORGANISM: Homo Bapiens
                           RESULT 57
US-09-779-050A-43
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                                                                                                       RESULT 55
US-10-861-049-36

Sequence 36, Application US/10861049

Publication No. US20050095243A1

GENERAL INFORMATION:

APPLICANT: Andrew Chan

APPLICANT: Flavius Martin

TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

FILE REFERENCE: P204001US

CURRENT FLING DATE: 2004-06-04

PRIOR PILING DATE: 2003-06-06

PRIOR PILING DATE: 2003-06-06

PRIOR PILING DATE: 2003-06-05

PRIOR FILING DATE: 2003-06-05

NUMBER OF SEQ ID NOS: 145

LENGTH: 265
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; Publication No. US20050163775A1
; GENERAL INFORMATION:
    APPLICANT: Andrew Chan
    APPLICANT: Andrew Chan
    APPLICANT: Andrew Chan
    APPLICANT: Plavius Martin
    TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
    FILE REFERENCE: P204011P1
    CURRENT APPLICATION NUMBER: US/11/021,874
    CURRENT FILING DATE: 2004-12-22
    PRIOR PILING DATE: 2004-06-04
    PRIOR PLING DATE: 2004-06-04
    PRIOR PLING DATE: 2003-06-05
    PRIOR APPLICATION NUMBER: US 60/476,481
    PRIOR PLING DATE: 2003-06-05
    PRIOR PLING DATE: 2003-06-05
    PRIOR FILING DATE: 2003-06-05
    NUMBER OF SEQ ID NOS: 165
    SEQ ID NOS: 165
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33.1%; Score 66.5; DB 5; Length 265;
Best Local Similarity 32.4%; Pred. No. 4.2;
Matches 11; Conservative 8; Mismatches 14; Indels
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| : : | : | | | | : | : | : | 34 CPEEGYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
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Best Local Similarity 32.4%;
Matches 11; Conservative
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US-11-021-874-36
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US-11-021-874-36
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Sequence 2, Application US/09302863
Publication No. US20030022233A1
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G
APPLICANT: Din, Warman S.
TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION FILE REPRENCE: 2519
CURRENT APPLICATION NUMBER: US/09/302,863
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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APPLICANT: BOYLE,
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT APPLICATION NUMBER: US/09/779,050A
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR PILING DATE: 2001-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 42
LENGTH: 293
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                  TITLE OF ANYBRANCE: PF524P1
CURRENT APPLICATION NUMBER: US/09/961,376
CURRENT FILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-12-13
PRIOR FILING DATE: 2000-12-13
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
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Pred. No. 4.6
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Best Local Similarity 32.4%;
Matches 11; Conservative (
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Best Local Similarity 32.4*
Matches 11, Conservative
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, ORGANISM: Homo sapiens
US-09-961-376-2
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ORGANISM: Homo sapiens
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Sequence 14, Application US/09855158

Sequence 14, Application US/09855158

PUBLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: 3, AND TACI

FILE REFERENCE: A-686A

CURRENT APPLICATION NUMBER: US/09/855,158

CURRENT APPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR PLING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATENTIN VUMBER: US 60/204,039

FROM PILING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 14

SEQ ID NO 14

LENGTH: 293
                                                                                          Sequence 14, Application US/09854864

Patent No. US200200812561

Patent No. US200200812561

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: TW, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT FILING DATE: 2001-09-11

PRIOR PELICATION NUMBER: US 60/204,039

PRIOR PLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 14
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Pred. No. 4.6;
8; Mismatches 14; Indels
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Best Local Similarity 32.4%;
Matches 11; Conservative E
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; ORGANISM: Homo sapiens
US-09-855-158-14
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ORGANISM: Homo sapiens
US-09-854-864-14
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Best Local Similarity
Matches 11; Conserv
                                                        RESULT 59
US-09-854-864-14
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US-10-084-971-2

Sequence 2, Application US/10084971

Publication No. US20020187526A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Neutrokine-alpha Binding Proteins and Methods Based Thereon;
FILE REFERENCE: PF524PCT

CURRENT APPLICATION NUMBER: US/10/084,971

CURRENT FILING DATE: EARLIER PILICATION NUMBER: US/09/533,822

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599

PRIOR FILING DATE: BARLIER FILING DATE: 1999-03-10

PRIOR FILING DATE: BARLIER FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 293
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; APPLICANT: Kindsvogel, Wayne; TITLE OF INVENTION: ALtibodies That Bind Both BCWA and TACI; TITLE OF INVENTION: ALtibodies That Bind Both BCWA and TACI; CURRENT FILIKO DATE: 2002-02-06; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12; NUMBER OF SEQ ID NOS: 5; SOFTWARE: FRAEKSEQ for Windows Version 3.0
; SEQ ID NO 4; LENGTH: 293
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32.4%; Pred. No. 4.6;
tive 8; Mismatches
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US-10-151-882-46
Sequence 46, Application US/10151882
Publication No. US20030059862A1
GENERAL INFORMATION:
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Matches 11; Conservative
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US-10-084-971-2
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SERVICE APPLICATION US/09855564

FUDICACION NO. US20030165986A1

GENERAL INFORMATION:

JENERAL INFORMATION:

APPLICANT: GOOGWIN, RAYMONG G

APPLICANT: DIN, WANWAN S

TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION

FILE REFERENCE: 2519

CURRENT FILING DATE: 1999-04-30

PRIOR APPLICATION NUMBER: 09/302,863

PRIOR APPLICATION NUMBER: 09/302,863

PRIOR APPLICATION NUMBER: 09/302,863

PRIOR PILING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2: SEQ ID NO 5: 5

LENGTH: 293
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33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels
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| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: Morris, David W. APPLICANT: Morris, David W. TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NAMBER: US/10/087,192 CURRENT FILING DATE: 2204-03-01 PRIOR FILING DATE: 2000-12-22 PRIOR PLILING DATE: 2001-12-22 PRIOR PLILING DATE: 2001-03-02 PRIOR PR
                                                                                                                                                                              DB 3;
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Pred. No. 4.6;
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33.1%; Score 66.5; D
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches
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; ORGANISM: Homo sapiens
US-10-087-192-1650
                                    ; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 65
US-10-087-192-1650
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US-09-855-564-2
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       LENGTH: 293
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JS-10-268-951-22
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US-10-152-363A-2
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APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PFS54
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Atentin version 3.0
SEQ ID NO 46
LENGTH: 293
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; Sequence 2, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, GGCz
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; FRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR APPLICATION NUMBER: US 08/200,333
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PSEC FOR Windows Version 4.0
; SEQ ID NO 2
: LENGTH: 293
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Pred. No. 4.6;
8; Mismatches 14; Indels
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; Sequence 8, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
A APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
APPLICANT: Henne, Randal M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT APPLICATION STELL SOUI-11-05
; NUMBER OF SEQ ID NOS: 46
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Best Local Similarity 32.4%;
Matches 11; Conservative E
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US-10-293-816-2
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 11; Conserva
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TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF2592
CURRENT APPLICATION NUMBER: US/10/268,951
CURRENT PILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/082,260
PRIOR PILING DATE: 2001-06-14
PRIOR PILING DATE: 2001-66-14
PRIOR PILING DATE: 2001-66-14
PRIOR PILING DATE: 2001-66-14
PRIOR PILING DATE: 1997-03-12
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-34
PRIOR PILING DATE: 2001-03-36
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CURRENT FILING DATE: 2002-05-20; PRIOR PILING DATE: 2002-05-20; PRIOR PILING DATE: 2001-05-24; NUMBER OF SEQ ID NOS: 70
SEQ ID NO 2; SEQ ID NO 2; SEQ ID NO 2; LENGTH: 293
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 8; LENGTH: 293; TYPE: PRT; TYPE: PRT; ORCANISM: Homo sapiens
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Best Local Similarity
Matches 11; Conserv
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Search completed: December 21, 2005, 16:30:38 Job time: 90.4 secs
; ORGANISM: human
US-10-618-797-4
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Publication No. US20040048296A1

Fublication No. US20040048296A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Ruben, Steven M

TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based Thereon

TILE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based Thereon

CURRENT APPLICATION NUMBER: US/10/618,797

CURRENT APPLICATION NUMBER: 09/848, 295

PRIOR APPLICATION NUMBER: 60/202,193

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.1
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537
PRIOR FILING DATE: 2000-06-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 293
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Publication No. US2004003674A1

GENERAL INFORMATION:

APPLICANT: Ambrose, Christine

APPLICANT: Ambrose, Christine

APPLICANT: Ambrose, Christine

APPLICANT: Rennert, Paul

APPLICANT: Rennert, Paul

TITLE OF INVENTION: Taci As As Anti-Tumor Agent

FILE REFERENCE: BIOCO130 NP of PCT/US01/40626

CURRENT APPLICATION NUMBER: US/10/258,368

CURRENT PILING DATE: 2002-10-21

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 293
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33.1%; Score 66.5; D
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches
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US-10-268-951-22
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 293
TYPE: PRT
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US-10-618-797-4
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US-10-258-368-1
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Sequence 7, Application US/10742634

Sequence 7, Application US/10742634

Sequence 7, Application Wo. US20040208824A1

GENERAL INFORMATION:

APPLICANT: Parmelee, David

APPLICANT: Renelee, David

APPLICANT: Ralperina, Olga

APPLICANT: Hibert, David

APPLICANT: Hibert, David

APPLICANT: Hibert, David

APPLICANT: Hibert, David

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses The FILE REFERENCE: 1488.1810002

FILE REFERENCE: 1488.181002

FILE REFERENCE: 1003-12-22

PRIOR APPLICATION NUMBER: US 60/435,262

PRIOR APPLICATION NUMBER: US 60/467,198

PRIOR PILING DATE: 2003-05-02

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 7

LENGTH: 293

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Query Match 33.1%; Score 66.5; Di
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches
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ORGANISM: Homo sapiens
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2834, Ap
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US-09-471-276-1590
US-09-252-991A-25721
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US-09-948-295-2
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US-08-349-471-20
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RESULT 2
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US-09-854-864-6

Sequence 6, Application US/09854864

Retent No. 6774106

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE.
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERBNCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT PILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-13

PRIOR PELING DATE: 2000-05-14,591

PRIOR FILING DATE: 2000-05-15

SOFTWARE PAPELICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-05-15

SOFTWARE PAPELICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-05-15

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US-09-854-864-21

Sequence 21, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:
PAPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLS/AGP-3, AND TACI

TITLE OF INVENTION: BLS/AGP-3, AND TACI

FILE REFERENCE: A-6868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR PILING DATE: 2000-06-27

NUMBER OF EXQ ID NOS: 31

SOFTWARE: Patentin version 3.1

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PRIOR FILING DATE: 2000-06-27
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Matches 34; Conservative
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; ORGANISM: Homo sapiens
US-09-854-864-7
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ORGANISM: Homo sapiens
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Sequence 7, Application US/09854864

Sequence 7, Application US/09854864

Setting Constraint Information Conference APPLICANT: THEIL, LARS EXDE

APPLICANT: THEIL, LARS EXDE

APPLICANT: THEIL, LARS EXDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
Sequence 2, Appli
Sequence 14, Appl
Sequence 9367, Ap
Sequence 2, Appli
Sequence 206, Appli
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                                        4, Appli
69, Appli
151, Appl
273, App
273, App
64, Appl
39208, A
11660, A
32903, A
48120, A
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13, Appl
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48, Appl
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105, App
49, Appl
13111, A
4, Appli
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Sequence 19,
Sequence 1,
Sequence 2,
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Sequence 1
Sequence 4
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      US-09-902-540-10416
US-09-917-254-81
US-09-917-254-81
US-09-949-016-11625
US-10-037-417-6
US-10-104-047-3105
US-10-104-047-3105
US-10-104-047-3105
US-10-104-047-3105
US-09-320-320-676
US-09-320-320-676
US-09-270-767-41054
US-09-270-767-56270
US-09-202-540-16212
US-09-202-540-16212
US-09-002-540-16212
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5-09-004-838-105
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5-09-902-540-13111
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US-09-94-016-11115

Sequence 11115, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHIGMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL0001307

CURRENT APPLICATION NUMBER: 60/29/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 1115
                                                                                                                                                                      ## SEQUENCE 11, Application US/09565423

## Patent No. 6475987

## GENERAL INFORMATION:

## PAPLICANT: SIN, HONG-Bing

## TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

## TITLE OF INVENTION: METHODS OF USE THEREOF

## TITLE OF INVENTION: METHODS OF USE THEREOF

## TITLE OF INVENTION: METHODS OF USE THEREOF

## CURRENT APPLICATION NUMBER: US/09/565,423

## CURRENT FILING DATE: 2000-05-05

## PRIOR FILING DATE: 1999-05-06

## PRIOR FILING DATE: 1999-05-06

## NUMBER OF SEQ ID NOS: 17

## SEQ ID NO 11

## SEQ ID NO 11
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Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 34; Conservative 0; Mismatches 0;
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CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                CSONEYFDSLLHACI PCOLRCSSNTPPLTCORYC 38
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US-09-565-423-11
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US-09-949-016-11115
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US-09-565-423-11
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US-09-854-864-9
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Sequence 13 Application US/09854864

Pacent No. 6774106

GENERAL INFORMATION:
PAPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLXS/AGP-3, AND TACI
FILE OF INVENTION: BLXS/AGP-3, AND TACI
FILE REFERENCE: A-6868

CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PLING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591
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| Sequence 5, Application US/09854864
| Patent No. 6774106
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: TU, GANG
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-6868
| CURRENT FILING DATE: 2001-09-11
| PRIOR FILING DATE: 2000-05-12
| PRIOR PLING DATE: 2000-06-12
| PRIOR FILING DATE: 2000-06-27
| NUMBER OF SEQ ID NOS: 31
| SEQ ID NO S: 31
| LENGTH 181
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100.0%; Score 201; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels
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                                                                                   DB 2; Length 58;
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                                                                             100.0%; Score 201; DB 2; 100.0%; Pred. No. 5e-17; iive 0; Mismatches 0
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Matches 34; Conservative
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; ORGANISM: Homo sapiens
US-09-854-864-21
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; ORGANISM: Consensus
US-09-854-864-13
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US-09-854-864-13
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US-09-854-864-5
                                                                                      Query Match
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Sequence 10, Application US/09854864

Sequence 10, Application US/09854864

Sequence 10, Application US/09854864

Sequence 10. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REPERBNER: A-6868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR RILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 10

LENGTH: 281
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APPLICANT: THEILL, LARS EYDE
APPLICANT: TY, GANG
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE. REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
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70.6%; Pred. No. 1.1e-08;
tive 2; Mismatches 6
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    CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR RELING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 11
LEMOTH: 185
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Patent No. 6774106
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Best Local Similarity 70.64
Matches 24; Conservative
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Best Local Similarity 70.6%
Matches 24; Conservative
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US-09-854-864-10
                                                                                                                                                                                                                                                           , ORGANISM: Murine
US-09-854-864-11
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US-09-854-864-12
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Sequence 9, Application US/09854864

Patent No. 6774106

GRNERAL INFORMATION:
PAPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: TU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-06-71

PRIOR FILING DATE: 2000-06-77

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 9

LENGTH: 283
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Batent No. 6774106.

GENERAL INFORMATION:

APPLICANT: THEIL, LARS EYDE

APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B
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Sequence 17, Application US/09565423

Patent No. 6475987

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPERENCE: 2879-72

CURRENT APPLICATION NUMBER: US/09/565,423

CURRENT FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-01

PRIOR PILING DATE: 1999-05-06

PRIOR FILING DATE: 1999-05-06
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Pred. No. 7.6e-09;
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-09-565-423-17
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Sequence 6, Application US/08810572A

Patent No. 5963102

GENERAL INFORMATION:

APPLICANT: Brain, Richard J.

AITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th
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                                                   Gaps
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Query Match 33.1%; Score 66.5; DB 2; Length 67; Best Local Similarity 32.4%; Pred. No. 0.48; Matches 11; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elam PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 23-6
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 1340-1-007
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Patent No. 6774106

General No. 6774106

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: THE LO. INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTHARE: Patentin version 3.1

SEQ ID NO 20

LENTH: 59
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| Sequence 16, Application US/09854864
| Patent No. 6774106
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: TY, GANG
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-6868
| CURRENT APPLICATION NUMBER: US/09/854,864
| CURRENT FILING DATE: 2001-09-11
| PRIOR APPLICATION NUMBER: US 60/204,039
| PRIOR APPLICATION NUMBER: US 60/214,591
| PRIOR PELING DATE: 2000-06-27
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 16
| LENTH: 67
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                                                                                                                                                                     46.5%; Score 93.5; DB 2; Length 117; 69.7%; Pred. No. 0.00052; tive 1; Mismatches 2; Indels 7
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1. Similarity 32.4%; Pred. No. 0.42;
11; Conservative 8; Mismatches 14;
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                                                                                                                                                                                                                                                                  2 SONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                  2 AQCEYFDSLLHAC-PC-LRCS----PPTCQ-YC 27
                                                                                                 ORGANISM: human-murine Consensus
    SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 117
                                                                                                                                                    Query Match
Best Local Similarity 69.7*
...ches 23; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-854-864-16
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US-09-854-864-20
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                                                                             TYPE: PRT
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 15
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            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: Unknown>
PRIOR APPLICATION BATA:

APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELEFAN: 201-487-5800
TELEFAX: 201-487-5800
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Pred. No. 1.1;
8; Mismatches 14;
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33.1%; Score 66.5; Di
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.1%;
Best Local Similarity 32.4%;
Matches 11; Conservative 8
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CRGANISM: Homo sapiens
US-09-854-864-15
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APPLICANT: Bram, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Bsq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                          NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                           COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NOWBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFFCATION: AUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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33.1%; Score 66.5; DB 2;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGNENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                     ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09782857A Patent No. 6500428 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                   CITY: Hackenback
STATE: New Jersey
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                                                                                                                                                                                                                                                      COUNTRY: USA
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ZIP: 07601
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US-09-782-857A-6
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APPLICANT: Bram, Richard J.
APPLICANT: Bram, Gotz
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 293;
COMPUTER READABLE FULL.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

FILING DATE: 12-APP-1999

CLASSIFICATION: AUTHOWN-
ATTORNEY/AGENT INFORMATION:

NAME: JGCKSON EGG., David A.

REFERENCE/DOCKET NUMBER: 1340-1-007 PCT

TELEPHONE: 201-487-5800

TELEPHONE: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 293 amino acids

"TVPE: amino acid

"TVPE: aligle
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 33.1%; Score 66.5; D Local Similarity 32.4%; Pred. No. 2; nee 11; Conservative 8; Mismatches
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APPLICATION NUMBER: 08/810,572
FILING DATE: <UNKNOWN>
ATTORNEY/AGERT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09782857A
Patent No. 6500428
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 10
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STATE: New Jersey
COUNTRY: USA
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Matches
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von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
                                                                  APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: ADDRESSE: David A. Sackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
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SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-FEB-1997

CLASSIFICATION: 536

ATVONEY/AGENT INPORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 26,742

RELEFAX: 201-343-1684

INFORMATION FOR EQ ID NO: 2: SEQUENCE CHARACTERISTICS:

LEMGTH: 293 amino acids

TYPE: amino acid

STRANDEDNESS: single

TYPE: Jinear
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Pred. No. 2;
                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
    Sequence 2, Application US/08810572A Patent No. 5969102 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 32.4%;
Matches 11; Conservative
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STATE: New Jersey
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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JS-09-854-864-14
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APPLICANT: Yu, Guo-Liang, et al.
APPLICANT: Yu, Guo-Liang, et al.
TITIE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P1
CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-13
PRIOR PRIOR DATE: 2000-10-13
PRIOR PRIOR DATE: 2000-10-23
PRIOR PRIOR PRILING DATE: 2000-10-23
PRIOR PRIOR PRILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-06-15
PRIOR PRILING DATE: 1997-03-12
PRIOR PRILING DATE: 1997-03-12
PRIOR PRILING DATE: 1997-03-12
PRIOR PRILING DATE: 1997-03-12
PRIOR PRILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO PRAGMENT TYPE: Noterminal ORIGINAL SOUNCE: ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09879919
Patent No. 6541224
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.44
Matches 11; Conservative
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Best Local Similarity 32.4
Matches 11; Conservative
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, ORGANISM: Homo sapiens
US-09-879-919-22
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-782-857A-2
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RESULT 23

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GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERBNCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 14
LENGTH: 293
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US-09-854-864-18
US-09-854-864-18
Sequence 18, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
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Sequence 4, Application US/09848295;
Sequence 4, Application US/09848295;
Patent No. 6623941
GENERAL INFORMATION:
APPLICANT: Baker, Keven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
TITLE OF INVENTION: Thereon
TITLE OF INVENTION: Thereon
TITLE OF ILING DATE: 2001-05-04
CURRENT APPLICATION NUMBER: 2001-05-04
PRIOR PLING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.1%; Score 66.5; DB 2; Length 293; 32.4%; Pred No. 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAARC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09854864
Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.19
Best Local Similarity 32.49
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.1'
Best Local Similarity 32.4'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-09-848-295-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Gaps
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APPLICANT: Hardy, Daniel M.
APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
APPLICANT: Garbers, David L.
ATTLE OF INVENTION: Species-Specific Egg-Binding Proteins of TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                               DB 2; Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 880;
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                                                                                                                                         9; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flloppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                     Sequence 2834, Application US/10104047
| Patent No. 6943241
| GENERAL INFORMATION:
| APPLICANT HELIX RESEARCH INSTITUTE
| TILE OF INVENTION: No. 6943241e1 full length cDNA
| FILE REFERENCE: H1-ADIOS
| CURRENT APPLICATION NUMBER: US/10/104,047
| CURRENT FILING DATE: 2002-03-25
| PRIOR APPLICATION NUMBER:
| PRIOR FILING DATE:
| NUMBER OF SEQ ID NOS: 4096
| SOFTWARE: PATENTIN Ver. 2.1
| SEQ ID NO 2814
                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQL------RCSSNT 25
                                                                                                                                                                                       --RCSSNT 25
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                                                                                          29.6%; Score 59.5; D
28.9%; Pred. No. 26;
tive 5; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
                                                                                                                                                                                       1 CSQNEYFDSLLHACIPCQL----
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Best Local Similarity 28.9°
Matches 11; Conservative
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-2834
  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2804
                                                                       Query Match
Best Local Similarity
.....hes 11; Conservat
                                                                                                                                                                                                                                                                                                                              US-10-104-047-2834
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| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                            Query Match 33.1%; Score 66.5; DB 2; Length 397; Best Local Similarity 32.4%; Pred. No. 2.7; Matches 11; Conservative 8; Mismatches 14; Indels
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US-10-104-047-2804
US-10-104-047-2804
US-10-104-047-2804
; Sequence 2804, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; TITLE OF INVENTION: No. 6943241e1 full length cDNA; FILE REFERENCE: H1-04105
; CURENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; RIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2804
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESELSEQ for Windows Version 4.0
SEQ ID NO 9626
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
FRIOR APPLICATION NUMBER: US 60/204,039
FRIOR FILING DATE: 2000-05-12
FRIOR APPLICATION NUMBER: US 60/214,591
FRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 397
                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-854-864-18
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US-09-949-016-9626
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, ORGANISM: Homo sapiens
US-09-471-276-1590
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US-09-252-991A-25721
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US-09-257-580-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-257-580-2
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; Sequence 1590, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Duclert A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CP1
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER FILING DATE: 1998-04-09
; EARLIER FILING DATE: 1998-04-09
; EARLIER FILING DATE: 1999-04-09
; MUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1590
LENGTH: 98
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                    DB 1; Length 2476;
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Similarity 38.1%; Score 54; DB 2; Length 98;
8; Conservative 4; Mismarches 6 7 7 7
                                                                                                                                                                                                                                                                                                                                                                                                                  AGENCIA 30
US-09-6130
Sequence 6330, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JODERT, S.
APPLICANT: Glordano, J.Y.
TITE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPRENCE: GENEET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILIG DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
LENGTH: 98
LENGTH: 98
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Pred. No. 2.7e+02;
8; Mismatches 14;
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TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
                                                                                                                                                                                                                                  Query Match 27.9%;
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-09-621-976-6330
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Best Local Similarity
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; Sequence 25721, Application US/09252991A
; Sequence 25721, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REPRENCE: 10796.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25721
; LENGTH: 431
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  Length 98
Query Match 26.9%; Score 54; DB 2; Best Local Similarity 38.1%; Pred. No. 21; Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yorkehire Cancer Research
TITLE OF INVENTION: Tumour Suppressor Gene
FILE REPERENCE: Canine p53
CURRENT APPLICATION NUMBER: US/09/257,580
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 9804178.3
PRIOR FILING DATE: 1998-02-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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48.3%; Pred. No. 89;
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                                                                                                         14 CIPCOLRCSSNTPPLTCORYC 34
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Patent No. 6307036
GENERAL INFORMATION:
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Best Local Similarity 48.3<sup>3</sup>
Matches 14; Conservative
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Sequence 2, Application US/09848295

Sequence 2, Application US/09848295

Patent No. 6623941

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

TITLE OF INVENTION: Thereon

TITLE OF INVENTION: Thereon

TITLE OF INVENTION: Thereon

FILE REFERENCE: PF5.7

CURRENT PILING DATE: 2001-05-04

PRIOR PILICATION NUMBER: 60/202,193

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2.
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26.1%; Score 52.5; DB 2; Length 142;
Best Local Similarity 29.4%; Pred. No. 45;
Matches 10; Conservative 8; Mismatches 15; Indels
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US-09-930-933A-65

Sequence 65, Application US/09950933A

Setent No. 6875907

GENERAL INFORMATION:

APPLICANT: Simmons. Carl R.

APPLICANT: Simmons. Carl R.

TITLE OF INVENTION: Use

FILE REPERENCE: 35718/238472

CURRENT APPLICATION NUMBER: US/09/950,933A

CURRENT PILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: 60/232,569

PRIOR PILING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FREUSEQ for Windows Version 4.0

FRINGEN NOS: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 115;
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Best Local Similarity 44.4%; Pred. No. 30; Matches 8; Conservative 4; Mismatches
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US-09-877-730-26
; Sequence 26, Application US/09877730
                                                                                             53 CKTRCSAHSRPNVCNRAC 70
                                                               17 CQLRCSSNTPPLTCQRYC 34
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-848-295-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-950-933A-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Navarro, Pedro;
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Use
FILE REPERENCE: 3518/238472
CURRENT APPLICATION NUMBER: US/09/950,933A
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/232,569
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 61
SEQ ID NO 61
SEQ ID NO 61
SEQ ID NO 61
TYPE: PRT
                                                                               GENERAL INFORMATION:
APPLICANT: MORIKAWA, MINORU
APPLICANT: HARDA, NACKI
TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Felease #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2733 CPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSONEYFDSLLHACI-PCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-111
TELEFONE: (703) 205-8000
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61, Application US/09950933A
Patent No. 6975907
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
                                       Sequence 9, Application US/08718388
Patent No. 6271362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5405 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-718-388-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
US-09-950-933A-61
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26.4%; Score 53; DB 2; Length 108;

Query Match

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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Friedrich, Glenn
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ## APPLICANT: Walke, D. Wade
## APPLICANT: Scoville, John
## APPLICANT: Scoville, John
## APPLICANT: Triedrich, Glenn
## APPLICANT: Triedrich, Glenn
## APPLICANT: Triedrich, Glenn
## APPLICANT: Triedrich, Glenn
## APPLICANT: Zembrowicz, Brian
## APPLICANT: Zambrowicz, Brian
## APPLICANT: Zambrowicz, Brian
## APPLICANT: Sands, Arthur T.
## TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
## TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
## PILE REFERENCE: LEX-0189-USA
## CURRENT APPLICATION NUMBER: US/09/877,730
## CURRENT APPLICATION NUMBER: US/09/877,730
## PRIOR APPLICATION NUMBER: US/09/877,730
## PRIOR FILING DATE: 2000-06-09
## PRIOR FILING DATE: 2000-06-09
## NUMBER OF SEQ ID NOS: 31
## SEQ ID NO 16
## SEQ 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 2; I
Pred. No. 2.4e+02;
6; Migmatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.9%; Score 52; DB 2;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 10; Conservative 6; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668 NSFIDAKVLSCGICCISRSSIPPPCVCKMY 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NEYFDSLLHACIPCOLRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 NEYFDSLLHACIPCOLRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09877730; Patent No. 6465632; GENERAL INFORMATION: APPLICANT: Walke, D. Wade; APPLICANT: Scoville, John APPLICANT: Turner, C. Alexander Jr. APPLICANT: Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09877730 Patent No. 6465632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.3%;
Matches 10; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-877-730-16
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JUNEARY: Walke, D. Wade

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Friedrich, Glenn

APPLICANT: Friedrich, Glenn

APPLICANT: Sambrowicz, Brian

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6465632el Human Phosphatages and Polymucleotides Encoding the FILE REPRENCE: LEX-0189-USA

FILE REPRENCE: LEX-0189-USA

CURRENT APPLICATION NUMBER: US 60/210,607

PRIOR APPLICATION NUMBER: US 60/210,607

PRIOR APPLICATION NUMBER: US 60/210,607

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 624
                                                                   APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Friedrich, Glenn
APPLICANT: Friedrich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT APPLICATION NUMBER: US 60/210,607
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.9%; Score 52; DB 2; Length 547; Best Local Similarity 33.3%; Pred. No. 1.9e+02; Matches 10; Conservative 6; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 NEYFDSLLHACIPCQLRCSSNTPPLTCQRY 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09877730 Patent No. 6465622 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: homo sapiens
US-09-877-730-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
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LENGTH: 547
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TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST STREET: TOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,080
FILING DATE:
FLING DATE: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 910562.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION NUMBER: GB 910564.6
FILING DATE: 19-MAR-1991
TELECOMMUTCATION NUMBER: GB 910564.6
FILING DATE: 19-MAR-1991
TELECOMMUTCATION NUMBER: GB 910564.6
FILING DATE: 19-MAR-1991
TELECOMMUTCATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELEFAX: (202) 86.1 300
TELEFAX: (202) 86.2 9044
TELEFAX: (202) 82-0944
TELEFAX: (202) 82-0944
TELEFAX: GATAGATERISTICS:
LENGTH: G3 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1025 NSFIDAKVLSCGICCISRSSIPPPCVCKMY 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 NEYFDSLLHACIPCQLRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN; JOZEF
APPLICANT: VANDERLEYDEN; JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08117080 Patent No. 5482928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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APPLICANT Turner, C. Alexander Jr.
APPLICANT Turner, C. Alexander Jr.
APPLICANT Turner, C. Alexander Jr.
APPLICANT Extedrich, Glenn
APPLICANT Extedrich, Glenn
APPLICANT Sambowicz, Brian
APPLICANT Sambowicz, Brian
APPLICANT Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEx. 0189-USA
CURRENT APPLICATION NUMBER: US 60/210,607
PRIOR PLILNG DATE: 2001-06-08
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SSOTTANEE FASESEQ for Windows Version 4.0
SSO ID NO 12
LENGTH: 991
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465613el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT APPLICATION NUMBER: US 60/817,730
CURRENT APPLICATION NUMBER: US 60/210,607
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR APPLICATION NUMBER: 06.09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.9%; Score 52; DB 2; Length 991; 33.3%; Pred. No. 3.4e+02; tive 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.9%; Score 52; DB 2; I Best Local Similarity 33.3%; Pred. No. 3.1e+02; Matches 10; Conservative 6; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  860 NSFIDAKVLSCGICCISRSSIPPPCVCKMY 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        947 NSFIDAKVLSCGICCISRSSIPPPCVCKMY 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NEYFDSLLHACIPCQLRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 NEYFDSLLHACIPCOLRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/0987730; Patent No. 6465632; GENERAL INFORMATION: APPLICANT: Walke, D. Wade APPLICANT: Scoville, John APPLICANT: Turner, C. Alexander Jr. APPLICANT: Triedrich, Glenn; APPLICANT: Abuin, Alejandro; APPLICANT: Zambrowicz, Brian; APPLICANT: Sands, Arthur T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09877730 Patent No. 6465632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 33.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: homo sapiens
US-09-877-730-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 43
US-09-877-730-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 44
US-09-877-730-2
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APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BEBOLLE, MIGUEL
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES:
ADDRESSER: CUSHWAN DARBY & CUSHWAN
STREET: 1000 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 15DT C. C.W.C.C.MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,142
FILING DATE: 20-AUG-1997
CLASSIFICATION DATA:
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11,080
FILING DATE: 20-DC-1993
APPLICATION NUMBER: PCT/0892/00423
FILING DATE: 10-MAR-1992
PRILING DATE: 10-MAR-1992
PRILING DATE: 11-MAR-1991
PRILING DATE: 11-MAR-1991
PRILING DATE: 11-MAR-1991
PRILING DATE: 11-MAR-1991
PRILING DATE: 19-MAR-1991
PRILING DATE: 19-MAR-1991
TELECOMMUNICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
PRILING DATE: 19-MAR-1991
TELEFHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEFAX: (202) 822-0944
TELEFAX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
24 MIEACIGNGGRCNENVGPPYCCSGFC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         Sequence 12, Application US/08915142
Patent No. 5942663
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-915-142-12
                                                                                                                         US-08-915-142-12
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                                                                                                                                                               Gaps
                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.6%; Score 51.5; DB 1; Length 63; Best Local Similarity 38.5%; Pred. No. 27; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                   Length 63;
                                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST STREET: TOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
STATE: D.C.
COUNTRY: USA
ZIP: 2005-3918

COMPUTER, ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/471,329
FILING DATE: 0.2-UN-1995
CLASSIFICATION NUMBER: US 08/117,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 08/117,080
FILING DATE: 10-MAR-1991
APPLICATION NUMBER: US 08/117,080
FILING DATE: 10-MAR-1991
APPLICATION NUMBER: US 0810568.6
FILING DATE: 11-MAR-1991
FILING DATE: 11-MAR-1991
APPLICATION NUMBER: US 0810568.6
FILING DATE: 11-MAR-1991
APPLICATION UMBER: US 0810568.6
APPLICATION UMBER: US 0810568.6
APPLICATION UMBER: US 0810568.
; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-117-080-12
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                                                                                                   DB 1;
                                                                                               Score 51.5; DE; Pred. No. 27; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN:
STREFT:
                                                                                                                                                                                                                            10 LLHACIPCQLRCSSNT-PPLTCQRYC 34
                                                                                                                                                                                                                                                                   24 MIEACIGNGGRCNENVGPPYCCSGFC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08471329
Patent No. 5689048
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
                                                                                               Ouery Match 25.6%;
Best Local Similarity 38.5%;
Matches 10; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-471-329-12
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   DB 1, Length 63;
                                        Indels
                                        11;
Query Match
25.6%; Score 51.5; 1
Best Local Similarity 38.5%; Pred. No. 27;
Matches 10; Conservative 4; Mismatches
                                        4; Mismatches
                                                                                                         24 MIEACIGNGGRCNENVGPPYCCSGFC 49
                                                                           10 LLHACIPCQLRCSSNT-PPLTCQRYC 34
                                                                                                                                                                                        US-08-465-380-4
; Sequence 4, Application US/08465380
; Patent No. 5863894
                                                                                                                                                                           RESULT 48
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10 LLHACIPCOLRCSSNT-PPLTCORYC 34

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Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.6%; Score 51.5; DB 1; Length 77; 29.3%; Pred. No. 33; tive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 CGENEWLDD-----GTTQKPCEAKCNEEPPEEEDPICKSKGC 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: GEORGE P. VLASUK, PATRICK ERIC
APPLICANT: HUGO STANSSENS; JORIS HILDA
APPLICANT: HUGO STANSSENS; MARC JOZEF
APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
APPLICANT: LAUWERY STEPHANE JESPERS; and
APPLICANT: LAUMEN STEPHANE JESPERS; and
APPLICANT: GANSEMANS
ITILE OF INVENTION: NEWATODE-EXTRACTED ANTI-
TITLE OF INVENTION: COAGULANT PROTEIN
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: SJA West FITCH Street
STREET: SLATE 4700
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 5.5" Diskette, 1.44 Mb MEDIUM TYPE: 5.5" Diskette, 1.44 Mb MEDIUM TYPE: 5.5" OOPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: MORD PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380 FILING DATE: June 5, 1995
CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTONNEY, ADENT INFORMATION:
NAME: BIGGS, SUZAMNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELECOMMUNICATION TOWN ADDITION:
TELEPHONE: (213) 489-1600
TELECOMMUNICATION TOWN ADDITION:
TELEPHONE: (213) 489-1600
TELECOMMUNICATION TOWN ADDITION:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/08480478 Patent No. 5864009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.34
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE:
                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/08465380

Patent No. 5863894

GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF SEQUENCES: 356
CORRESPONDENES: 356
CORRESPONDENES ADDRESS:
ADDRESSEE: LYON & LYON
                   APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTEIN
WUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATIOS SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acids
TYPE: maino acids
TYPE: mino acids
                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide ORIGINAL SOURCE:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 49
US-08-465-380-40
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                                                                                                                                                                                                                                                                                                                                                                                      25.6%; Score 51.5; DB 1; Length 77; 29.3%; Pred. No. 33; trive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yean R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATOBE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TIPE: BUCHGABE
COMPUTER: IBM Compacible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOR'D Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CILASSIFICATION ADATA:
APPLICATION NUMBER: 08/326,110
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
ATTONNEY/AGENT INPORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 313/269
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Ancyclostoma caninum US-08-486-397-40
                                                                                                                                                                                                                                                                                         ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/08486397
Patent No. 5866542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INPORMATION FOR EEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYBE: amino acids
TYBE: amino acids
TYPE: yellogy
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                             INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.34
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
   67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
TELEX: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 52
US-08-486-397-40
                                                                                                                                                                                                                                                                                                                          US-08-486-397-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.6%; Score 51.5; DB 1; Length 77; Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Laroche, Laurent S. Jespers, APPLICANT: Yees R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 357 CORRESPONDENCE ADDRESSES: ADDRESSEE: Lyon & Lyon STREET: G.J. West Fifth Street STREET: Suite 4700 CITY: Los Angeles STREE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
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SOFTWARE: FABLEEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE I.
REGISTRATION NUMBER: 30,158
REFERNEK/POCKET NUMBER: 30,158
REFERNEK/POCKET NUMBER: 208/290
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARATERICES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08486397
Patent No. S866542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-480-478-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-486-397-4
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Query Match 25.6%; Score 51.5; DB 1; Length 77; Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                     APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yors R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT
TITLE OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
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TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
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Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 31,159
REFERENCE/DOCKET NUMBER: 213/270
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     90071
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US-08-461-965-4
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                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Lancens, Marc J. Lauwereys,
APPLICANT: Voes R. Laroche, Laurent S. Jespers,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Perex W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                            1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                         6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CGENEWLDD-----CGTOKPCEAKCNEEPPEEEDPICRSRGC 42
                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.6%; Score 51.5; D
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches
     Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: Storage
COMPUTER: BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSETECATION TATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 31,270
TELERONMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-486-399-40
; Sequence 40, Application US/08486399
; Patent No. 5866543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                      Sequence 4, Application US/08486399 Patent No. 5866543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
  29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 77 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Best Local Similarity 29.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-486-399-4
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25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
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Sequence 33, Application US/08326110A

Sequence 34, Application US/08326110A

Patent No. 2945275

GENERAL INFORMATION:
APPLICANT: HUGO STANSSENS; DORIS HILDA
APPLICANT: HUGO STANSSENS; DORIS HILDA
APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
APPLICANT: LAUWERT STEPHANE USSPERS; and
APPLICANT: AUNIENT GEORGES JOZEF
APPLICANT: GANSEMANS
TITLE OF INVENTION: COGGULANT PROTEIN
TITLE OF INVENTION: COGGULANT PROTEIN
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: LYON
STREET: SUILE 1700 & LYON
STREET: SUILE 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FREESEN VARIAGON 1.5
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/326,110A
FILING DATE: 18 OCTOBER 1994
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
                                                                                                                                                                                                  210/243
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-461-965-40
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Factor No. 5872098

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOTIS H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Year W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 336
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%; Score 51.5; DB 1; Length 7
29.3%; Pred. No. 33;
tive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSQNEYFDSLLHAC --- IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                          COMPUTER PREADBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IEM COMPATIBLE
COMPUTER: EM COMPATIBLE
COMPUTER: MOTG PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFCATION NUMBER: 08/326,110
APPLICATION NUMBER: 08/326,110
APPLICATION NUMBER: 08/326,110
ATTONEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELECHONE: (213) 489-1600
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.39
Watches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                       Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                       STREET:
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Gaps

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Mensens, Jorie Hilda Lieven
APPLICANT: Mensens, Jorie Hilda Lieven
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon F
STREFT.
                                                                                                                                                                                                                                                                                                                  Query Match 25.6%; Score 51.5; DB 1; Length 7
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CGENEWLDD----CGTOKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSONEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/634,641
FILING DATE: April 19, 1996
RIGH APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/136
TELECOMMUNICATION INFORMATION:
                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-634-641-40
; Sequence 40, Application US/08634641
; Patent No. 5955294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 633 West Fifth Street STREET: 633 West Fifth Street STREET: LOS PARTY.
  (213) 955-0440
                                                                                                          77 amino acids
                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                             TOPOLOGY: line
TELEFAX:
                                                                                                                                                                                                                                                                US-08-634-641-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 59
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                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                         25.6%; Score 51.5; DB 1; Length 77; 29.3%; Pred. No. 33; tive 6; Mismatches 12; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
TITLE OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 4 storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOSTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,641
FILING DATE: April 19, 1996
FILING DATE: October 17, 1995
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/426,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/426,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/426,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/136
TELECHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vlasuk, George P. Vlasuk
Stanssens, Patrick Eric Hugo
Mensens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08634641
Patent No. 5955294
GENERAL INFORMATION:
APPLICANT: Vlasuk, George P. Vla
APPLICANT: Stanssens, Patrick El
APPLICANT: Mensens, Joris Hilda
TELECOMUNICATION INFORMATION:
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                         Query Match 25.6
Best Local Similarity 29.3
Matches 12, Conservative
                                                                                                                                                                                 TYPE: amino acid;
TOPOLOGY: linear
US-08-326-110A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 90071
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US-08-634-641-4
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GENERAL INCORMATION:

APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Measens, Joris Hilds Lieven
APPLICANT: Measens, Joris Hilds Lieven
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Genemans, Yannick Georges Jozef
APPLICANT: Genemans, Yannick Georges Jozef
APPLICANT: Genemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Genemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Genemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Governion: NEMATOBE-EXTRACTED SERINE PROTEIN
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADRESS:
ADDRESSES: Lyon & Lyon
ADDRESSES: Lyon & Lyon
ADDRESSES: Lyon & Lyon
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Galifornia
COUNTRY: U.S.A.
ZIF: 9071
COMPUTER READABLE FORM:
MEDIUM TYPE: Storesege
COMPUTED: THE SECONDERINE FORM:
MEDIUM TYPE: Storesege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/U895/13231
PILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 61
US-09-449-471-40
; Sequence 40, Application US/09249471
; Sequence 10, 604041
                        REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 anino acids
TYPE: amino acids
TOPOLOGY: linear
BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-249-471-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Vlasuk, George Phillip
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Stansens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Gensemans, Yannick Georges Jozef
APPLICANT: Gensemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Nathew
APPLICANT: Moyle, Nathew
APPLICANT: Moyle, NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.6%; Score 51.5; DB 1; Length 77; Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 08/09,455
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 08/09,455
FILING DATE: APPLICATION NUMBER: 08/09/455
FILING DATE: APPLICATION NUMBER: 08/09/455
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FILING DATE: October 17, 1995
FILING DATE: Unne 5,1995
APPLICATION NUMBER: 08/486,397
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            ; ORGANISM: Ancyclostoma caninum US-08-634-641-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 60
US-09-249-471-4
'S Sequence 4, Application US/09249471
', Patent No. 6040441
   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Vlasuk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Georges, Jaurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMADOB-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 25.6%; Score 51.5; D
Local Similarity 29.3%; Pred. No. 33;
He 12; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
ATTONEY/ACENT INFORMATION:
NAME: BIGGS, NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
ITELERAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 7 maino acide
TYPE: amino acide
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/09/249,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-249-472-40
; Sequence 40, Application US/09249472
; Patent No. 6046318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
APPLICATION NUMBER: UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-249-472-4
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APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Stansens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.6%; Score 51.5; DB 2; Length 77; Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIF: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/ACENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 216/270
REEFERNCE/DOCKET NUMBER: 216/270
TELEFHONE: (213) 489-1600
TELEFAK: (213) 955-0440
TELEFK: (7-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09249472
Patent No. 6046318
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Philli
APPLICANT: Stanssens, Patrick Ex
APPLICANT: Messens, Joris Hilda
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-249-471-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 62
US-09-249-472-4
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11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSQNEYFDSLLHAC---IPCOLRCSSNTP----PLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stanseens, Patrick Eric Hugo
APPLICANT: Stanseens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: STOTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                17, 1997
PCT/US95/13231
                APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/1323
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 19,94
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/09249451
Patent No. 6087487
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-249-451-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vlasuk, George Phillip
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Stansens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Mod-Le, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: SEQUENCES: 356
CORRESPONDENCE ADDRESSE: ADDRESSEE: LAURANTION: STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51.5; DB 2; Length 7 Pred. No. 33; 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CGENEWLDD----CGTOKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
RECISTRATION NUMBER: 216/270
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-040
TELEPRAX: (213) 955-040
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,451
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Ancyclostoma caninum
US-09-249-472-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09249451
Patent No. 6087487
GENERAL INFORMATION:
APPLICANT: Vlauk, George Phill:
APPLICANT: Stanssens, Patrick En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.6'
Best Local Similarity 29.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICKSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSQNEYFDSLLHAC --- IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 25.6%; Score 51.5; D
Local Similarity 29.3%; Pred. No. 33;
nes 12; Conservative 6; Mismatches
            MEDLUM TYPE: storage
COMUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,455
FILING DATE: APALI 17, 1997
PRICH APPLICATION NUMBER: OS/486,399
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEYAGENT INRORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 316/270
TELLEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-809-455-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.6%; Score 51.5; DB 2; Length 77; Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stansene, Patrick Eric Hugo
APPLICANT: Annesene, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jacoche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganeemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE STREATED STRINE PROTEIN
TITLE OF INVENTION: NEMATORES AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSONEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
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1: Stanssens, Patrick Eric Hugo
1: Messens, Joris Hilda Lieven
1: Lauwereys, Marc Josef
1: Laroche, Yves Rene
1: Jespers, Laurent Stephane
1: Gansemans, Yannick Georges Jozef
2: Moyle, Matthew
                                                                       PRING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRESENTING DATE:
PRILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486, 399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465, 380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465, 380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465, 380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326, 110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326, 110
FILING DATE: June 5, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30, 158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OCCUPATION:
TELECOMMUNICATION OCCUPATION OCCUPATION
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Galifornia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Ancyclostoma caninum US-09-249-451-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08809455
Patent No. 6090916
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phill:
Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6%; Score 51.5; DB 2; Length 7 Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHAC---IPCOLRCSSNTP----PLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                      COMPOTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE: APILIT, 1997
APPLICATION NUMBER: 08/809,455
FILING DATE: OCCODER 17, 1997
APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: 08/46,399
FILING DATE: OCCODER 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Ancyclostoma caninum US-09-249-461-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-249-461-40
; Sequence 40, Application US/09249461
; Patent No. 6096877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 77 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.6%; Score 51.5; DB 2; Length 77; Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gasemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
COMPUTER: SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,455
FILING DATE: April 17, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELECHOMENE CHARACTERISTICS:
LENGTH: 77 amino acids
TELENCE: amino acids
TELENCE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-249-461-4; Sequence 4, Application US/09249461; Patent No. 6096877; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                       TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
MUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.6%; Score 51.5; D
29.3%; Pred. No. 33;
tive 6; Mismatches
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Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US95/13231
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Jespers, Laurent Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRILING DATE:
PRIOR APPLICATION NUMBER: 08/09/455
PRILING DATE: APPLICATION NUMBER: 08/09/455
PILING DATE: APPLICATION NUMBER: 07/0895/1323
PILING DATE: October 17, 1995
PILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
PILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATONNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-249-448-40
; Sequence 40, Application US/09249448
; Sequence 40, Application US/09249448
; Patent No. 6121435
; GENERAL INFORMATION:
APPLICANT: Stansens, Patrick Eric APPLICANT: Lauwercys, Marc Josef APPLICANT: Lauwercys, Marc Josef APPLICANT: Laroche, Yves Rene APPLICANT: Jespers, Laurent Stephan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30,158
ER: 216/270
                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 216/;
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.6
Best Local Similarity 29.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-249-448-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.6%; Score 51.5; DB 2; Length 77; Best Local Similarity 29.3%; Pred. No. 33; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
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Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE: World Perfect 5.1
APPLICATION NUMBER: 08/809,455
FILING DATE: 06/809,455
FILING DATE: 06/809,455
FILING DATE: 06/801,17,1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/466,397
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5,1995
APPLICATION NUMBER: 216/270
FILING DATE: June 5,1995
APPLICATION NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELETAX: 67-3510
TELETAX: 67-3510
TELETAX: 67-3510
TELETAX: 67-3510
TELETAX: 07-3510
TELE
Li Lyon & Lyon Careet Lie 633 West Fifth Street Lies Angles STATE: California COUNTRY: U.S.A.
ZIP: 90071

"OMPUTER READ"

"APPTORE TEAD"
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Patent No. 6121435
GENERAL INPORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric
APPLICANT: Lawereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stepha
APPLICANT: Gensemans, Yannick Geor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Ancyclostoma caninum US-09-249-461-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Moyle, M. APPLICANT: Bergum, J. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 70
US-09-249-448-4
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25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels
                  APPLICANT: Lawerey, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Gengeman, Yannick Georges Jozef
APPLICANT: Gengeman, Yannick Georges Jozef
APPLICANT: MOYLe, Matthew
APPLICANT: MOYLE, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE CANTESPONDENCE ADDRESSE: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: John & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPACTION
SOFTWARE: WORD PEFFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION TOTAE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PELICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: APPLI 17, 1995
APPLICATION NUMBER: PCT/U895/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: Coctober 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFEROCHMONICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
       Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 73
US-09-249-473-40
; Sequence 40, Application US/09249473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IELEFAX: (213) 489-1600
TELEX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amin 77 amin 179F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
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APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
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APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA
PRIOR APPLICATION DATA
PRIOR APPLICATION DATA
PRIOR APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 316/270
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Ancyclostoma caninum US-09-249-448-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-249-473-4; Sequence 4, Application US/09249473; Patent No. 6534629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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25.6%; Score 51.5; DB 2; Length 77;
29.3%; Pred. No. 33;
.ive 6; Mismatches 12; Indels 11; Gaps
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IITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                  Stanssens, Patrick Bric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-Feb-200

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/USS5/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/361,110
FILING DATE: October 18, 1994
ATTORNEY/ASEMT INCREMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di8kette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 Weet Fifth Street
Suite 4700
                                                           US-09-498-556-4
Sequence 4, Application US/09498556
Patent No. 6872808
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-16(
TELEFAX: (213) 955-0440
TELEX: 67-3510
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LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4:
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STATE: California
COUNTRY: U.S.A.
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Best Local Similarity 29.3
Matches 12; Conservative
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                                                                                       APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
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                                                       Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,473
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
PRILING DATE:
PREPIREATION NUMBER:
PRILING DATE:
PREPIREATION NUMBER:
PRILING DATE:
PREPIREATION NUMBER:
PREPIRENCE/DOCKET NUMBER:
PREPIRENCE/DATENTION
PREPIRENCE/DOCKET NUMBER:
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ORGINAL SOURCE:
CRGANISM: Ancyclostoma caninum
US-09-249-473-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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TOPOLOGY: linear
Patent No. 6534629
GENERAL INFORMATION:
APPLICANT: Vlasuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
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FRACER NO. 6812800

GENERAL INCHARACTER ALC GEOGE PHILID

FRACER NO. 6812800

GENERAL INCHARACTER ALC GEOGE PHILID

FRACER NO. 6812800

GENERAL INCHARACTER ALC FROM EAST FROM EA
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yre version 5.1.6 193 - 2005 Compugen Ltd. y sw model 15:43:09 ; Search time 106.4 Seconds (without alignments) 140.403 Million cell updates/sec	-10-077-137-1_COPY_8_41 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34 ASUM62 ipop 10.0 , Gapext 0.5 43163 seqs, 439378781 residues ts satisfying chosen parameters: 2443163 gth: 0 igth: 0 igth: 2000000000 igth: 2000000000 istimum Match 04 instimum Match 1004 isting first 300 summaries	s:* s:* s:* s:* s:* bs:* results predicted by chance to have a results proceed by chance to have a 1 to the score of the result being printed, of the total score distribution. SUMMARIES ID	AAB15486 Aae15486 Human B-C ADA43366 Ada49366 Human BCM ADZ67761 Human BCM AADZ67761 Human BCM AADZ67761 Human BCM AAE12485 Human B-C AEC02032 Amino aci AAE11484 Aae15501 Human B C AAE11484 AAA00843 Amino aci AAX1484 AAA001 A human B C AAX11484 AAX199 AA001 A human B C AAX11799 AAS0698 Human BCM AAX71979 AAS06698 Human BCM AAX11799 AAE00506 Human BCM AAB1487 AAE00506 Human BCM AAB26698 Aae00506 Human BCM AAE28461 AAE28461 AAE3611 Human BCM AAE28461 AAE3616 Human BCM AAE28461 AAE3616 Human BCM AAE3616 AAE3616 Human BCM AAE3616 AAE3616 Human GCN AAE3616 AAE3616 Human GCN AAB16161 AAE3616 Human GCN AAB16162 AAE3616 Human GCN AAB16161 AAE3616 Human GCN AAB16161 AAE3616 Human GCN AAB16161 AAE3616 Human CON AAB161717 AMINO aci AAB661527 AUMAN LWM AB661527 AUMAN LWM AAC661727 AAE3616 Human BCC AAC661727 AAE3616 HUMAN AAC661727 HUMAN
GenCore Copyright (c) 1993 OM protein - protein search, using sw Run on: December 21, 2005, 15	Title: Perfect score: 201 Sequence: 1 CSQNEYFDSLLHACIPCQI Scoring table: BLOSUM62 Gapop 10.0, Gapext C Gapop 10.0, Gapext C Total number of hits satisfying chose Minimum DB seq length: 200000000 Maximum DB seq length: 2000000000 POSEL-processing: Minimum Match 0% Listing first 300 su	Database: A_Geneseq_21:* 1: geneseq_1980s:* 2: geneseq_1990s:* 3: geneseq_2000s:* 4: geneseq_2000s:* 5: geneseq_2001s:* 7: geneseq_2003as:* 7: geneseq_2003as:* 8: geneseq_2003as:* 9: geneseq_2004s:* 9: geneseq_2004s:* 9: geneseq_2004s:* and is derived by analysis of t. Result No. Score Match Length DB ID	2 201 100.0 34 5 5 201 100.0 34 6 3 201 100.0 34 6 5 201 100.0 40 6 5 2 9 5 6 201 100.0 6 52 9 6 201 100.0 6 52 9 6 201 100.0 184 3 3 201 100.0 184 4 4 112 201 100.0 184 4 4 113 201 100.0 184 4 4 114 201 100.0 184 6 118 201 100.0 184 6 5 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 100.0 184 6 201 201 201 201 201 201 201 201 201 201

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				AMEACASE AMEACASE ABGO76975 ABGO76976 ABM84359 AMM84359 AMM84357 AMM84357 AMM84357 AMM84357 AMM84357 AMM84357 AMM84357 AMM84357 AMM84357 AMM84354 AMM84354 AMM84354 AMM84444 AMM844444 AMM8444444 AMM84444444444
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6.5 33.1 293 7 ADF7737 6.5 33.1 293 7 ABB574 6.5 33.1 293 8 ADS7075 6.5 33.1 293 8 ADS7075 6.5 33.1 293 8 ADS7217 6.5 33.1 293 8 ADV3217 6.5 33.1 293 8 ADQ9444 6.5 33.1 293 9 ADQ9444 6.5 33.1 294 8 ADQ9444	6.5 33.1 294 9 ADW0344 6.5 33.1 312 5 AAO1413 6.5 33.1 334 5 AAO1413 6.5 33.1 348 6 AAE3522 6.5 33.1 348 6 AAE3522 6.5 33.1 357 6 AAE3522 6.5 33.1 357 6 AAE3522 6.5 33.1 366 5 AAO1413 6.5 33.1 397 5 AAE352 6.5 33.1 397 6 AAE352 6.5 33.1 397 6 AAE352 6.5 33.1 397 6 AAE352 6.5 33.1 398 8 ADR1891 61 30.3 1887 6 ABU2211	61 30.3 1887 7 ADM2932 5. 29.6 138 4 ABB7595 5. 29.6 418 5 ABB0623 5. 29.6 418 5 ABB0623 5. 29.6 581 7 ADB64625 5. 29.6 735 5 AAG6825 5. 29.6 845 5 AAG6825 5. 29.6 845 6 ABU209 5. 29.6 845 6 ABU209 5. 29.6 845 6 ABU209 5. 29.6 845 6 ABG6880 5. 29.6 845 6 ABG6880 5. 29.6 845 7 ADB6468 6.5 29.6 897 4 AAG6888 6.5 29.6 897 4 AAG6888	29.6 897 7 ADE0785 29.6 897 7 ADE0894 5.5 29.6 914 8 AAE2993 5.5 29.6 974 7 AAE380 5.5 29.6 974 7 AAE380 5.5 29.6 985 7 ADM0418 5.5 29.6 991 6 AAC2030 5.5 29.6 993 8 ADI2763 6.5 29.6 993 8 ADI2763	8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9
	<i>•••••••••••••••••••••••••••••••••••••</i>			1533 5 1155 4 1155 4 1155 4 1155 4 1155 6 11

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Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 10A; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA49366 standard; peptide; 34
                                                                                                                                                                                                  12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                                                                                                                                                                             14-MAY-2001; 2001WO-US015567.
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                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                             Yu G;
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                                                                                                                            WO200187979-A2.
                                                                                                      Homo sapiens.
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Aac22254
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Adx88417
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Abb62442
Abb62442
Abu10466
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Adj92151
Adn22513
Abp34972
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Ade29295
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AAB15298
ADY37282
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ABU10461
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AAY30383
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AAO13678
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AAO21310
ADX88417
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1142
1422
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166
       AAE15486;
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a precisic binding partner for APRLL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA actracellular consensus sequence, bur not the extracellular region of TACI and/or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, astrointestinal, pancreatic or prostate tumour. APRLL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, acopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn s disease, colitis), sclerodermi, autoimmune disease (mittiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infilitation of the skin or organs. The present sequence with a protozoal and viral infections from the present sequence or the sequence of the standard and the standard and the sequence or the sequence o
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100.0%; Pred. No. 2.8e-18;
iive 0; Mismatches 0;
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ID ADA4
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AC ADA4
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DT 20-N
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DE Huma
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Human; transmembrane activator and intracellular CAML interactor; TACI; Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

(first entry)

12-MAR-2002

Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;

Human tumor necrosis factor receptor BCMA Cys-rich domain.

14-JUL-2005 (first entry)

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Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
                    antiarthritic; dermanological; antidiabetic; neuroprotective; antiarthritic; dermanological; antidiabetic; neuroprotective; antipyretic; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; myasthaenia gravis; Grave's disease; autoimmune themolytic anaemia; autoimmune thrombocytopenic purpura; Goodpasture's syndrome; pempligus vulgaris; acute theumatic fever; post etreptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
           antagonist; immunosuppressive; antirheumatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                      CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 616, 618pp, English.
                                                                                                                                                                                                                                                                                                                                    (NAJE-) NAT JEWISH MEDICAL & RES
                                                                                                                                                                                                                                                                                                                                                                Xu L;
                                                                                                                                                                                                                                                                 24-OCT-2001; 2001US-0345106P.
14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
                                                                                                                                                                                                                                        24-OCT-2002; 2002WO-US034376.
                                                                                                                                                                                                                                                                                                          2002US-0403364P
                                                                                                                                                                                                                                                                                                                                                               Shu H, Liu Y,
                                                                                                                                 cysteine rich domain
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                                                                                                                                                                                   WO2003035846-A2
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                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                          13-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                               Zhang G,
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New tumor necrosis factor receptor (TNFR) polypeptides, useful as detecting ligands, and for modulating tumor growth, metastasis and immunity, such as separating resting from stimulated immune cells.

Disclosure; SEQ ID NO 9; 132pp; English.

Sheppard PO, Dillon SR

16-OCT-2003; 2003US-0511698P. 18-OCT-2004; 2004US-0619552P. 18-OCT-2004; 2004WO-US034375

WO2005037865-A2

28-APR-2005

Homo sapiens.

cytostatic

(ZYMO) ZYMOGENETICS INC.

Fox BA, Holloway JL, WPI; 2005-315682/32

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The invention provides novel tumor necrosis factor receptor zinfild polynuclectides ADZ67753 and polypeptides ADZ67754, expression vectors and antibodies. Zinfild polynuclectides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant zinfild polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Zinfild polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastasis, and immunity such as separating resting from stimulated immune cells. The present sequence is that of the Cysrzich domain of human TUNE BUMA ADZ67760. This sequence was compared with that of zinfild in the identification of zinfild as a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEO ID NO:2, or amino acids 134-285 of SEO ID NO:2, by at least one modification in the region connecting &bgr; strands or and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antitheumatic, antithialmancory, antiathritic, dermatological, antidiabetic, neuroprotective, antiathyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal. TC is useful for inhibiting TALL-1 chickles are remmatorid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, Grave's disease, autoimmune hemolytic anaemia, autoimmune thromatoric purpura, Goodpasture's syndrome, pemphigus vulgaris, cutte rheumatic fever, post-serreptococcal glomerulonephritis and coldmann (CRD) module of human BCMA.
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100.0%; Pred. No. 2.8e-18;
iive 0; Mismatches 0;
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Best Local Similarity
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ADZ67761 standard; protein; 40 AA

Matches

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ADZ67761

RESULT 3
ADZ67761
ID ADZ6
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AC ADZ6

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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                     Human B-cell maturation (BCMA) protein extracellular domain.
  Length 40;
                                        Indels
100.0%; Score 201; DB 9; 100.0%; Pred. No. 3.3e-18;
                                                                                                       CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 36
                                                                               1 CSONEYPDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                        Mismatches
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                                                                                                                                                                                                                               AAE15485 standard; peptide; 51
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                     Local Similarity 100.
1es 34; Conservative
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Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; pooriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCWA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple sclerows; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence
                                                                                                                                                                                                                                                                                                     New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human B cell maturation protein cysteine rich extracellular region.
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; Pred. No. 4.3e-18;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 21; 140pp; English
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27-JUN-2000; 2000US-021459IP.
14-MAY-2001; 2001US-00214591.
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                                                                                    04-AUG-2004; 2004WO-US025247
                                                                                                                              29-JAN-2004; 2004US-0540271P.
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                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                        Patel D;
                                                                                                                                                                                                                                                                  WPI; 2005-555932/56.
WO2005075511-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
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                                            18-AUG-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 10A; 94pp; English.
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27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                                                                                                                                                           14-MAY-2001; 2001WO-US015567.
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Best Local Similarity 100.
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                              Homo sapiens
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WO200187979-A2.
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                                                                                                                                                                                                                                                                                                          The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a pecific binding partner for APRIL (G70, a tumour necrosis factor-INF family ligand), having the consensus region of TACI, BCMA, or the TACI GMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA, in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointesitnal, pancreatic or prostate tumour. ARRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumarcid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region
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                                                                                                                                           Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
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100.0%; Pred. No. 4.8e-18;
iive 0; Mismatches 0;
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  (AMGE-) AMGEN INC.
                                                 Yu G;
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Region
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRLL (GTO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA extracellular region of TACI activity of the TACI/ BCMA. The method is useful for inhibiting activity of TACI and/or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in amammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatities, respiratory allergic disease (asthma, hypersensitivity ung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, thematoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
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Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
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100.0%; Pred. No. 1.5e-17;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                   Disclosure; Fig 10A; 94pp; English
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Matches 34; Conservative
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The present sequence represents a BCWA (not defined) polypeptide. BCWA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCWA activity (and thus NF-kB activity compounds which modulate BCMA activity dand thus NF-kB activity. The specification describes a method of identifying a lorease gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for indentifying polypeptides which increase or decrease gene expression from a pramaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthitis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane activator and CAML-interactor; tumour necrosis factor; rNF; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; mysthemia gravis; multiple sclerosis; rheumatoid arthritis; asthms, bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropath; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
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                                                                                                                                                                                                                                                                               Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
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                                                                                                                                 99US-0121485P.
                                                                                             24-FEB-2000; 2000WO-US004925
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Best Local Similarity
                                                                                                                                                                                                                                                WPI; 2000-558405/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 184 AA;
                                                                                                                                                                                                            Seed B, Ting A;
                  WO200050633-A1
                                                                                                                                   24-FEB-1999;
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                                                      31-AUG-2000
                                                                                                                                                                                                                                                                                                                                               expression.
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Homo sapiens

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The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAMI-interactor (TACI) receptor. Traci is a tumour necrosis factor (TARI) receptor. The extracellular domains of BR43x2 (an isoform of TACI). TACI or BCMA (a related B cell protein) receptor contain a cysteline rich domain, and are used for protein receptor contain a cysteline rich domain, and are used for inhibiting ztiff a activity. Ztiff is a TYR ligand. They may also be used for inhibiting stiff a cities a BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The ztiff a cities activity and Stax2, TACI or BCMA receptor-ligand engagement is associated with cashma, bronchitis, emphysems, enghysems, nephritis, nephritis, pyelonephritis, renal complasms, multiple myelomas, lymphomas, light chain neuropathy, amplement of any production, graft versus host disease, inflammation, insulin dependent rejection, graft versus host disease, inflammation, insulin dependent conference smellitus, Crohn's disease, joint pain, swelling, and engage conference agonists or antagonists can be used to treat hypertension, renal artery constants, or ceptic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, stenosis, or occlusion, and cholesterol or renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, TNF, tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACL; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                      Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 201; DB 3;
100.0%; Pred. No. 1.5e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 152; 175pp; English
                                                                                                                                                                                                                       Yee DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE09241 standard; protein; 184 AA
                                                                                                 07-JAN-2000; 2000WO-US000396
                                                                                                                                          99US-00226533
                                                                                                                                                                                                                       Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                              WPI; 2000-452538/39.
N-PSDB; AAA58559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BCMA protein.
                                                                                                                                                                                                                          Gross JA, Xu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 184 AA;
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               WO200040716-A2
                                                                                                                                          07-JAN-1999;
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                                                          13-JUL-2000
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99US-0132892P

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present invention relates to Tumour necrosis factor (TNF) and ApoL-
                                                                                                                                                                                                                                 Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
                                                                                                                                                                                                                                                                                                             Claim 37; Page 104-105; 112pp; English.
                                                                                                          (NAJE-) NAT JEWISH MEDICAL & RES CENT.
                 05-MAY-2000; 2000WO-US012266.
                                                                    01-MAY-2000; 2000US-0201012P
                                                                                                                                                                                WPI; 2001-016094/02.
                                                                                                                                                                                                   N-PSDB; AAD02125
                                                     06-MAY-1999;
                                                                                                                                              Shu HS
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                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or between APRIL and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, architis, multiple solon and autocimmune diseases e.g. rheumatoid arthitis, multiple solerosis, psoriasis and lupus erythematosus. The present sequence is human BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; hamemolytic ansemia; Grave's disease; mysathenia gravis; chromosome 16; post-streptococcal glomerulonephitis; polyarteritis nodosa; BCWA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                                               Grewal I, Kim KJ, Marsters SA, Pitti RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                       Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 201; DB 4; 100.0%; Pred. No. 1.5e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       maturation factor (BCMA) protein.

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    /label= Extracellular_domain

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY71979 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 2; 160pp; English
                                    28-NOV-2000; 2000WO-US032378
                                                                    16-FEB-2000; 2000US-0182938P
22-AUG-2000; 2000US-0226986P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2001 (first entry)
                                                                                                                                                               Ashkenazi AJ, Dodge KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
Les 34, Conservative
                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                    WPI; 2001-541628/60.
                                                                                                                                                                                                                                     N-PSDB; AAD15902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184 AA;
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23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The present invention retails actor (1781). Incleic acid molecules, crime present invention in the present invention in proteins (including homologues), and their antibodies. The invention in particular relates to methods for regularing the interaction between Table of particular relates to methods for regularing the interaction between Table of regulare monocyte, macrophage and B lymphocyte mediated immune responses. Table 1 protein is useful for identifying compounds that regulare B components is useful for identifying compounds that regulare B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus crythematosus (SLE), insulin dependent diabetes mellitus, multiple solerosis, mysathenia gravis, Grave's disease, autoimmune haemolytic anemaia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The Table 1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a human B cell maturation factor (BCMA) protein. The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for Table 1 protein. BCMA gene is located on chromosome CC in tis usecle, heart, lung, kidney, pancreas, testis and placenta. BCMA mann in the pro-B lymphocyte stage but its expression increases with B lymphocyte maturation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 1.5e-17;
cive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB60698 standard; protein; 184 AA
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Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 184 AA;
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RESULT 14
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EXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the as BCMA) protein, or a BAFF-R fusion protein as an agent for the creatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory capent, and also plays a role in the development of hypertension and containing it, and BAFF-R. Specific antibodies can be used for inhibiting B-cell growth, dendritic call-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. The BAFF-R proteins may also condition, and in the treatment of immunosuppressive disorders and HIV conteins or BAFF-R specific antibodies may be used for treating, pathway suppressing or altering an immune response involving a signalling pathway contained and maturation in the treating diseases inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythemacous, autoimmune haemolytic anaemia, capenoses in which as glomerulonephritis, and lymphomas. Nucleic acids encoding contained and informative B-cell carcinomas, lymphomas, lymphomas, autoimmune disorders. The contained and informative B-cell carcinomas, lymphomas, lymphomas, autoimmune disorders. The contained and informative B-cell carcinomas, lymphomas, lymphomas, lymphomas, autoimmune disorders and inherited B-cell carcinomas, lymphomas, lym
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                                                                                                                                                                                                                                                                                                                                  Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                 Browning J, Ambrose C, Tschopp J, Schneider P;
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100.0%; Pred. No. 1.5e-17;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents human BAFF-R
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Fig 1; 59pp; English.
                                                                                                                17-AUG-1999; 99US-0149378P.
11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
                                                                                   16-AUG-2000; 2000WO-US022507.
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                                                                                                                                                                                                    (APOT-) APOTECH R & D SA
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                                                                                                                                                                                  (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                     N-PSDB; AAF59998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 184 AA;
                    WO200112812-A2
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                                                                                                                                                                                                                                                      Thompson J;
                                                    22-FEB-2001
                                                                                                                                                                                                                                      Mackay F,
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the invention tractes to a merinou of treating a mominal tota condition.

Sesociated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell meturation protein (BFW or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is interaction between APRIL and its cognate receptor(s). This method is carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systematic lupus erythematous-EBP); hypertension, cardiovascular diseases, systematic lupus erythematous-EBP; hypertension, cardiovascular diseases, systematic services and for treating autoimmune diseases, cardiovascular immunosuppressive diseases, organ transplantation, inflammation and human immune response involving a signalling pathway between APRIL-R and its lighand. APRIL-R DNA is also useful in gene therapy. The present sequence is human APRIL-R also referred as BCMA or BCM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCMA; B cell maturation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of treating a mammal for a condition
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11-FEB-2000; 2000US-0181807P.
30-JUN-2000; 2000US-0215688P.
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Matches 34; Conservative
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(APOT-) APOTECH R & D SA.
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                                                                                                                                                                                               Homo sapiens.
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Colorectal cancer; metastasis; differential expression; cytostatic;

diagnosis; gene therapy; vaccine.

Metastatic colorectal cancer-associated polypeptide.

(first entry)

30-DEC-2002

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The present invention describes a human tumour necrosis factor receptor designated Zthff12 [1]. [1] has cytostatic, immunosuppressive, dermathological, antiinflammatory, neuroprotective, antidiabetic, antinflammatory, neuroprotective, antidiabetic, antinflammatory, neuroprotective, antidiabetic, antisthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. [1] can be used for inhibiting, in a mammal, the activity of a ligand that binds Zthf12 (e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour calls. [1] is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel disease, graft rejection and Crohn's disease, such and crohn's disease and characterized and crohn's disease and construction the immune system for requiating B cell responses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention
                  nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; myloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.
     neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 135-136; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grant FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-2000; 2000US-0246449P.
20-DEC-2000; 2000US-0257131P.
28-JUN-2001; 2001US-0301715P.
29-AUG-2001; 2001US-0315565P.
                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001; 2001WO-US047018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu W, Henne RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                             WO200238766-A2.
                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gross JA,
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New genes that are up- or down-regulated in colorectal cancer, useful for diagnosing colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating

Claim 8; Page 255; 260pp; English.

colorectal cancer,

(UYCA-) UNIV CASE WESTERN RESERVE.

Mack DH, Markowitz SD

2002-698677/75

N-PSDB; ABQ81560

(EOSB-) EOS BIOTECHNOLOGY

02-APR-2001; 2001US-0281149P. 17-APR-2001; 2001US-0284555P.

27-FEB-2002; 2002WO-US006001. 27-FEB-2001; 2001US-0272206P.

WO200268677-A2. Homo sapiens.

06-SEP-2002.

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The present sequence is the protein sequence of a human polypeptide encoded by a gene that exhibits decreased expression in colon cancerderived metastases compared to normal colon tissue. It is an example of claimed polypeptides that are encoded by genes which are differentially expressed in metastatic colorectal cancer cells. Such polypeptides are useful in diagnostic and prognostic assays, for raising antibodies are e.g. in immunotherapy, and in screening for modulator compounds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, tumour, B-cell maturation antigen, transmembrane activator; calcium-modulator; cyclophilin ligand-interactor; TAC1; gene therapy; neoplasm; chronic lymphocytic leukaemia; lymphoproliferative dieasse; non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
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Best Local Similarity
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es 34; Conservative
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BCMA; multiple myeloma

sapiens

Homo

ABP54694 standard; protein; 184 AA

RESULT 15 ABP54694 ID ABP54 XX

Query Match

tches

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Gaps

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Length 184; Indels Gross JA;

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The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZINF) 2 or INF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft ejection, anaemia and septic shock. The fusion proteins are also used in gene, therapy, The present sequence is human B-cell maturation receptor
                                                                                                                                                                                                                                                                               Transmembrane activator and calcium modulator and cyclophilin ligand-
interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
diabetes, comprises a TACI receptor group and an immunoglobulin group.
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 100; 71pp; English
                                                                                                                                       24-MAY-2001; 2001US-0293343P.
                                                                                                         20-MAY-2002; 2002WO-US015910.
                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                       WPI: 2003-148455/14.
                                                                                                                                                                                                                                                        N-PSDB; AAD53754
                                           WO200294852-A2
             Homo sapiens.
                                                                           28-NOV-2002
                                                                                                                                                                                                       Rixon MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the manufacture of a composition for inhibiting the proliferation of tumour cells. The method involves using an antibody component that binds both the B-cell maturation antigen (BCMA) and the transmembrane activator and calcium-modulator and cyclophilin ligand-interactor (TACI). BCMA and TACI binding antibody compositions are useful for inhibiting proliferation of tumour cells, particularly inhibiting production or a disorder consisting of neoplasm, chronic lymphocycic production or a disorder consisting of neoplasm, chronic lymphocycic lymphoproliferative disease or light chain gammopathy or inflammation lymphoproliferative disease or light chain gammopathy or inflammation e.g. asthma. The invention is also useful in gene therapy. The present is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antimilammatory; immunosuppressive; glomerulonephritis; athma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; B-cell maturation receptor; BCMA; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    B-cell maturation antigen and transmembrane activator and calcium-modulator and cyclophilin ligand-interactor, useful for treating disorders e.g. inflammation or lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 201; DB 5;
100.0%; Pred. No. 1.5e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human B-cell maturation receptor (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                               8. .41
/note= "Cysteine rich region"
                                                                           /note= "Extracellular domain"
                                             note= "Antigenic epitope"
                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 63; 67pp; English.
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                                                                                                                                                                                                                                          20-FEB-2001; 2001US-0270274P.
12-APR-2001; 2001US-0283447P.
                                                                                                                                                                                                            06-FEB-2002; 2002WO-US003500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC
                                                               .48
                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-723183/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD46410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 184 AA;
                                                                                                                                              WO200266516-A2
                                                                                                                                                                                                                                                                                                                           Kindsvogel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-2003
                                                                                                                                                                              29-AUG-2002
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                            Region
                                                                 Domain
                                                                                               Region
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AAE35216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; TALL-1; antagonist; immunosuppressive; antirheumatic; antinflammatory; antiarchritic; dermatological; antidiabetic; neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple solerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; goodpasture s syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                           ..
0
                                                                                                                                                   Length 184;
                                                                                                                                                                                                           Indels
                                                                                                                                             100.0%; Score 201; DB 6;
100.0%; Pred. No. 1.5e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                  1 CSONBYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                       8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
gene therapy. The present sequence in (BCMA) protein used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA49361 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2003 (first entry)
                                                                                                                                                                                                                 34; Conservative
                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BCMA protein.
                                                                                            Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003035846-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA49361;
                                                                                                                                                         Query Match
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APRIL; scFV; immunospecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antinflammatory; antirheumatic; antiarhetritic; cyroscatic; antianemanic; antiallergic; antiasthmatic; neuroprotective; ophthalmological; tuberculostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; antipsoriatic; cancer; autoimmune disease; graft versus host disease; GVHD; inflammatory diseate; proliferative disease; single chain antibody; antibody; human; BCMA; tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the use of an agonist or antagonist of Genoxit activity for preventing or treating obesity. Genoxit is a member of the Tumour Necrosis Factor Receptor Super Family and is a Type III transmembrane protein. The agonists or antagonists of the invention are useful for treating or preventing obesity-related diseases or disorders, e.g. obesity, insulin resistance, atherosclerosis, atheromatrous disease, heart disease (e.g. cardiac insufficiency, coronary insufficiency, high blood pressure), hypertension, stroke, syndrome X, diabetes mellitus (complications, e.g. microangiopathic lesions, ocular lesions, cular lesions, retinopathy, neuropathy and renal lesions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New use of agonist or antagonist of Genoxit activity for preventing or treating obesity-related diseases or disorders, e.g. hyperlipidemia and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 201; DB 6;
100.0%; Pred. No. 1.5e-17;
iive 0; Mismatches 0;
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                                                                                               78. .184
/label= Intracellular_domain
                                                   55. .77
/label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 32; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP60552 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour necrosis factor BCMA.
                       /label= Gln, Lys
                                                                                                                                                                                                                                                                                                                                                                                                                         Briggs K;
                                                                                                                                                                                                                                                                                                                       06-AUG-2001; 2001US-0310754P.
                                                                                                                                                                                                                                                                         05-AUG-2002; 2002WO-IB003498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Lucas J, Dialynas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-268160/26
                                                                                                                                                                                                                                                                                                                                                                        GEST ) GENSET SA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 184 AA;
  Misc-difference
                                                                                                                                                                         WO2003013582-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2003
                                                                                                                                                                                                                        20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP60552;
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                                                Domain
                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &bgr; strands CD and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antirheumatic, antiinflammatory, antiarhitic, dermatological, antidabetic, neurotective, altithyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 a vaccine. A protein of the invention is useful for inhibiting TALL-1 considers in the invention at useful for inhibiting TALL-1 andependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, crimcombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephitis and acute rheumatic fever, post-streptococcal glomerulonephitis and collaborate in the present sequence represents human BCMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant; antidiabetic; hypotensive; ophthalmological; neuroprotective; nephrotropic; obseity; Tumour Necrosis Factor Receptor Super Family; Type III transmembrane protein; insulin resistance; atherosclerosis; atheromatous disease; heart disease; hypertension; stroke; syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia.
                                                                                                                                                                                                                                                                                                                                                                                             Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 100.0%; Score 201; DB 6; Local Similarity 100.0%; Pred. No. 1.5e-17; Nes 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
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/label= Extracellular_domain
                                                                                                                                                                                                                        (NAJE-) NAT JEWISH MEDICAL & RES CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 62; Page 613; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR40082 standard; protein; 184 AA
                                                                                                                                                                                                                                                                         Xu L;
                                                                                            24-OCT-2001; 2001US-0345106P.
14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
13-ANG-2002; 2002US-0403364P.
                                                24-OCT-2002; 2002WO-US034376
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                                                                                                                                                                                                                                                                         Shu H, Liu Y,
                                                                                                                                                                                                                                                                                                                       WPI; 2003-403345/38
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADA49360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Genoxit.
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  01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonist.
                                                                                                                                                                                                                                                                         Zhang G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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Best Loc Matches

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RESULT 19 ABR40082

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Gaps . 0

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Key Domain

Length 184; Indels

Ruben SM

syndrome

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The present sequence represents a human BCMA polypeptide. The specification also describes TACI and BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNP) family ligands TALL-1 and April bind to the TACI receptor, while TNF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haematological malignancy; immunoconjugate; cytostatic; immunostimulant; vaccine; immunotherapy; cancer; multiple myeloma cell; chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hematological malignancy-related genes and polypeptides, useful for screening anti-cancer agents, and generating antibodies or immunoconjugates for treating e.g. multiple myeloma cell or chronic
                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
preparing a composition for treating systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparing a composition for treating systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                         Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
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                                                                                                                                                                                                                         Grewal I, Ridgway J,
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                                                 24-JUL-2002; 2002WO-US023487.
                                                                                              03-AUG-2001; 2001US-0310114P.
30-APR-2002; 2002US-0377171P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-2002; 2002US-00057475
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Mcneill PD;
                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-598749/56.
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                                                                                                                                                                                                                                                                          WPI; 2003-256560/25
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                                                                                                                                                                                                                                                                                                     N-PSDB; ABZ68871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003062401-A2
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20-FEB-2003
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Carter L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD67527;
                                                                                                                                                                                                                         Dixit V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).

The antibody of the invention has dermatological, immunosuppressive, antiallergic, antiatharthic, cytostatic, antianaemic, antiallarthritic, cytostatic, antianaemic, antiallarthritic, cytostatic, antianaemic, antiallarthritic, antistally, and haemostatic activity.

The antibody or its fragment are useful for treating, preventing or ameliorating cancer such as autoimmune disease, and graft versus concertion of antistally prognosing, treating, preventing or erythematool arthritis or Sjogren's syntamome. The antibody is useful for detecting, diagnosing, prognosing, treating, preventing or ameliorating adisease or disorders ancolosing, treating, preventing or ameliorating adisease or disorders includes autoimmune and inflammatory disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis, asthma, allergic encephalomyelitis, myccarditis, multiple solerosis, or uveitis, multiple solerosis, diabetes mellitus, psoriasis, cancer of the immune system, particularly B call cancers, immunedficiency syndrome (ADDS), and infectious diseases (e.g. laukemia). The present sequence represents equired immunodeficiency syndrome (ADDS), and proliferative disorders (e.g. acquired immunodeficiency syndrome (ADDS)), and proliferative disorders (e.g. acquired immunodeficiency syndrome (ADDS)), and the tumour necrosis factor BCMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                            Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand; TALL-1; April; systemic lupus erythematosus; BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 201; DB 6; 100.0%; Pred. No. 1.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of human BCMA receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 222; 225pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP97717 standard; protein; 184 AA
                                                                                 22-MAY-2002; 2002WO-US016106.
                                                                                                                                24-MAY-2001; 2001US-0293100P.
                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 184 AA;
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                                    28-NOV-2002
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Query Match

RESULT 21

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Claim 8; Page 68-69; 72pp; English
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                                                                                                                                     The present invention describes an isolated polymucleotide (I), which is overexpressed in haematological malignancies, and which encodes a colymposition or an immunogenic fragment of the polympositie. Also described: (1) an isolated polympositie; (2) an expression vector described: (1) an isolated polympositie; (2) an expression vector comprising an expression vector; (4) an isolated antibody that perfect ones cell comprising an expression vector; (4) an isolated antibody that specifically binds to the polympositie or its immunogenic fragment; and (5) immunoconjugates comprising the antibody above, or an antibody that specifically binds to a polympositie or its immunogenic fragment, encoded by (1). (1) has cytostatic and immunostimulant activities, and can be used in vaccines and immunotherapy. The immunoconjugates are useful in composition for treating cancer, e.g. multiple myeloma cell, chronic composition for treating cancer, e.g. multiple myeloma cell, chronic lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep, or immunoconicotide (1) or polypeptide can be used for screening anti-cranted agents, and generating antibodies or immunoconjugates for treating corposition the above-mentioned diseases. The polymucleotide, contracting antibody can be used for detecting, diagnosing or prognosticating the above-mentioned diseases. The polymucleotide, prognosticating the haemaclological malignancies described above. The prognosticating the haemaclological halps and the prognosticating the prognosticating the prognosti
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Central Nervous System, CNS, inflammation, B-cell maturation antigen,
BCMA; multiple sclerosis, neuroprotective, nootropic, antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating a neurodegenerative immunological disorder, e.g. demyelination or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Match 100.0%; Score 201; DB 7; Local Similarity 100.0%; Pred. No. 1.5e-17; les 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
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                                                                            Claim 9; SEQ ID NO 4; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG43715 standard; protein; 184 AA
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lymphocytic leukemia.
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Best Local S
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             immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand (the mammal has or is at risk of developing multiple sclerosis). The method of the invention has neuroprotective, nootropic, and antilniflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
relates to a novel method for treating a neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an isolated monoclonal antibody which binds to a transmembrane activator of and CAML interactor (TACI) receptor. The TACI antibodies are useful for modulating TALL-1 or TACI polypeptide biological activity in mammalian cells, or for diagnosing arreating pathological conditions associated with TNF and TNF receptorrelated molecules, e.g. cancer or immune-related disease, such as systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome, systemic vasculitis, diabbetes mellitus, Crohn's disease, such as gyatemic vasculitis, multiple sclerosis, psoriasis, asthma, urticaria or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-TACI receptor monoclonal antibody, useful for diagnosing and treating pathological conditions associated with tumor necrosis factor, e.g. cancer or immune-related disease, such as rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;
Antidabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
Antibacterial; antiparastic; systemic lupus erythematosus;
diabetes mellitus; AIDS; BCMA.
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                                                                                                                                                                                                                                                                          Length 184;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                          inflammation. The present sequence represents human BCMA
                                                                                                                                                                                                                                                                            Score 201; DB 7;
Pred. No. 1.5e-17;
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                                                                                                                                                                                                                                                                                                                                                                                        8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
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                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 6; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK00756 standard; protein; 184 AA
                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                         34; Conservative
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Native human BCMA
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                                                                                                                                                                                                                                      Sequence 184 AA;
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The invention
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents neutrokine-alpha, BCMA, which may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein conjugate of the invention. The neutrokine-alpha protein conjugate of the invention. The neutrokine-alpha protein conjugate comprises neutrokine-alpha protein and chelator, where the neutrokine-alpha protein (also known as B-lymphocyte stimulator (BLyS), TALL-1, THANK and BAFF) is capable of binding neutrokine-alpha receptor and is selected from full length or mature neutrokine-alpha protein. The protein conjugate of the invention is useful in a complex with a metal ion associated with the chelator which is useful for administering radiotherapy to a subject such as human who is in need of radiotherapy, which involves administering the complex to the subject, where it is administered as an injectable solution, and the subject has a B-cell mediated disease. The subject has a condition chosen from non-Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus
                                                                                                                                                                                                                                                                                                                                                  neutrokine-alpha; chelator; B-lymphocyte stimulator; BLyS; TALL-1; THANK;
BAFF; neutrokine-alpha receptor; complex; metal ion; radiotherapy;
B-cell mediated disease; non-Hodgkin's lymphoma;
infectious diseases including AIDS, hepatitis infection, bacterial infection, fungal infection, protozoal infection and parasitic infection. The present sequence represents native human BCWA.
                                                                                                                                                                                                                                                                                                                                                                                           chronic lymphocytic leukaemia; multiple myeloma; chronic lymphocytic leukaemia; multiple myeloma; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; Crohn: a disease; diabetes; Wegener's granulomatosis; myasthenia gravis; asthma; cancer; Sjogren's syndrome; diagnostic imaqing; lymphocyte; B cell; cancerous cell; metastasis; lymphatic system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neutrokine-alpha conjugate useful for targeting complexed metal ion to cells expressing receptor (predominantly lymphoid) for radiotherapy treatment of, for example, non-Hodgkin's lymphoma comprises neutrokinealpha protein and chelator.
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                                                                                    Length 184;
                                                                                                               Indels
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                                                                                    100.0%; Score 201; DB 8;
100.0%; Pred. No. 1.5e-17;
ive 0; Mismatches 0;
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                                                                                                                                           1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilbert D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 9; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galperina O,
                                                                                                                                                                                                                                           ADQ94442 standard, protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-2002; 2002US-0435262P. 02-MAY-2003; 2003US-0467198P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-2003; 2003WO-US040979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                             Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                           Neutrokine-alpha, BCMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parmelee D, Yeh R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-553134/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004058309-A1.
                                                             Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                  07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2004.
                                                                                                                                                                                                                               ADQ94442
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c erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's disease, diabetes, Wegener's granulomatosis, myasthenia gravis and asthma, correlarably non-Hodgkin's lymphoma. The complex is useful for treating cancer, which involves administering it to a subject haring cancer, where cancer expresses a neutrokine-alpha receptor on its a call of the cancer expresses a neutrokine-alpha receptor on its surface. The cancer is a B cell cancer, which is chosen from non-Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia. The complex is also useful for treating an autoimmune disease or disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis and Sjoaren's syndrome. The complex may also be used for diagnostic useful for killing a cell chosen from a cell bearing a neutrokine-alpha useful for killing a cell chosen from a cell bearing a neutrokine-alpha caepara cancerting an early bearing an entrokine-alpha capha receptor, which involves contacting the cell with the composition to kill the cell. The cell is lymphocyte, B cell or cancerous cell that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antiansemic; antiarthritic; antiatentatic; antidiabetic; antinflammatory; antisortatic; antirhermatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO polynucleotides and polypeptides, useful in useful in diagnosing treating an immune related disease, e.g. systemic lupus hematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated PRO nucleic acid (I). Also described: (I) a vector comprising (I); (2) a host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaрв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
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100.0%; Pred. No. 1.5e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO protein sequence SEQ ID NO:1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1990; 3009pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virucide; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-376182/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 184 AA;
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isolated PRO polypeptide; (5) a chimeric molecule comprising the isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a antagonist of the polypeptide or an antibody that binds to the polypeptide or an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide of a mammal; (10) a method of identifying a compound that inhibits or manufact the activity of or expression of a gene encoding a PRO polypeptide in mammal; (12) a method of identifying a compound that inhibits or manufact the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of esimulating the immune response in a mammal. The PRO sequences have antialleric, antialnaemic, antialpeoriatic, antialnaemic, antialpeoriatic, antialnaemic, antialpeoriatic, antialnaemic, antialpeoriatic, antialnaemic, antialpeoriatic, antialpeoriatic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune response and in estimulating an immune response. The present sequence represents a human properior.

PRO protein from the present invention.
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Martin F;

Gong Q,

Chan A,

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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New tumor necrosis factor receptor (TNFR) polypeptides, useful as detecting ligands, and for modulating tumor growth, metastasis and immunity, such as separating resting from stimulated immune cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
                                                     Depleting B cells from a mixed population of cells by contacting cells with a BLyS antagonist and a CD20 binding antibody, useful treating B cell malignancies and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 184;
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100.0%; Pred. No. 1.5e-17;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumor necrosis factor receptor BCMA.
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/note= "Сув-rich domain"
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                                                                                                                         Disclosure; Fig 2; 114pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fox BA, Holloway JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-315682/32.
             WPI; 2005-058069/06.
N-PSDB; ADW03431.
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2005037865-A2
                                                                                                                                                                                                                                                                                                                                    BCMA protein.
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Matches
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The invention provides novel tumor necrosis factor receptor ztnfr14 polynucleotides ADZ67754, expression vectors and antibodies. Ztnff14 polynucleotides are used in claimed methods for detecting a cancer in a patient. Recombinant ztnff14 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Ztnff14 polypeptides, optionally conjugated to a polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastasis, and immunity such as separating resting from stimulated immune cells. The present sequence is that of human TNPR BCMA. This sequence was compared with that of ztnff14 in the identification of ztnff14 as a member of the TNPR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of inhibiting the growth of a cell that expresses a protein comprising contacting the cell with an antibody, oligopeptide or organic molecule that binds to the protein, the binding of the antibody, oligopeptide or organic molecule to the protein and causing an inhibition of growth of the cell. Also described is a method for treating or preventing a cell proliferative disorder associated with archaed expression or activity of a protein having at least 80 % amino acid sequence identity to: a polypeptide having any of SEQ ID NO: 2, 8, 10, 12, 16, 20, 22, 49 and 51; a polypeptide having the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting the growth of a cell that expresses a protein by contacting the cell with anti-tumor antigens of hematopoietic origin (TAHO) polypeptide, antibody or organic molecule, useful for treating hematopoietic and malignant tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; therapy; cell growth; protein purification; DNA purification; hyperproliferation; neoplasm; tumor antigen of hematopoietic origin; TAH023.
                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           1 CSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                  CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor antigen of hematopoietic origin TAHO23.
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA23348 standard; protein; 184 AA
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24-DEC-2003; 2003US-0532426P.
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                                                                                                                                                                                                                                                                                                                                                    34; Conservative
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                          Sequence 184 AA;
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sequence of (a), lacking its associated signal peptide; an extracellular domain of the polypeptide having the amino acid sequence of (a), with or without its associated signal peptide; a polypeptide encoded by any of SEQ ID NO: 1, 7, 9, 11, 15, 19, 21, 48 and 50; or a polypeptide encoded by the full-length coding region of the nucleotide sequence of (d), comprising administering to a subject in need of such treatment an antagonist of the protein, and effectively treating or preventing the cell proliferative disorder. Also disclosed are anti-tumor antigens of hematopoietic origin (TAMO) polypeptides, encoding nucleic acids, the invention. The methods and compositions of the present invention are useful for treating hematopoietic and malignant tumors in mammals. This is the amino acid sequence of tumor antigen of hematopoietic origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA; B-cell maturation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                  Length 184;
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                                                                                                                                                                                                                                                                                                                  Score 201; DB 9;
Pred. No. 1.5e-17;
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                                                                                                                                                                                                                                                                                                                                                                                           1 CSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amin acid sequence of a BCMA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEC02031 standard; protein; 184 AA
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                                                                                                                                                                                                                                                                                                                                                         Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     Sequence 184 AA;
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (GT0, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in amammal which is useful for inhibiting activity of TACI and/or BCMA in amammal which is useful for inhibiting activity of TACI and/or BCMA in amammal which is useful for inhibiting activity of TACI and/or BCMA in amammal which is useful for inhibiting activity of TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic atsaces such as diarrhoea, psoriasis, allergies, pneumonia, atopic disease, drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; pymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; corbn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; transmembrane activator and intracellular CAML interactor; TACI;
                                                                                   Gaps
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                                      Length 184;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Human BCMA-immunoglobulin Fc region fusion protein.
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0
                                      100.0%; Score 201; DB 9; 100.0%; Pred. No. 1.5e-17;
                                                                                                                                                     CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                            1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                               AAE15488 standard; protein; 283 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                             Query Match
Best Local Similarity 100.0%;
Matches 34; Conservative (
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Sequence 184 AA;
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AAE15488
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                                                                                                                                                                                                                                                              Chromosome aberration; oncogenic fusion protein; cancer; proliferative disease; cellular protein isoform; heat shock protein 90; hisp-90; rheumatoid arthritis; cancer; heamatopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; acute myeloid leukaemia; ALL; APL; NIL; solid tumour; papillary thyroid carcinoma; Bwing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90.
                                                                    Gaps
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is human BCMA protein-immunoglobulin Pc region fusion protein
                                           Length 283;
                                                                   Indels
                                           Score 201; DB 5;
Pred. No. 2.4e-17;
; Mismatches 0;
                                                                                         1 CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                        5 CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 38
                                                                                                                                                                                                                                          Human translocation (4; 16) (q26; p13) protein.
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                                                                                                                                                                         ABG95060 standard; protein; 288 AA
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                                             100.0%;
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                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fritz LC, Burrows FJ;
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N-PSDB; ABS73235.
                                                     Local Similarity
                      Sequence 283 AA;
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                                             Query Match
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Matches
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Homo sapiens
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31-JUL-2001
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
                                                                                                                                                                                                                                                                                                            Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor;
b-cell maturation inhibitor; immunoglobulin production inhibitor;
autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
renal disorder; immunosuppressive disorder; HIV infection;
organ transplantation; antiinflammarory; systemic lupus erythematosus;
autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
                                                                                                                                                                                                                                                                                        Mouse 1gG signal/human BAFF-R/human 1gG Fc fusion protein, BAFF-R-Fc.
synovial sarcoma. The method is also useful for treating viral infections. This represents a protein encoded by the DNA sequence of chromosome aberration
                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Browning J, Ambrose C, Tschopp J, Schneider P;
                                                                     Length 288;
                                                                                              Indels
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0
                                                                        100.0%; Score 201; DB 5; 100.0%; Pred. No. 2.4e-17;
                                                                                                                                     112 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 145
                                                                                                                      1 CSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                               0; Mismatches
                                                                                                                                                                                                        AAB60699 standard; protein; 302 AA
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(first entry)
                                                                      Query Match
Best Local Similarity 100.
Matches 34; Conservative
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(APOT-) APOTECH R & D SA.
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                                                  Sequence 288 AA;
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22-MAY-2001
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Thompson J;
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Chimeric.
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c and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV confiction, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, conteins or BAFF-R specific antibodies may be used for treating. Since BAFF-R suppressing or altering an immune response involving a signalling pathway conteins or BAFF-R and BAFF-R thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, cach as systemic lupus erythematosus, autoimmune haemolytic anaemia, crapidly progressive glomerulonomburitis, and lymphomas. Nucleic acids encoding chance may research in Berapy to treat tumours, lymphomas, cutoimmune disorders and inherited B-cell-associated disorders. The comparising a mouse IgG-kappa signal sequence, residues 1-153 of human constrains a human IgG-Rappa signal sequence, residues 1-153 of human constrains a human IgG-Rappa signal sequence, residues 1-153 of human constrains a human IgG-Rappa signal sequence, residues 1-153 of human constrains a human IgG-Rappa signal sequence.
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/label= Mature_human_BCMA_IgG_Fc_fusion_protein
23. 75
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/label= Signal peptide
/note= "Derived from murine Ig kappa sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Derived from human IgG Fc region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BCMA-Immunoglobulin G Fc region fusion construct.
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/note= "Derived From human BCMA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 201; DB 4;
Pred. No. 2.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE00507 standard; protein; 302 AA.
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Best Local Similarity
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(GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 302 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                nvention.
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                                                                                                                                                                                                                                                                                         interaction between ARRIL and its cognate receptor(8). This method is useful for treating undesired cell proliferation such as cancer or carcinoma, approach and its cognate receptor(8). This method is useful for treating undesired cell proliferation such as cancer or carcinoma, and other carcinoma, colon carcinoma, breast carcinoma, disease, estemic lupus erythematosus-SLB); hypertension, cardiovascular disease, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and human immune response involving a signalling pathway between ARRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is a fusion construct containing human APRIL-R also referred as BCMA or sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
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                                                                                                                                             Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
                                                                                                                                                                                                                                The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (ECM or ECMA) antagonist that antagonises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human, neurodegenerative immunological disorder; demyelination;
Central Nervous System; CNS; inflammation; B-cell maturation antigen;
BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
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                                                                                     Rennert P;
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/note= "Murine IgGkappa signal sequence"
                                                                                     Cachero T, Ambrose C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human B-cell maturation antigen-Fc SEQ ID NO:3.
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06-OCT-1999; 99US-0157933P.
11-FEB-2000; 2000US-0181807P.
30-JUN-2000; 2000US-0215688P.
                                                                                    Thompson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                               (BIOJ ) BIOGEN INC.
(APOT-) APOTECH R & D SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; mouse.
                                                                                                            WPI; 2001-266242/27
                                                                                                                        N-PSDB; AAD03847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 302 AA;
                                                                                    Schneider P,
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The invention relates to a novel method for treating a neurodegenerative immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand (the mammal has or is at risk of developing multiple sclerosis). The method of the invention has neuroprotective, nootropic, and antiinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence is used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating a neurodegenerative immunological disorder, e.g. demyelination or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
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       "Human BCMA extracellular domain"
/note= "Human BCMA extracellular domain
75. .302
/note= "Human Ig heavy chain Fc region"
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100.0%; Pred. No. 2.6e-17;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                    21-FEB-2003; 2003WO-US005147.
                                                                                                                                                                                                                                                                                                                                                         21-FEB-2002; 2002US-0358427P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalled SL, Reid H;
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Best Local Similarity
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Synthetic.
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                                                                                                                             The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The dolypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleromi; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see AEC02021), that that bind BAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
                                                      useful
                                                   New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                   ch 98.0%; Score 197; DB 9; 1 Similarity 97.1%; Pred. No. 9.1e-18; 33; Conservative 1; Mismatches 0
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                                                                                                               claim 13; SEQ ID NO 15; 140pp; English.
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           Kelley RF, Patel D;
                                  WPI; 2005-555932/56
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                                                                                                                                                                                                                                                                 Sequence 34 AA;
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polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroma; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see AEC02021), that that bind BAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder; immunomodulator; antiinflammatory; cancer;
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                                                                                                                                                                                                                                                                                          Length 34;
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                                                                                                                                                                                                                                                                                          Score 196; DB 9;
Pred. No. 1.2e-17;
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                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                               ch 97.5%;
1 Similarity 97.1%;
33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAFF; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2005075511-A1.
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The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis Family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroms; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a BCMA-Fc fusion protein, where I22 of BCMA is changed to Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
                                                                                                                                                                                                                                                                                                   New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.
cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Formula II derived polypeptide D that binds BAFF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.5%; Score 194; DB 9;
llarity 97.1%; Pred. No. 2e-16;
Conservative 0; Mismatches
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               B-cell maturation antigen, Fc.
                                                                                                                                                     04-AUG-2004; 2004WO-US025247.
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Best Local Similarity
Local 33; Conserve
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                                                                                                                                                                                                                                                                           WPI; 2005-555932/56.
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                                                                                         WO2005075511-A1
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                                              Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell macuration antigen (BCMA). APRIL and BAFF are tumor necrosis family (TMF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroma; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents polypeptide of the invention that binds APRIL, derived from
                                                                                                                                                                                                               APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides that inhibit APRIL and/or BAFF binding to BCNA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
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                                                                                                                                                                                  Formula I derived polypeptide F that binds APRIL.
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97.1%; Pred. No. 2.2e-17;
iive 0; Mismatches 1;
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CSQNEYFDSLLHACIPCQLYCSSNTPPLTCQRYC 34
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                                                                                         AEC02017 standard; peptide; 34
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Best Local Similarity
                                                                                                                                                                                                                                                                                          WO2005075511-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation.
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                                                                                                                                                                                                                                                             Synthetic
                                                                                                                       AEC02017;
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Matches
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34

9; Length 296; Indels

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WO2005075511-A1.
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Best Local Simi
Matches 33;
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                                                                                                                              The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCWA). APRIL and BAFF are tumor necroals family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleromi, or T-cell mediated disease such as graft rejection, graft versus host disease (GYHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see AEC02021), that that bind BAFF.
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                                            New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
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                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                           Claim 13; SEQ ID NO 14; 140pp; English.
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                                                                                                                                                                                                                                                                                                                       33; Conservative
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                                                                                                                                                                                                                                                                        Sequence 34 AA;
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                                                                                      inflammation
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  Kelley RF,
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diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroma; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see AEC02021), that that bind BAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APRID; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic; B-cell maturation antigen; BCMA.
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95.5%; Score 192; DB 9;
Best Local Similarity 97.1%; Pred. No. 4e-17;
Matches 33; Conservative 0; Mismatches
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The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroms; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents polypeptide of the invention that binds APRIL, derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APRIL, BAFF, immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
                                                                                                                                                                                                                                                  New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Formula II derived polypeptide H that binds BAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.0%; Score 189; DB 9;
94.1%; Pred. No. 9.6e-17;
ive 0; Mismatches 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                Claim 7; SEQ ID NO 7; 140pp; English.
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                                                                                                     04-AUG-2004; 2004WO-US025247.
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                                                                                                                                  29-JAN-2004; 2004US-0540271P.
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Best Local Similarity
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                                             WO2005075511-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34 AA;
                                                                                                                                                                                                                                                                                                    inflammation
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               Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen BCRAA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleroms; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence
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                                                                                                                                                                                            APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.
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 1 SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 33
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                                                                          AEC02020 standard; peptide; 34 AA
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                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                          Synthetic
                                                                                                        AEC02020;
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AEC02018
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Length 34; Indels

WPI; 2005-555932/56

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The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
                                                                                                                                                 The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCWA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple scleromi, or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents a polypeptide of the invention, derived from formula II (see ABC02021), that that bind BAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic.
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                                          for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and
                               polypeptides that inhibit APRIL and/or BAFF binding to BCMA,
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Pred. No. 9.6e-17;
0; Mismatches
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                                                                                                                     Claim 13; SEQ ID NO 18; 140pp; English.
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Best Local Similarity 94.1
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Length 34; 2; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
scleroma; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents polypeptide of the invention that binds AFRIL, derived from
                                                                                                                                                                     Gaps
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                                                                                                                                 Length 34;
                                                                                                                                                                     Indela
                                                                                                                 90.5%; Score 182; DB 9; Li
91.2%; Pred. No. 7.5e-16;
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                                                                                                                                                                                                                                                                                                                                           AAB60700 standard; protein; 157
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2000US-0181684P.
2000US-0183536P.
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                                                                                                                                                                         31; Conservative
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                                                                                                                                 Query Match
Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAF60000
                                                                                                  Sequence 34 AA;
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11-FEB-2000; 2:
18-FEB-2000; 2
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                                                               AEC02012.
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useful

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be used in the treatment of immunosuppressive disorders and HIV prifection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, rapidla grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents a human BAFF-R protein sequence as encoded by plasmid PASTS35. However, this BAFF-R protein sequence is 27 amino acids shorter than that given in AABG0698
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Sequence 157 AA;

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Gaps
                         æ,
79.4%; Score 159.5; DB 4; Length 157;
                       0, Indels
             Pred. No. 2.6e-12;
                                                 3 QNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                       0; Mismatches
          90.6%;
                       29; Conservative
           Similarity
Query Match
             Local
                      Matches
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ONEYFOSLLHACIPCQLR---NTPPLTCQRYC 35

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ADI53060 standard; peptide; 26 AA ADI53060 ID ADI5

(first entry) 22-APR-2004 AD153060;

protein co-ordinate data, cytostatic, antiallergic; immunosuppressive; antirheumatic; antiarthritic; neuroprotective; antinflammatory; antiabbetic; dermatological; antiasthmatic; neutrokine-alpha; crystallography; cancer; allergic disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes; systemic lupus erythematosus; asthma; receptor. Human BCMA receptor binding site.

Ното варіеля

WO2003050134-A2

07-NOV-2002; 2002WO-US035661

07-NOV-2001; 2001US-0331049P.

(HUMA-) HUMAN GENOME SCI INC.

Volovik Y; Arnold E, Oren DE, Li Y,

WPI; 2003-532895/50.

crystalline Neutrokine-alpha protein, useful for designing compounds that bind, inhibit or mimic a Neurrokine-alpha protein or enhance the activity of a Neutrokine-alpha protein for treating e.g. cancer or allergic disorders.

Disclosure, Fig 4; 362pp; English.

The invention relates to a neutrokine-alpha protein in crystalline form. The crystalline neutrokine-alpha protein is useful for designing molecules that have biological activity or compounds that bind, inhibit or mimic a neutrokine-alpha protein and/or enhance the activity of a neutrokine-alpha protein. The three-dimensional structure of a neutrokine-alpha protein is useful in determining the three-dimensional of other neutrokine-alpha proteins and their homologs. The compounds that mimic,

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The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a cotivity). The specification describes a method of identifying a cotivity increases gene expression from a promoter. The method involves contacting a library of with a cell which expression of the reporter recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for from a promoter. The BCMA polypeptide or nucleic acid are useful for treparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
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            cancer, allergic disorders, or autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus erythematosus or asthma. This sequence represents the residues in the receptor for binding a cytokine ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCWA, necrosis factor-kB activator; NP-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
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prevent or inhibit the activity of the protein are useful for treating
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                               0; Indels
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/note= "putative transmembrane domain"
                                                                                                                                                      DB 7; L
5.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of murine BCMA polypeptide.
                                                                                                                                            75.1%; score 100.0%; Pred. No. ... 0; Mismatches
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                                                                                                                                                                                                                                                                         1 EYFDSLLHACIPCOLRCSSNTPPLTC 26
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                                                                                                                                   Query Match
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"heg 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-558405/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seed B, Ting A;
                                                                                                                 Sequence 26 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAB08844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                     RESULT 50
                                                                                                                                                                                                                                                                                                                                                          AAB08844
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Theill LE,
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                                                                                                                                                              RESULT 52
                                                                                                                                                                            AAE15490
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                                                                                                                     요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Tumour necrosis factor (TNF) and Apoliciated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B TALL-1 protein is useful for identifying compounds that regulate B sponses. TALL-1 protein is useful for identifying compounds that regulate B sponses. TALL-1 protein is useful for identifying compounds that regulate B second architis, systemic lupus cervitematosus (SLB), insulin dependent diabetes mellitus, multiple cervitematosus (SLB), insulin dependent diabetes mellitus, multiple cervitematosus (SLB), insulin dependent diabetes mellitus, multiple cervitematosus (SLB), insulin dependent diabetes mellitus, systemic lupus cancematosus autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a murine B cell maturation factor (BCMA). BCMA is
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                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation; post-streptococcal glomerulonephritis; polyarteritis nodosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                   Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
                                                                                5
                                                    DB 3; Length 185;
                                                                                Indels
                                                                                9
                                                                                                                                                                                                                                                                                        Murine B cell maturation factor (BCMA) protein.
                                                                                                                          Score 136; DB 3;
Pred. No. 3e-09;
                                                                                                         CSQNEYFDSLLHACI PCQLRCSSNTPPLTCQRYC
                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 37; Page 107-108; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NAJE-) NAT JEWISH MEDICAL & RES CENT.
                                                                                                                                                                                                         Ź
                                                                                                                                                                                                         AAY71980 standard; protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-2000; 2000WO-US012266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999; 99US-0132892P.
                                                      67.78;
                                                                                                                                                                                                                                                              (first entry)
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-016094/02.
                                                                    Similarity
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                            Sequence 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200068378-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                              28-MAR-2001
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                                                                              24;
    designing
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                                                      Query Match
Best Local S
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                                                                                  Matches
                                                                                                                                                                               RESULT 51
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tunmour necrosis factor-TNF c family ligand), having the consensus region of TACI, BCMA, or the TACI/C GMA, The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal whoch is useful for inhibiting activity of TACI and/or BCMA in a mammal whoch is useful for inhibiting activity. BCMA and TACI c antagonists are useful for treating inflammation and immune function diseases such as diarkhoea, pooriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (CCohn's disease, colitis), scleroderma, autommune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, cancer bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; dury allergy; dermatitis; neumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
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                                                                                                                                                       Gaps
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7
                                                                       DB 4; Length 185;
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                                                                                                                                                                                                                                                                                                          5 CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36
                                                                                                                                                                                                                                            1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                       Score 136; DB 4;
Pred. No. 3e-09;
                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse B cell maturation (BCMA) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE15490 standard; protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-2001; 2001WO-US015567.
                                                                       67.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002 (first entry)
                                                                           Query Match
Best Local Similarity 70.6
Matches 24; Conservative
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Sequence 185 AA;
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Mouse BCMA-human immunoglobulin Fc region fusion protein.

(revised)
(first entry)

29-AUG-2003 12-MAR-2002

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AAE15489;

AAE15489 standard; protein; 281 AA

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RESULT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides novel tumor necrosis factor receptor zinfil4 polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors and antibodies. Human zinfil4 polypucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant zinfil4 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Zinfil4 polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides to be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastasis, and immunity such as separating resting from stimulated immune cells. The present sequence is that of mutine TMFR BCMA. This sequence was compared with that of mutine zinfil4 ADZ67756 in the identification of zinfil4 as a member of
with leucocyte infiltration of the skin or organs. The present sequence
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumor necrosis factor receptor (TNFR) polypeptides, useful as detecting ligands, and for modulating tumor growth, metastasis and immunity, such as separating resting from stimulated immune cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
                                                                                                                                                             ..
7
                                                                                                                Length 185;
                                                                                                                                                             6; Indels
                                                                                                                DB 5;
                                                                                                                                                                                                                               S CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon SR
                                                                                                                                                                                                       1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                Score 136; DB 5;
Pred. No. 3e-09;
                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse tumor necrosis factor receptor BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 10; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                              ADZ67762 standard; protein; 185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2004; 2004WO-US034375.
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                                                                                                              67.7%;
70.6%;
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                                                                                                                                                           24; Conservative
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                       is mouse BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-315682/32.
                                                                                                            Query Match
Best Local Similarity
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                                                                    Sequence 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005037865-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                             ADZ67762;
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                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                      RESULT 53
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ADZ67762

ADZ6

ADZ6
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular repairs of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for irreating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), selenoderma, autoinemune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leurcoyche infiltration of the skin or organs. The present sequence is mouse BCMA protein-human immunoalobulin for region fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                   cytostatic; B cell maturation protein; BCMA, tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
Human; transmembrane activator and intracellular CAML interactor; TACI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 10B; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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DB 5; Length 281;

67.7%; Score 136;

Query Match

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Gaps

.. 7

6; Indels

2; Mismatches

24; Conservative

Matches

δ

Best Local Similarity

Query Match

CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36 1 CSONEYFDSLIMACIPCOLRCSSNTPPLICORYC 34

67.7%; Score 136; DB 9; Length 185; 70.6%; Pred. No. 3e-09;

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(revised)
(first entry)

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Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                   cytostatic; B cell maturation protein; BCMA, tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriaals; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; mouse.
                                                                                                                                                          Human; transmembrane activator and intracellular CAML interactor;
                                                                                                                              Human-murine B cell maturation protein (BCMA) consensus sequence.
                           AAE15491 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-2001; 2001WO-US015567
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                                                                                                                                                                                                                                                                                                                                                          WO200187979-A2
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                    29-AUG-2003
12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheill LE,
                                                         AAE15491;
                                                                                                                                                                                                                                                                                                                            Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligand
RESULT 56
               AAE15491
                                         The invention relates to a novel TALL-1-binding polypeptide comprising a defined sequence in the specification. The composition is useful in modulating the activity of TALL-1, and in treating, preventing, amediated autoimmune disease (e.g. systemic lupus prythematosus) or B-cell-mediated cancer or lymphoma. The composition may also be used in treating inflammations (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease, asthma, atherosclerosis, cachexia, cirrhosis, diabetes, aplomerulonephritis, Hashimoto's thyroiditis, ischemen's disease, and vasculitis, Bashimoto's thyroiditis, parkinson's disease, and vasculitis. Disorders may be treated with the novel composition using gene therapy. This sequence represents a TALL-1 related protein of the
               ä
                                                                                                                                                                                                                                                                 TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease; systemic lupus erythematosus; B-cell-mediated cancer; lymphoma; inflammation; rheumatosid arthritis; acute pancreatitis; atheroselerosis; Alzheimer; G disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis; glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New TALL-1-binding polypeptide, useful for modulating the activity of TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune diseases, cancers or lymphomas.
               Gaps
               5
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               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.7%; Score 124; DB 6; Lo
100.0%; Pred. No. 2.3e-08;
ive 0; Mismatches 0;
 Pred. No. 4.6e-09;
2; Mismatches 6;
                                            34
                                                                CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36
                                            1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
                                                                                                                                                                                                                                        TALL-1 related protein SEQ ID No 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 26; 236pp; English.
                                                                                                                                                  ABJ38417 standard; protein; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-2002; 2002WO-US015273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-2001; 2001US-0290196P.
 70.6%;
                                                                                                                                                                                                           (first entry)
                24; Conservative
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   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                             12-JUN-2003
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                                                                                                                                                                               ABJ38417;
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   Best Local
                  Matches
                                                                                                                                 RESULT
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Yu G;

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a pecific binding partner for APRLI (GTO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA extracellular consensus sequence, but not the extracellular region of TACI or TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI or TACI or ECMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRLI, BCMA and TACI deragonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, alexiples, promemonia, atophocidermaticis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, but neucographs, protozoal and viral infections (HIV), atherosclerosis, fungal, but he control or the skin or organs. The present sequence of the skin or organs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is human-murine B cell maturation protein (BCMA) consensus sequence. (Updated on 29-AUG-2003 to standardise OS field)
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Pred. No. 0.0005;
1; Mismatches 2; Indels 7
Disclosure; Fig 11; 94pp; English.
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Best Local Similarity 69.7%;
Matches 23; Conservative
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Gaps

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Indels

21

1 CSQNEYFDSLLHACIPCQLRC

Conservative

Best Local Similarity

21;

Matches

ð g

22 CSQNEYFDSLLHACIPCQLRC 42

Sequence 24 AA;

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCWA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCWA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCWA. The method is useful for inhibiting activity of TACI and/or BCWA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointeetinal, pancreatic or prostate tumour. APRIL, BCWA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, clitis), soleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, soleroderma, and murine B cell maturation protein (BCWA) consensus sequence is human-murine B cell maturation protein (BCWA) consensus sequence cystelne rich region. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                                              Human; transmembrane activator and intracellular CAML interactor; TACI;
                                                                                                                                                                                                                                                                                                                    Human-murine BCMA consensus sequence cysteine rich region.
                     2 AQCEYFDSLLHAC-PC-LRCS----PPTCQ-YC 27
34
SQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC
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                                                                                                                                                           AAE15492 standard; peptide; 24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-2001; 2001WO-US015567
                                                                                                                                                                                                                                                (revised)
(first entry)
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12-MAR-2002
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                                                                                                              RESULT 57
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                           Gape
                           7;
  Length 24;
                           Indels
Score 90.5; DB 5;
Pred. No. 0.00025;
0; Mismatches 1;
                                                                                                                                                                                                                    A murine ztnf4, a tumour necrosis factor ligand.
                                                    5 EYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                           2 EYFDSLLHAC-PC-LRCS----PPTCQ-YC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 163; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yee DP;
                                                                                                                                             AAY94006 standard; protein; 249 AA
  45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2000; 2000WO-US000396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1999; 99US-00226533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gross JA, Xu W, Madden K,
                                                                                                                                                                                             (first entry)
              Best Local Similarity 73.3
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                            WO200040716-A2.
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                             20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-2000.
                                                                                                                                                                     AAY94006;
     Query Match
                                                                                                                              AAY94006
ID AAY9
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fumor necrosis factor receptor; TACI; cancer; neoplasm; diagnosis;

WO2005037865-A2 Mus musculus.

cytostatic.

Mouse tumor necrosis factor receptor

(first entry)

14-JUL-2005

ADZ67773;

ADZ67773 standard; protein; 249 AA.

RESULT 60

4DZ6777

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pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCWA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
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                                                                                                                                                                                                                                                                        Length 249;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                        35.6%; Score 71.5; DB 3;
35.3%; Pred. No. 0.69;
tive 8; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic, carcinoma, lymphoma, cancer, murine,
                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 1647; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM85744 standard; protein; 249 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse protein sequence mCP1369.
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Best Local Similarity 35.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                            Local Similarity 35.3
nes 12; Conservative
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                                                                                                                                                                                                               Sequence 249 AA;
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ABBRE 5744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         necrosis factor receptor (TNFR) polypeptides, useful as ligands, and for modulating tumor growth, metastasis and such as separating resting from stimulated immune cells.
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18-OCT-2004; 2004US-0619552P.
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Best Local Similarity
Matches 12; Conserv
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CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38 1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34

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New isolated mucin-like polypeptides, useful for diagnosing or treating, e.g. bacterial infections, allergic asthma, inflammation, allergic conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung
                                                                                                                                                                                                                                                The present invention relates to novel mucin-like proteins (I) and their coding sequences. The mucin-like proteins and coding sequences are useful in the therapy or in the prevention of a disease when the increase in the mucin-like activity of a polypeptide is needed e.g. bacterial infections, allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced disease, allergic conjunctivitis, otitis, tissue injury, epithelial adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia, chronic cholecystitis, or skin cancer. The present sequence is a mucin glycoprotein which was used in a sequence alignment with the mucin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory; Ophthalmological; Auditory; Vulnerary; Gastrointestinal; Cytostatic; Gene Therapy; Mucin-like protein, human; mucin; bacterial infection; allergic asthma; inflammation; viral infection; allergic conjunctivitis; otitis; tissue injury; epithelial wounding; inflammatory; bowel disease; crohn; a disease; small adenocarcinoma of the lung; lung cancer; gastric intestinal metaplasia; chronic cholecystitis; skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated mucin-like polypeptides, useful for diagnosing or treating,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 1569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1179 CSQDEYFDHEEGVCVPCM-----PPTTPQ 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ 31
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            (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68.5;
Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR18914 standard; protein; 2240 AA
                                                                                                                                                                                                                     Example 2; Fig 1; 170pp; English.
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                                               Bienkowska J, Mcallister G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.2'
                                                                                                                                                                                  cancer, or skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-604324/58
                                                                                 WPI; 2004-604324/58
                                                                                                  GENBANK; AAQ82434
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1569 AA;
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                                                                                                                                                                                                                                                                                                                                        Characterizing proteins present in a plasma membrane of a cell, useful in identifying diagnostic markers and potential drugs, comprises subjecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial, Virucide, Antiallergic, Antiasthmatic, Antiinflammatory, Ophthalmological, Auditory, Vulnerary, Gastrointestinal, Cytostatic, Gene Therapy; Mucin-like protein, human; mucin; bacterial infection; allergic asthma, inflammation; viral infection; allergic conjunctivitis, otitis, tissue injury, epithalial wounding; inflammatory bowel disease; Crohn's disease; small adenocarcinoma of the lung; lung cancer; gastric intestinal metaplasia; chronic cholecystitis; skin cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of characterizing proteins present in the plasma membrane (PM) of live calls. The proteins of the invention are useful in identifying diagnostic markers and potential drugs. The invention is useful for identifying drugs for diagnosing and treating disorders such as cancer which are associated with abnormal representation of cell surface proteins. The present sequence is mouse tumor necrosis factor receptor superfamily member lib protein.
Plasma membrane; diagnosis; therapeutic; cancer; cytostatic; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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Pred. No. 0.69;
8; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 54; 196pp; English.
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                                                                                                                                                                                                                                                                                                                                                                           cell to a protease treatment
                 tumor necrosis factor receptor
                                                                                                                                                    25-NOV-2004; 2004WO-IL001085
                                                                                                                                                                                     26-NOV-2003; 2003US-0524885P
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Best Local Similarity 35.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                         Inberg A,
                                                                                                                                                                                                                                                                                        WPI; 2005-418017/42.
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                                                                                                                                                                                                                                                                                                        REFSEQ, NP 067324
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                                                                                   WO2005052182-A2
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                                                   Mus musculus
                                                                                                                    09-JUN-2005
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                                                                                                    The present invention relates to novel mucin-like proteins (I) and their coding sequences. The present sequence is one such human mucin-like protein. The mucin-like proteins and coding sequences are useful in the therapy or in the prevention of a disease when the increase in the mucin-like activity of a polypeptide is needed e.g. bacterial infections, allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced disease, allergic conjunctivitis, otitis, tissue injury, epithelial wounding, inflammatory bowel disease, Crohn's disease, small adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia, chronic cholecystitis, or skin cancer.
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e.g. bacterial infections, allergic asthma, inflammation, allergic conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung cancer, or skin cancer.
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                 Score 68.5; DB 8; Length 2240;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mucin-like protein, SCS0004, variant SEQ ID 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1161 CSQDEYFDHEEGVCVPCM-----PPTTPQ 1184
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/label= Signal_peptide
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/label= Mature_protein
                                                                         Claim 2; SEQ ID NO 4; 170pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR18913 standard; protein; 2258 AA
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                                                                                                                                                                                                                                                                                                                                        34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.2
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                       Sequence 2240 AA;
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                                The present invention relates to novel mucin-like proteins (I) and their coding sequences. The present sequence is one such human mucin-like protein. The mucin-like proteins and coding sequences are useful in the therapy or in the prevention of a disease when the increase in the mucin-like activity of a polypeptide is needed e.g. bacterial infections, allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced disease, allergic conjunctivitis, oritis, tissue injury, epithelial wounding, inflammatory bowel disease, Crohn's disease, small adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia, chronic cholecystitis, or skin cancer.
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                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                              8; Length 2258;
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                                                                                                                                                                                                                                                                                                                34.1%; Score 68.5; I
45.2%; Pred. No. 15;
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Claim 2; SEQ ID NO 3; 170pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR18915 standard; protein; 2264 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                   Local Similarity 45.2
les 14; Conservative
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                                                                                                                                                                                                                                                                         Sequence 2258 AA;
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                                                                                                                                                                                                                                                                                                                  Query Match
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The invention describes a transgenic mouse (I) comprising a disruption in an subtilisin-like protein convertase (SPC6) gene, where there is no native expression of an endogenous SPC6 gene. The therapeutic agent is administered by inhalation or insufflation or cal, buccal, buccal, parenteral, intraocular, intraperitoneal, intravenous, intrapleural, intraocular, intraperitoneal, parenteral, intraocular, intraperitoneal, or rectal route. The transgenic mouse and associated methods are useful for identifying potential therapeutic associated with SPC6 agonists and antagonists) for treating conditions associated with SPC6. The identified agents are potentially useful for treating diseases such as schizophrenia. The mouse is useful for sequence of mouse SPC6.
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adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia, chronic cholecystitis, or skin cancer.
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                              7;
                                                                                                                                                             Length 2264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroleptic; subtilisin-like protein convertase 6 agonist; subtilisin-like protein convertase 6 antagonist; transgenic; subtilisin-like protein convertase 6; SPC6; schizophrenia.
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse subtilisin-like protein convertase 6 (SPC6).
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                                                                                                                                                                                                                                                                                                  1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ 31
                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                             Score 68.5; I
Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC71568 standard; protein; 1548 AA
                                                                                                                                                         34.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-2002; 2002US-00180903
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                                                                                                                                                                                                                                    14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-777261/73
                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1548 AA;
                                                                                                   Sequence 2264 AA;
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24-SEP-2001;
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ADC
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This sequence shows a murine subtilase. The homologous human subtilase coding sequence is located on chromosome 9421.13. Related EST's are expressed in kidney (renal cell adenocarcinoma), head and neck tissue, heart, multiple sclerosis lesions, cervix, pooled germ cell tumours. Uterus tumour, adenocarcinoma, retina ii and stomach. The subtilisin cuterus tumour adenocarcinoma, retina ii and stomach. The subtilisin convertase subtilisin. There are two blocks of 11 furincomman proprotein convertase subtilisin. There are two blocks of 11 furincommembrane domain, also in the C-terminal portion, suggesting that the transmembrane domain, also in the C-terminal portion. Suggesting that the potent is localised on the outside of the membrane. The subtilase compounds, which may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. Ocerors comprising the collocatide are useful for modulating the activity of subtilase in a disease, e.g. a central nervous system disorder, a gestrointestinal catisorder, cancer, a cardiovascular disorder, a genitourinary disorder, cancer, a partin, polvit pain, colon tumour, pre-oesophageal dysphagia, cransplant rejection, pelvit pain, colon tumour, pre-oesophageal dysphagia, congestive heart failure, myocardial infarction, ovary tumour, lung tumour, thyroid tumour, carcinoma, lymphoma, Kaposi's sarcoma, congestive heart failure, myocardial infarction, ischaemia, hypertensive comgestive heart failure, myocardial side useful for preventing or ameliorating the diseases eited above
                                                                                                                                                                                                                                                                                                                                                                                    pooled germ cell; tumour, uterus; adenocarcinoma; retina II; stomach; proprotein convertase subtilisin; furin-like repeat; Alzheimer's disease; Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia; gastritis; ulcers; urinary incontinence; lupus nephritis; renati rejection; myocardial infarction; erectile dysfunction; ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma; congestive heart failure; ischaemia; hypertensive vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New subtilase-encoding polynucleotide and its encoded protein, useful for identifying modulators of subtilase activity, and in gene therapy for treating e.g. Alzheimer's disease, cancers, congestive heart failure or
                                                                                                                                                                                                                                                                                                                                          Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney; renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;
Disclosure; Page 122-26; 135pp; English.
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                                                                                                                                                      ABB80243 standard; protein; 1877
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29-JUL-2002; 2002US-0398734P.
                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                               Murine subtilase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003060109-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
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Best Local Similarity 37.8 Matches 14; Conservative

Query Match

1;

Gaps

2

33.6%; Score 67.5; DB 7; Length 1548; 37.8%; Pred. No. 14; ive 4; Mismatches 14; Indels 5.

Length 33;

DB 5;

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is human TACI cysteine-rich consensus region
                                                      Query Match
Best Local Similarity
                           Sequence 33 AA;
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                                                                                                                                                                                                                                                                                         Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
                                                          Gaps
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                             33.6%; Score 67.5; DB 7; Length 1877; 37.8%; Pred. No. 17;
                                                        Indels
                                                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQR 32
                                                        14;
                                                                                                                                                                                                                                                                     Human TACI cysteine-rich consensus region #1
                                                        4; Mismatches
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                                                                                                                                                                                     AAE15495 standard; peptide; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-021459IP.
14-MAY-2001; 2001US-00214591.
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                                                                                                                                                                                                                                           (first entry)
                                                          14; Conservative
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                                           Best Local Similarity
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    Sequence 1877 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                           12-MAR-2002
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                                Query Match
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The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &bgr; strands D and E that reduces the biological activity of the TALL-1 antagonist as immunosuppressive, antirheumatic, attinifiammatory, antiathritic, dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic, neuroprotective, antithyroid, antipyretic, newportory, antiathritic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal. TC is useful for treating autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, Grave's disease, autoimmune hemolytic anaemia, autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory; antiarthritic; dermatological; antidiabetic; neuroprotective; antipyreid; antipyreitc; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever; post-sireptococcal glomerulonephritis; polyarteritis nodosa; TACII; CRD; cysteine rich domain.
                                                                    Gaps
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                                                                    Indela
                                                                 14;
                                                                                                                                                                                        1 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 33
                                                                                                                                         1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
Score 66.5; DE pred. No. 0.39; B; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        ADA49368 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TACI1 cysteine rich domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
13-AUG-2002; 2002US-0403364P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2002; 2002WO-US034376
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       33.1%;
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                                                                           11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA49368;
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                                                                                                                                                                                                                                                                                                                      RESULT 69
ADA49368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; neuroprotective; nootropic; immunomodulator; metabolic; antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; antidiatemen; antipartine; vasotropic; antibacterial; asthma; AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor; rheumatorid arthritis; graft-versus-host disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn's disease; panctrophic lateral sclerosis; ALS; Alzheimer's disease; disease; alsoherulonephritis; inflammatory bowel disease; ischaemia; multiple sclerosis; Parkinson's disease; transgenic animal.
thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis and polyarteritis nodosa. The present sequence represents a cysteine rich domain (CRD) module of human TACII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor ligand family member) receptor and encoding nucleic acids.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
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                                                                                                                                                Length 33;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human AGP-3 receptor cysteine rich repeat region #1.
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                                                                                                                                                                                                                                                     Score 66.5; DB
Pred. No. 0.39;
                                                                                                                                                                                      8; Mismatches
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                                                                                                                                              33.1%;
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                                                                                                                                                                   Best Local Similarity
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                                                                                                       Sequence 33 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAU10951;
                                                                                                                                              Query Match
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composition of hybridoma cells which are derived from B cells, which continuous treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are cusful for treating acute panorcaetitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosis, cachexia/anorexia, catheres, fever, glomenlonephritis, inflammatory bowel disease, catheres, fever, glomenlonephritis, inflammatory bowel disease, catheres, ever, glomenlonephritis, inflammatory bowel disease, catheres, especies, parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for developing transgenic animals expressing (II), which are useful for producing the present sequence represents the amino acid sequence of human AGP-3 cysteine-rich repeat region #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides novel tumor necrosis factor receptor (TNFR) ztnfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors and antibodies. Ztnfr14 polynucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Ztnfr14 polypeptides and be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastasis, and immunity such as separating resting from stimulated
                                                                                                                                                                                                                                                                                                                                                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor necrosis factor receptor; TACI; cancer; neoplasm; diagnosis; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                   Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumor necrosis factor receptor TACI Cys-rich domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 33.1%; Score 66.5; DB Local Similarity 32.4%; Pred. No. 0.44; nes 11; Conservative 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                  Sequence 37 AA;
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Matches
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AAW75785
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                                                                                                               1,
                                                                                                                                                                                                                                                                                                                                                 Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
immune cells. The present sequence is that of the Cys-rich domain of human TNFR TACI ADZ67771. This sequence was compared with that of ztnfr14 in the identification of ztnfr14 as a member of the TNFR family.
                                                                                                               Gaps
                                                                                                               1;
                                                                                   Length 48;
                                                                                                               Indels
                                                                                                              14;
                                                                                   Score 66.5; DB 9;
Pred. No. 0.57;
8; Mismatches 14;
                                                                                                                                           1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                              | : : | | | : | : | : | : | : | : | CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 45
                                                                                                                                                                                                                                                                                                                              Human TACI cysteine rich extracellular region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 13; 94pp; English.
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                                                                                                                                                                                                                                            AAE15500 standard; peptide; 59
                                                                                   33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-2001; 2001WO-US015567.
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27-JUN-2000; 2000US-021459IP.
14-MAY-2001; 2001US-00214591.
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                                                                                                                11; Conservative
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                                                                                      Query Match
Best Local Similarity
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                                                            Sequence 48 AA;
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This is the amino acid sequence of the N-terminal, i.e. the extracellular, domain of novel human transmembrane activator and CAML-extracellular, domain of novel human transmembrane activator and CAML-interactor (TACI) protein (see AAW15783). TACI is a lywphoryte receptor protein that is involved in the calcium activation pathway. It is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically cregulate B cell responses without affecting T cell activity. The extracellular domain of TACI functions as a binding site for a ligand that stimulates the activation of the cell by inducing the binding of the CTC terminal portion (see AAW75784) of TACI to the N-terminal domain of CAML. A recombinant form of the extracellular portion of TACI acts as cominant-negative or blocking agent and acts to suppress the immune system. It can be used to treat or prevent autoimmune disease, graft rejection or graft versus host disease. The extracellular region is also used in a claimed method for identifying a ligand for TACI, in which binding of a candidate molecule is determined by detecting cellular
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(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human TACI cysteine-rich extracellular region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACI; transmembrane activator and CAML-interactor; calcium signal-modulating cyclophilin ligand; human; lymphocyte surface receptor; human; B-call; B lymphocyte; infection; cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis; immunosuppressive; graft versus host disease; transplant rejection; therapy; signal transduction.
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                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                     33.1%; Score 66.5; DB 5; 32.4%; Pred. No. 0.7; iive 8; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW75785 standard; protein; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US004270
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                                                                                                                                                                                                                                         Sequence 59 AA;
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inflammatory diseases
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                                                                                                                                                 Local Similarity
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                                                                                           Sequence 166 AA;
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Matches
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                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; cronh's disease; scleroderma; autocimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription factor, or of NF-AT dependent transcription
                                                                                                                                  Gaps
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                                                                                           Length 166;
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                                                                                                                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                             BB
                                                                                                                                  8; Mismatches
                                                                                             Score 66.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                 AAE15494 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                              Human TACI extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 12A; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
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                                                                                         33.1%;
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Best Local Similarity
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                                                         Sequence 166 AA;
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sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human TACI protein extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane activator and CAML interactor; TACI; extracellular domain; trinerising polypebtide; homotrimeric protein complex; antiinflammatory; antiartric; antiinflammatory; antiartric; anticheumatic; immunosuppressive; antiarteriosclerotic; cytostatic; gene therapy; inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; autoimmune disease; atherosclerosis; osteoporosis; allograft rejection; cancer; human; heat shock binding protein; HSBP; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising an extracellular domain of the transmembrane activator and calcium-signal modulating cyclophilin ligand (CAML) interactor (TACI), and a trimerizing polypeptide, useful for treating
                                                                                                                                                                                                  Gaps
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                                                                                                                                                          DB 5; Length 166;
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                                                                                                                                                     Score 66.5; DB 5; I pred. No. 2; 8; Mismatches 14;
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                                                                                                                                                                                                                                                                                  34 CPEEQYWDPLLGTCMSCKTICNHQS-ORTCAAFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TACI-HSBP fragment SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                ADN03188 standard; protein; 171 AA
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                                                                                                                                                     ch 33.1%;
1 Similarity 32.4%;
11, Conservative 8
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activities, and can be used in gene therapy. The polypeptides are useful for treating and controlling inflammatory diseases, e.g. rheumatoid arthritis or inflammatory bowel disease, autoimmune disease, attherocalerosis, osteoporosis, allograft rejection and cancer. The present sequence represents a human TACI and heat shock binding protein (HSBP) fusion protein fragment, which is used in the exemplification of the present invention.
                88888888888
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Sequence 171 AA;

1; 1; Gaps Query Match
33.1%; Score 66.5; DB 8; Length 171;
Best Local Similarity 32.4%; Pred. No. 2.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1

1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34

CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 38

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R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Teapis, FEMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16 A;Refearence number: S31208; MUID:93010984; PMID:1396583
A;Accessionale type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-184 < LA2>
A;Cross-references: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 4-184 < LA3>
A;Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955
C;Genetics:
A;Cenetics: A;Genetics: A;Genetics
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R;Nakagawa, T.; Murakami, K.; Nakayama, K.
RESE Lett. 327, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a i
A;Reference number: S34583; MUID:93327934; PMID:8335106
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A;Molecule type: mRNA
A;Residues: 1-1548 cNAK>
A;Cross-references: UNIPROT:004592; UNIDARC:UPI000016CF9E; GB:D17583; NID:g407344; PIDN:E
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: T42215
R;Gao, Z.; Garbers, D.L.
Biol. Chem. 273, 3412-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro A;Reference number: Z22080, MUID:98123114; PMID:9452463
A;Accession: T42215
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A;Anlecule type: mRNA
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A;Residues: 1-5376 <GAO>
C,Genetics: NIPROT:088799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:G3327420; PI
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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N;Alternate names: sperm-specific membrane protein
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                                                                                                                                                                                                                                                          A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor
                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 34; Conservative 0
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ses 14; Conserv
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B-Call maturation sapiens (man)
C;Species: Home sapiens (man)
C;Species: Anomes 1995 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43466; S31208; Sascel
B, A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire
A;Reference number: S43466
B,Accession: S4346
B,Accession: S4346
B,Accession: Dralimnary
B,Molecule type: DNA
B,Residues: 1-184 < LAA>
A;Residues: UNIPROT: Q02223; UNIPARC: UPI0000034D1B; EMBL: Z29574; NID: 9471244; PID
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cathepsin B (EC 3.
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H64888
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B32669
I51060
B42822
T32379
KHRTB
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JC8020
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T39228
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T01999
T06702
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S34968
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A82787
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T20125
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S11926
G88968
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T42992
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T16840

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NiAlternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serine CiSpecies: Spodoptera frugiperda (fall armyworm)
CiSpecies: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                             C;Accession: T43251
R;Cieplik, M.; Klenk, H.
R;Cieplik, M.; Klenk, H.
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiperons, A;Reference number: Z22368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: S07127
R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A;Fitle: The isoinhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the priman A;Reference number: S07127; MUID:84255715; PMID:6564898
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R;Rocbrock, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.;
J. Biol. Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proce
A;Reference number: A43434; MUID:92381036; PMID:1512259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1680 <ROE>
A;Cross-references: UNIPROT;P30432; UNIPARC;UPI000016BC03; GB:M94375; NID:g157461; PID:g1
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Description: responsible for the endoproteolytic processing of proproteins with specifi
C, Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1299 «CIE»
A;Cross-references: UNIPROT:Q26489; UNIPARC:UPI0000083055; EMBL:Z68888; NID:g1167859;
A;Experimental source: clone Sfurin 6; ovary
C;Function:
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C;Species: Ascaris lumbricoides (common roundworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Drosophila melanogaster
C,Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.9%; Score 58; DB 2; Length 1299; Best Local Similarity 37.1%; Pred. No. 29; Matches 13; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
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furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                   A,Accession: T43251
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 1-63 48AB>
A,Crosa - references: UNIDARC:UPI000012D146
C,Superfamily: roundworm trypsin inhibitor
                              furin (EC 3.4.21.75) - fall armyworm
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1 Similarity 37.1%;
13; Conservative
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Best Local Similarity
Matches 13; Conserv
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A;Gene: CESP:T10E10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residudes: 1-1101 (GEI>
A;Crose-references: UNIPROT:Q22378; UNIPARC:UP1000017BB8F; EMBL:U39644; NID:g1049339;
A;Experimental source: strain Bristol N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T10E10.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T16840 R;Geisel, C. RiGeisel, C. Ribbert C, Caenorhabdited to the EMBL Data Library, October 1995 A;Description: The sequence of C. elegans cosmid T10E10. A;Reference number: Z18588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C23G10.8 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004 C; Accession: T1S77 R; Latraille, P. Submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid C23G10. A; Reference number: Z18372 A; Accession: T15577
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0
                                                                                                                                                                                  DB 2; Length 5376;
A;Map position: 5
C;Function:
A;Description: functions in multiple cell adhesion processes
A;Note: found exclusively on the apical region of the sperm head
C;Keywords: cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61, DB 2; Length 1101, Pred. No. 11; 7; Mismatches 11; Indels
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Pred. No. 14;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                      16; Indels
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A;Gene: CESP:C23G10.8
A;Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
                                                                                                                                                                                                                                                                                                                                                        3300 CPTNSOFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
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A;Molecule type: DNA
A;Residues: 1-758 <LAT>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                            Query Match
32.1%; Score 64.5; DE
Best Local Similarity 35.1%; Pred. No. 16;
Matches 13; Conservative 5; Mismatches
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Best Local Similarity 37.5%;
Matches 12; Conservative
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Best Local Similarity 42.9%;
Matches 9; Conservative
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C,Accession: T01519

R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gotte R;Johnson, A.F.; wCcombie, W. Buhartienssen, R.; wCcombie, W. Buhartienssen, R.; McCombie, W. Buhartiensted to the BWBL Data Library, May 1997
A;Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-989 «JOH»
A;Cross-references: UNIPROT:Q9ZU00; UNIPARC:UPI00000A0E3D; EMBL:AF001308; NID:g2104523; I
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:018118; UNIPARC:UPI00006118C; EMBL:281129; PIDN:CAB03405.1;
A;Experimental source: clone T23F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pupochetical protein T23F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25169
R;Wilkinson, J:
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19990
A;Recession: T25169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
                                                                                                                                                                                              hypothetical protein T10M13.17.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                               1851 CSAHSVYTSCVPSCLPSCQDPEGQCTGAGAPSTCEEGC 1888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55.5; DB 2;
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Pred. No. 20;
7; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 41.9%;
Matches 13; Conservative
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Residues: 1-330 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 16/3
C;Superfamily: gliadin
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Zonadhesin - pig

C,Species: Sus scrofa domestica (domestic pig)

C,Species: Sus scrofa domestica (domestic pig)

C,Species: Sus scrofa domestica (domestic pig)

C,Accession: T34022

R,Hardy, D.M.; Garbers, D.L.

J. Biol. Chem. 270, 26025-26028, 1995

A,Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
A,Reference number: Z21464; MUID:96064658; PMID:7592795

A,Accession: T34022

A,Status: preliminary, translated from GB/EMBL/DDBJ

A,Rolecule type: mRNA
A,Robidus: 1.2476 - ALAR-
A,Robidus: 1.2476 - ALAR-
A,Robidus: UNIPROT:Q28983; UNIPARC:UP1000013C373; EMBL:U40024; NID:g1066465; PI
A,Experimental source: strain Meishan; testis
C,Genetics:
A,Genetics:
A,Genetics:
A,Genetics:
A,Description: may be involved in sperm adhesion to the zona pellucida
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(S.Superfemanly: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C;Superfemanly: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
P;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1717/Product: epidemanl growth factor receptor homolog 1 #status predicted <MAT>
F;1018-1323/Domain: protein kinase homology <KIN>
P;1026-1034/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: M86396; NID:g160957; PID
                                                                                                                                                                                                                                                                                                                                                                                                                     "Contains protein-tyrosine kinase (BC 2.7.1.112)
N'Contains: protein-tyrosine kinase (BC 2.7.1.112)
C'Specise: Schistcosoma mansoni
C'Specise: Schistcosoma mansoni
C'Adcession: A45558, 827836
R'Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Blochem. Parasitol. 53, 17-32, 1992
A;Title: Alternative splicing of the Schistcosoma mansoni gene encoding a homologue of A;Accession: A45558
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                                                                                                                             Length 1680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1717;
                      transmembrane protein
                                                                                                                                                                                   Indels
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A;Molecule type: mRNA
A;Rosidues: 1-117 - NAIPA
A;Cross-references: UNIPROT:026566; UNIPARC:UPI000007DCD7; El
A;Cross-references: Grim NCBI backbone (NCBIP:111129)
                      C:Keywords: hydrolase; serine proteinase; transmembrane pro
P;409-652/Domain: subtilisin homology <SBT>
P;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                     1 CSQNEYFDSLLHACIPCQLRCSS-NTPPLTCQRYC 34
                                                                                                                           ; Score 57.5; DB
; Pred. No. 41;
5; Mismatches
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illarity 40.9%; Pred. No. '
Conservative 2; Mismatch
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A; Cross-references: FlyBase: FBgn0004598
                                                                                                                             ch 28.6%;
1 Similarity 34.3%;
12; Conservative
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Best Local Similarity
Matches 12; Conserva
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nes 9; Conserva
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Best Local Similarity
Matches 12; Conserv
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A;Residues: 1-2022 <WIR>
A;Residues: 1-2022 <WIR>
A;Cross-references: UNIPOT:(14788; UNIPARC:UPI0000161189; GB:U42391; NID:g1147782; PIDN: R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overlapping expression of multiple unconventional myosin gent A;Reference number: A55758; MUID:94294418; PMID:8022818
A;Accession: I67700
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Molecule type: mRNA
A;Mosediues: 234-322 <RES>
A;Cross-references: UNIPARC:UPI0000073918; GB:L29149; NID:g457257; PIDN:AAA20912.1; PID:c
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Cipate: 13-Jan-1995 #sequence_revisiae
Cipate: 13-Jan-1995 #sequence_revisiae
Cipate: 13-Jan-1995 #sequence_revisiae
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
Cipate: 1235-1249, 1994
A.Pritle: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
A.Fritle: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
A.Fritle: The sequence of a 16 kb segment on the left arm of yeast chromosome X identifies
A.Fritle: The sequence of a 16 kb wn
A.Reference number: S4662; MUID:95274326; PMID:7754713
A.Residues: 1-758 <PUR>
A.Reference number: F:; Goffeau, A.Reference number: S56977
A.Reference number: S56977
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A;Residues: 1-758 <PUW>
A;Cross-references: UNIPARC:UPI000013B60A; EMBL:249481; NID:g1015584; PIDN:CAA89502.1; Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.
J. Cell Sci. 109, 653-661, 1996
A;Title: Human myosin-IXb, an unconventional myosin with a chimerin-like rho/rac GTPase-&
A;Reference number: A59256; MUID:97063843; PMID:8907710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Map position: 19p13.1
C;Superfamily: myosin motor domain homology; protein kinase C zinc-binding repeat homolog
C,Reywords: nucleotide binding; P-loop
F;149-941/Domain: myosin motor domain homology #status atypical <MMO>
F;239-246/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 31-Dec-2004
C;Accession: A59256; 161700
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N;Alternate names: probable membrane protein YJL206c; protein J0316
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Pred. No. 1.3e+02;
2; Mismatches 6; Indels
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
                              Indela
                                 9
                                 Mismatches
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ilarity 52.9%;
Conservative
                                                                                                                                                                                                                                                                                                                      myosin-IXb [similarity] - human
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                                 9; Conservative
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Best Local Similarity
Matches 9, Conserv
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                                 Matches
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30197
R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.
J. Biol. Chem. 272, 8791-8801, 1997
A;Tille: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com A;Reference number: 220771; MUID:97236843; PMID:9079715
A;Accession: T30197
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-2155 <LEGS.
A;Cross-teferences: UNIPROT:008523; UNIPARC:UPI00002793C; EMBL:X99805; NID:g1915908; PI
A;Experimental source: strain CD1; whole cochleae
A;Note: non-collagenous protein only expressed in the inner ear, by cells both in and sy
R;Matthews, L.

submitted to the EMBL Data Library, November 1996

A;Reference number: 219781

A;Accession: T23681

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-1513 <WIL>
A;Residues: 1-1513 <WIL>
A;Residues: 1-1513 <WIL>
A;Reperimental source: Clone M02G9

C;Genetics:
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C,Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zi
C,Keywords: nucleotide binding; P-loop
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()Species: Rattus norvegicus (Norway rat)

()Species: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

()Accession: 554307

R)Reinhard, J; Scheel, A.A.; Diekmann, D; Hall, A.; Ruppert, C.; Baehler, M.

R)Reference number: 54307

A; Reference number: 554307; MUID:95188874; PMID:7882973

A; Accession: S54307

A; Status: preliminary; nucleic acid sequence not shown

A; Residues: 1-1980 (REL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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F;239-246/Region: nucleotide-binding motif A (P-loop)
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>
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A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 2; Length 1513;
Pred. No. 75;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1980;
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29.4%; Pred. No. 1.2e+02;
tive 6; Mismatches 15;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 DSCQNVCQNVCQGACVSQNSPPAVCQQTC 169
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Best Local Similarity 44.8%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 29.4 Matches 10; Conservative
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Best Local Similarity
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A; Cross-references: UNIPROT: Q12307; UNIPARC: UPI00006A6BC; EMBL: 267750; NID: 91061256; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-118 <POW>
A;Cross-references: UNIPARC:UPI00006A6BC, EMBL:274210; NID:g1431255; PIDN:CAA98735.1; P
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: A84544
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
w.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallans.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: Q9SLE1; UNIPARC: UPI00000A1869; GB: AE002093; NID: 94581120; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypochetical protein M02G9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09.Jul-2004
C;Accession: T23682
R;Matthews, L.
                        hypothetical protein YDL162c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D1510
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S61051; S67714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g16770 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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C;Superfamily: Saccharomyces hypothetical protein YDL162c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 CSMDSFFDELLRDSHACTHTHTCNPPGPENTHTHTC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 CNRNSYCSRWFYCCLTLSSFCSLRC---VPPL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.5; DB Fred. No. 17; 4; Mismatches
                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1995
A;Reference number: S61010
A;Accession: S61051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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Pred. No. 3
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Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: SGD: S0002321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S67708
A;Accession: S67714
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-118 <POH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-255 <STO>
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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A; Map position: 2
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C;Species: Caenorhabditis elegans
C;Species: Tacoct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22759
R;Dobson, R.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19610
A;Accession: T22759
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: J-2224 «WIL»
A;Residues: 1-2224 «WIL»
A;Coss-references: UNIPROT:P90891; UNIPARC:UPIO00017BA22; EMBL:Z81091; PIDN:CAB03143.1;
A;Experimental source: clone F55H12
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
C;Accession: T13954
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUD:98360089; PMID:9633030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mENA
A,Residues: 1-1574 <NAK>
A,Residues: 1-1574 <NAK>
A,Residues: 1-1574 <NAK>
A,Cross-references: UNIPROT:08281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293;
A,Experimental source: strain Sprague-Dawley; brain
C,Genetics:
A,Gene: MEGF6
                           A,Map position: 10L
C;Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc
F;42-78/Domain: GAL4 zinc binuclear cluster homology <GAL4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB 2; Length 1574;
Pred. No. 1.4e+02;
6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        966 CSAGAPCDAVTGSCI-CPAGRWGPRCAQSCPPLTFGLNCSQIC 1007
                                                                                                                                                                                                                             Indels
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                                                                                                                                                               Length
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                                                                                                                                                               DB 2;
                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                               Score 53.5; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                    46 ACIACRKRVRCSGNIPCRLCQ 67
                                                                                                                                                                                                                                                                                           13 ACIPC---QLRCSSNTPPLTCQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 26.4%;
Local Similarity 32.6%;
les 14; Conservative (
                                                                                                                                                           Query Match 26.6%;
Best Local Similarity 50.0%;
Matches 11; Conservative
A;Cross-references: SGD:S0003741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 18
T13954
MEGF6 protein - rat
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Best Local &
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Aintrons: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12(493/1; 2555/1; 2720/1; 2739/3; 2819/1
P;220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>P;342-95/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>P;442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>P;442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>P;642-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>P;654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>P;1651-116/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3-P;1651-116/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3-P;1651-116/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3-P;1651-116/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3-P;1
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Rjde Bolle, M.F.C.; Eggermont, K.; Duncan, R.E.; Osborn, R.W.; Terras, F.R.G.; Broekaert, Blant Mol. Biol. 28, 713-721, 132-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-721, 140-7302, 140-721, MUID:95375234; PMID:7647302
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A;Status: preliminary
A;Molecule type: manA
A;Rolecule type: manA
A;Rolecule type: manA
A;Rolecule type: manA
A;Residues: 1-63 < DEB>
A;Residues: 1-63 < DEB
A;Coss-references: UNIPROT:P25404; UNIPARC:UPI000002D6AF; EMBL:UI5539; NID:9558864; PIDN
R;Cammue, B.P.; De Bolle, M.F.; Terras, P.R.; Proost, P.; Van Damme, J.; Rees, S.B.; VanC
J. Biol. Chem. 267, 2228-2233, 1992
A;Ritle: Isolation and characterization of a novel class of plant antimicrobial peptides
A;Reference number: A42316; MUID:92129292; PMID:1733929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <BPI8><BPI9><BPI0>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caenorhabditis elegans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S28291
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C;Species: Mirabilis jalapa (garden four-o'clock)
C;Date: 28-0cr-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
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    Gaps
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submitted to the EMBL Data Library, December 1992
A,Reference number: 828285
A,Stecesion: $28291
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-2844 <THO>
A,Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCE9; EMBL:Z19157
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A;Note: sequence extracted from NCBI backbone (NCBIP:78217)
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; Pred. No. 3e+02
3; Mismatches
    3; Mismatches
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                                                                                       6 YFDSLLHACIPCQ-LRCS-SNTPPLTC 30
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                                                                                                                                                      Query Match 25.6%;
Best Local Similarity 38.5%;
Matches 10; Conservative
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Best Local Similarity 44.4%;
Matches 12; Conservative
    12; Conservative
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    Matches
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Cispecies: Caenorhabditis
Cispe
                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-294 <WILL>
A; Cross-references: UNIPROT: Q9XUSO; UNIPARC: UP10000076A8F; EMBL: 281573; PIDN: CABO4626.1;
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A,Molecule type: DNA
A,Residues: 1-1474 «STO»
A,Cross-references: UNIPROT:062504; UNIPARC:UP100000781E7; GB:chr_III; PIDN:CAA79570.1;
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C;Genetics:
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A;Introns: 33/3; 50/2; 95/1; 118/3; 181/2; 293/3; 342/1; 371/3; 390/2; 451/1; 484/2
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Pred. No. 1.7e+02;
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Pred. No. 73;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SQNEYFDSLLHACIP-COLRCSSNTPPLTCQRYC 34
                                      A;Reference number: 219781
A;Accession: T23682
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A;Residues: 1-547 <NHA>
    submitted to the EMBL Data Library, November 1996
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                                                                                                                                                                                                                                                                                                                                A;Experimental source: clone M02G9
C;Genetics:
A;Gene: CESP:M02G9.3
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nes 8; Conservative
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Best Local Similarity
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A;Map position:
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A;Gene: ZC84.6
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Cross-references: UNIPARC:UPI000002AIC9; EMBL:281110; PIDN:CAB03263.1; GSPDB:GN00023; C
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A;Cross-references: UNIPROT:002364; UNIPARC:UPI0000086677; EMBL:281527; PIDN:CAB04279.1;
A;Experimental source: clone F35E12
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T21772; T24296
                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T01D3.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21773; T24297
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A;Introns: 38/2; 87/3; 128/2; 242/2; 374/3; 404/3; 722/3; 830/3; 845/1
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Pred. No. 1.3e+02;
3; Mismatches 19; Indels 13
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                                                                                                                                  2; Length 497;
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                                                                                                                                                                                          Indels
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A;Molecule type: DNA
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                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Steward, C.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19470
A;Acession: T21773
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submitted to the EMBL Data Library, November 1996
submitted to the EMBL Data Library, November 1996
A.Reference number: Z19470
A.Accession: T21772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1996 A;Reference number: Z19870 A;Accession: T24296
                                                                                                                               Score 51.5; DE
Pred. No. 77;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n, oreward, c.
submitted to the EMBL Data Library, October 1996
A.Reference number: 219870
A, Accession: T24297
                                                                                                                                                                                                                                                14 CIPCOLRCSSNTPPL----TCORYC 34
                                                                                                                                                                                                                                                                                                        CVASÓGRCSADTCPCVAARKTCDEHC 40
                       A;Gene: CESP:2K287.1
A;Map position: 5
A;Introns: 20/1; 44/2; 99/3; 339/3; 443/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone T01D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.6%;
Best Local Similarity 25.5%;
Matches 12; Conservative 3
                                                                                                                                     25.6%;
                                                                                                                                     Query Match 25.6
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :Residues: 1-915 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-915 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: T01D3.6b
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 148764; 835754
R;Della, N.G.; Senior, P.V.; Bowtell, D.D.
Development 117, 1333-1343, 1993
A;Pitle: Isolation and characterisation of murine homologues of the Drosophila seven in A;Reference number: 148764
A;Pitle: Isolation and characterisation of Multi-8404535
A;Accession: 148764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-282 <RES-
A;Cross-references: UNIPROT:Q06985; UNIPARC:UP1000002451E; EMBL:Z19580; NID:g297801; PID
C;Superfamily: Drosophila developmental protein sina; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-497 < WIL>
A; Cross-references: UNIPROT: Q23460; UNIPARC: UPI000007F2F3; EMBL: Z70757; PIDN: CAA94805.1;
A; Experimental source: clone ZK287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Rolidus: 1-282 <RES2
A;Roliduse: 1-282 <RES2
A;Cross-references: UNIPROT:P61092; UNIPARC:UP1000000B9B3; EMBL:Z19579; NID:g297034; PID
C;Superfamily: Drosophila developmental protein sina; RING finger homology
                                                                                                                                                                                                                              Biah-lA protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148763; S35753
R;Della, N.G.; Senior, P.V.; Bowtell, D.D.
Development 117, 1333-1343, 1993
A;Title: Isolation and characterisation of murine homologues of the Drosophila seven in A;Reference number: I48763; MulD:94008536; PMID:8404535
A;Accession: I48763
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:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
:Accession: T27827
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Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.6%; Score 51.5; DB 2; Length 282; Best Local Similarity 41.9%; Pred. No. 47; Matches 13; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.6%; Score 51.5; DB 2; Length 2 Best Local Similarity 41.9%; Pred. No. 47; Matches 13; Conservative 3; Mismatches 12; Indele
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A,Accession: T27827
A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 FDSLLHACIPCQ---LRCSSNTPPLTCQRYC 34
                             10 LLHACIPCOLRCSSNT-PPLTCORYC 34
                                                                 24 MIEACIGNGGRCNENVGPPYCCSGFC 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
C;Superfamily: Arabidopsis thaliana probable transcription factor F12K22.14; RING finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable transcription factor F12K22.14 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: E96612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                 Indels
                                                                                                                                                                                                            1345 CPPNSHYES----CVSLCQPRCAAIRLKSDCGHYC 1375
Local Similarity 31.4%; Pred. No. 2.6e+02; nes 11; Conservative 6; Mismatches 13;
                                                                                                                                           34
                                                                                                                                                     1 CSQNEYFDSLLHACIP-CQLRCSSNTPPLTCQRYC
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Best Local Similarity 45.8%;
Matches 11; Conservative
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Best Local Similarity 42.3%;
Matches 11; Conservative
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A;Residues: 1-653 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA A; Residues: 1-641 <STO>
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A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: F12K22.14
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         Best Loc
Matches
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A; Residues: 1-999 <WILD.
A; Cross-references: UNIPROT:Q17969; UNIPARC:UPI0000079A41; EMBL:Z37139; PIDN:CAA85494.1;
A; Experimental source: clone C14B1
R; Kershaw, J.
A; A; Ccession: T21723
A; Accession: T21723
A; A; Ccession: T21723
A; Ccession: T21723
A; Ccession: DNA
A; Residues: 1-999 <WIZ>
A; Residues: 1-999 <WIZ>
A; Cross-references: UNIPARC:UPI0000079A41; EMBL:Z34799; PIDN:CAA84320.1; GSPDB:GN00021;
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A,Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870
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A;Residues: 1-2120 <CCU>
A;Residues: 1-2120 <CCU>
A;Cross-references: UNIPROT:09YH85; UNIPARC:UPI00000FD14C; EMBL:AJ012287; NID:e1361091;
A;Note: non-collagenous protein only expressed in the inner ear
    A;Residues: 1-927 <W12>
A;Cross-references: UNIPARC:UPI000086677; EMBL:Z81110; PIDN:CAB03262.1; GSPDB:GN00023;
A;Experimental source: clone T01D3
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C;Species: Gallus gallus (chicken)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T302A3
R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.
Hear. Res. 130, 62-74, 1999
Hear. Res. 130, 62-74, 1999
A;Reference number: 220783; MUID:99251817; PMID:10320099
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CiSpecies: Caenorhabditis elegans
CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccesion: T19275; T21723
RiHarris, B.
Submitted to the EMBL Data Library, September 1994
A;Reference number: Z19099
A;Accession: T19275
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                C;Genetics:
A;Gene: CESP:T01D3.6
A;Map position: 5
A;Introns: 38/2; 87/3; 128/2; 242/2; 374/3; 416/3; 734/3; 842/3; 857/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 CTEFTYFLOYCOLALPOVAMNONWRAQINCPLACPLNAHPSTCTSSC 514
                                                                                                                                                                                                                                                                                                                                                                                          Length 927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSONEYFDSLLHACIP------CQLRCSSNTPPLICQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                     Score 51.5; DB 2; Length 92
Pred. No. 1.3e+02;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F34D10.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 YEDSLLKTCIGRAFERVKKMTPPLRIQSY 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 YFDSLLHACIPCQL-RCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.6%; Score 51.5;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.6%;
Best Local Similarity 25.5%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: F34D10.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
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Gape

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Gaps

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C;Species: Ascaris lumbricoides (common roundworm)
C;Bate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S08572
R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A;Title: The isoinhibitors of chymotrypsin/elastage from Ascaris lumbricoides: the prima?
A;Reference number: S07127; MUID:84255715; PMID:6564898
A;Accession: S08572
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P19379; UNIPARC:UPI000017715C; EMBL:X53011
C;Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; ubiqu:C;Superfamily: ubiquitin/ribosomal protein CEP52; ribosome; zinc finger
C;Keywords: DNA binding; protein biosynthesis; ribosome; zinc finger
F;1-2/Product: ubiquitin (fragment) #starus predicted <UBI>F;3-74/Product: ribosomal protein CEP52 #starus predicted <RIB>F;3-74/Domain: ribosoomal protein CEP52 homology <CPH>F;2-61/Region: zinc finger CCCC motif
F;68-74/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ORF23 - Lymantria dispar nuclear polyhedrosis virus C.Species: Lymantria dispar nuclear polyhedrosis virus, LdWNPV C.Species: Lymantria dispar nuclear polyhedrosis virus, LdWNPV C.Accession: T30370
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr: Virology 253, 17-34, 1999
A;Tile: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d A;Reference number: Z20836; WUID:99124785; PMID:9887315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT: Q9YMV1; UNIPARC: UPI00000F34B2; EMBL: AF081810; PIDN: AAC70208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubiquitin / ribosomal protein CEP52 - common tobacco (fragment)
NyAlternate names: ubiquitin fusion protein
Cispecies: Nicotiana tabacum (common tobacco)
Cispecies: Nicotiana tabacum (common tobacco)
Cipate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
Ciscossion: 51032
Rigenschik, P.; Parmentier, Y.; Criqui, M.C.; Fleck, J.
Nucleic Acids Res. 18, 4007, 1990
A;Title: Sequence of a ubiquitin carboxyl extension protein of Nicotiana tabacum.
A;Reference number: 510332; MUID:90326543; PMID:2165257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|| : | :|: | :|: | CGROEVWIE----CTGCELKCGQDENTPCALMCRPPSCE 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%; Score 50; DB 2; ilarity 44.4%; Pred. No. 23; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
24.9%; Score 50;
Best Local Similarity 30.8%; Pred. No.
Matches 12; Conservative 6; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 1-63 «BAB»
A,Cross-references: UNIDARC:UDI0000176391
C,Superfamily: roundworm trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRKCYVRCPRRTPORTCR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 CIPCQLRCSSNTPPLTCQ 31
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S10332
A;Molecule type: DNA
A;Residues: 1-74 <GEN>
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C4b-binding protein alpha chain - bovine
C5pecies Bos primigenius taurus (cattle)
C5pecies Bos primigenius 241300
R5Hilarp, A.; Thern, A.; Dahlback, B.
J. Immunol. 153, 4190-4199, 1994
A;Rillarp, A.; Thern, A.; Dahlback, B.
J. Immunol. 153, 4190-4199, 1994
A;Reference number: 146001
A;Recession: 146001
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-610 cHIL>
A;Cross-references: UNIPROT;Q28065; UNIPARC;UP10000126C27; EMBL:Z31693; NID:g469117; PIE
C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology <FH3>
F;174-234/Domain: complement factor H repeat homology <FH4>
F;239-294/Domain: complement factor H repeat homology <FH5>
F;174-234/Domain: complement factor H repeat homology <FH5>
F;259-362/Domain: complement factor H repeat homology <FH5>
F;259-284/Domain: complement factor H repeat homology <FH5>
F;36-425/Domain: complement factor H repeat homology <FH5>
F;36-425/Domain: complement factor H repeat homology <FH6>
F;487-541/Domain: complement factor H repeat homology <FH8>
F;487-541/Domain: complement factor H repeat homology <FH8>
F;487-541/Domain: complement factor H repeat homology <FH8>
                                                                                                                                                                                                                                                                                                                                                     Objection At2g21840 [imported] - Arabidopsis thaliana (Species Arabidopsis thaliana) (Species Arabidopsis thaliana) (Species Arabidopsis (Species (Species Arabidopsis (Species A
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 2; Length 746;
Pred. No. 1.2e+02;
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                                                                                                                                                      204 FDEMFYHCSACNFTLDLRCVSLPPPL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 CKETVVYDRFYYLCVECDLKC 287
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Best Local Similarity
Matches 6; Conserv
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A,Map position: 2
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Length 342;

Score 50; DB 2; Pred. No. 85;

24.9%; 50.0%;

Query Match Best Local Similarity

chymotrypsin/elastase inhibitor - common roundworm

receptor

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A; Molecule type: protein
A; Residues: 30-38;41-53, X', 55-79, XX', 82-94, 'NK'; XX', 100-104;107-128;162-167,'X', 169-20
A; Residues: 30-38;41-53, X', 55-79, 'XX', 82-94, 'NK'; XX', 100-104;107-128;162-167,'X', 169-20
A; Residues: 30-38;41-53, X', 55-79, 'XX', 82-94, 'NK'; XX', 100-104;107-128;162-167, 'X', 165-179;
A; Note: the purified protein, called tumor necrosis factor binding protein, is a soluble R; Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A; Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rec A; Reference number: A38281; MUID:91017809; PMID:2170974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-455 cGRA-
A;Residues: 1-455 cGRA-
A;Cross-references: UNIPARC:UPI000002CE11; GB:M37764
A;Notes: UNIPARC:UPI0000002CE11; GB:M37764
A;Notes: The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann,
EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
le form of the receptor.
A;Reference number: S12057; MUID:91006021; PMID:1698610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: S1205.
A,Accession: S12057
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-455 < NOP>
A,Cross-references: UNIPARC: UPI000002CE11; EMBL: X55313; NID: 937223; PIDN: CAA39021.1; PID: A,Cross-references: UNIPARC: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, We R. Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
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A,Residusa: 41-43, X',45-53, X',55-57 <SEC>
A,Cross-references: UNIPARC:UD10000072FDB
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Ler
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A,Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: renal failure patient urine
R; Engelmann, H.; Novick, D.; Wallach, D.
C Biol. Chem. 255, 1531-1536, 1990
A; Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence 1
A; Reference number: A35010; MUID:90110215; PMID:2153136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence A;Reference number: A60231; MUID:90292116; PMID:2113477
                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 1-455 <HIM>
A,Cross-references: UNIPARC:UPI000002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:
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A; Title: Isolation and characterization of a tumor necrosis factor binding protein from A; Reference number: A60594; MUID:89171156; PMID:2924890
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rat tumor necrosis factor
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A,Residues: 41-60 cGAT>
A,Zross-references: UNIPARC:UP100001736E1
A,Experimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf,
     ritle: Molecular cloning and expression of human and r
Reference number: A36555, MUID:91090841, PMID:1702293
Accession: A36555
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A;Accession: A38258
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A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>
A;Cross-references: UNIPARC:UP100001736E2
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A;Residues: 1-13 <KEM>
A;Cross-references: UNIPARC:UP10000155CFB
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A;Residues: 41-45 <ENG>
A;Cross-references: UNIPARC:UP100001736E3
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Unifornate names: P55 tumor necrosis factor receptor; TNF receptor type 1

N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
R;Puchis P, P; Strehl, S; Dworzak, M; Himmler, A.; Ambros, P.F.
A;Pierence number: A38208; MUID:92250049; PMID:1315717
A;Accession: A38208
A;Accession: A38899; MUID:90235284; PMID:2158862
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CG81272

probable aminotransferase (degT family) Cj1294 [imported] - Campylobacter jejuni (strain CjSpedales: Campylobacter jejuni (strain CjSpedales: Campylobacter jejuni (strain CjSpedales: Campylobacter jejuni (strain CjSpedales: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Ju1-2004

R; Paccession: CB1272

R; Paccession: CB1272

R; Paccession: CB1272

A; Reference number: B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel A; Reference number: A81250; MUD:20150912; PMID:10688204

A; Recession: C81272

A; Residues: DNA

A; Residues: 1-376 *PMA

A; Residues: 1
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A,Genetics: C31294
C,Superfamily: erythromycin resistance protein
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cossion: 1-655 < LOE2
A; Cossion: 1-655 < LOE2
A; Cossion: 1-655 < LOE2
A; Cossion: 1-650 < LOE3
A; Experimental source: placenta
A; Note: part of this sequence, including the amino end of the mature protein, confirmed
A; Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.Cell 61, 361-370, 1990
A; Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.
A; Reference number: A34900; MUID: 90235285; PMID: 2158863
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A;Residues: 1-455 <SCH:
A;Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:
R;Himmler, A: Maurer-Fogy, I:; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
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92;
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                              Conservative
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A; Gene: CESP: Y69H2.3b
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A,Molecule type: DNA
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R; McMurray, A.
C; Accession: T27319
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Ajrange position: 12p13.2-12p13.2
Ajrange position: 12p13.2-12p13.2
Ajintrons: 13/5, 55/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
Ajintrons: 13/5, 55/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
Ajintrons: 13/5, 55/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor; transmembrane protein
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
C;Keywords: duplication; glycoprotein; receptor; receptor; factor acceptor | #status predicted <&XT>
F;12-210/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F;44-82Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: transmembrane #status predicted <MEM>
F;212-234/Domain: intracellular #status predicted <MEM>
F;24,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27318
R;Mcurray, A.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z20343
A;Accession: T27318
A;Construction: UNIPROT:O9U1T6; UNIPARC:UPI0000164288; EMBL:298877; PIDN:CAB54472.1;
A;Construction: Construction: Construction: Construction: Caenoric Caenoric Construction: Caenoric Construction: Caenoric Construction: Caenoric Construction: Caenoric Caenoric Construction: Caenoric Caeno
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A,Residues: 41-53, X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A,Residues: 41-53, X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A,Cross-rences: UNIPARC:UP100001736E4
A,Experimental source: urine
C,Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
                                              R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified
A;Areference number: JC2404; MUID:95128033; PMID:7765720
A;Accession: JC2404
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Map position: 5
A;Introns: 183/1; 247/1; 288/1; 318/1; 364/1; 388/2; 457/1; 481/2; 521/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.9%; Score 50; DB 1; Length 455; Best Local Similarity 35.3%; Pred. No. 1.1e+02; Matches 12; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSQNEYFDSLLHACIPCOLRCSS --- NTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSQNE---YFDSLLHACIPCOLRCSSNTPPLTCQ 31
               A, Experimental source: normal urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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T27319
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hypothetical protein T5A14.15 [imported] - Arabidopsis thaliana hypothetical protein T5A14.15 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Boccies: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: P56596
C;Accession: P56596
Chin, C. M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marziall, Rizzo, M.; Romely, D.; Sakano, H.
Rizzo, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsie.
A;Reference number: P56591
A;Reference number: P5651
A;Reference number: P56591
A;Reference number: P56591
A;Reference number: P56591
A;Reference number: P56591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Gross-references: UNIPROT:021418; UNIPARC:UPI00000762C2; EMBL:Z75545; PIDN:CAA99886.1; A.Experimental source: clone K10D3
                                                                                                                                                                                                                         A;Cross-references: UNIPROT:09U1T5; UNIPARC:UPI0000164289; EMBL:298877; PIDN:CAB54473.1; A;Experimental source: clone Y69H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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A;Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 546/2; 586/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein K10D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
A;Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 CRSNEKFE-----PCKTVCSDTKCNEEPRFCPQVC 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSQNEYFDSLLHACIPCOLRCSS---NTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 24.9%; Score 50; DB 2; I
Local Similarity 32.4%; Pred. No. 1.4e+02;
hes 12; Conservative 3; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match
Local Similarity 29.3%; Pred. No. 2e+02;
hes 12; Conservative 7; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-922 <WIL>
                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-626 <WIL>
submitted to the EMBL Data Library, August 1997 A;Reference number: Z20343 A;Accession: T27319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June 1996
A;Reference number: 219762
A;Accession: T23573
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Query Match 24.4%;
Best Local Similarity 41.2%;
Matches 7; Conservative
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T48828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor A,Reference number: A62950; MUID:20437337; PMID:10984043
A,Accession: 683398
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-216 <STO>
A,Cross-references: UNIPROT:0912C8; UNIPARC:UPI00000C553D; GB:AE004624; GB:AE004091; NID
A,Experimental source: strain PAO1
C,Genetics:
A,Gene: PA1979
А;кевідцев: 1-1360 <STO>
A;Crose-references: UNIPROT:Q9ZVU3; UNIPARC:UPI00009D265; GB:AE005173; NID:g4204269; PI
C;Genetics:
A;Gene: T:Ai4.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable two-component sensor PA1979 [imported] - Pseudomonas aeruginosa (strain PAO1) [Species: Pseudomonas aeruginosa (cispecies: Cispecies: Cis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:O9XXP6; UNIPARC:UPI000007EED1; EMBL:AL021503; PIDN:CAA16424. A;Experimental source: clone Y68A4A
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sacession: T27303
R;Steward, C
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20340
A;Reference number: Z20340
A;Reference pumber: Z20340
A;Reference pumber: DNA
A;Residues: L392 WIL>
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                                                                                                                                                                                                                                                                                                                        24.9%; Score 50; DB 2; Length 1360; 50.0%; Pred. No. 2.8e+02; ive 4; Mismatches 4; Indels
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A;Map position: 5
A;Introns: 45/2; 74/3; 139/3; 175/2; 190/3; 241/3; 305/3; 356/3
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                   A; Map position: 1
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T27303
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C.Species: Lactuce sativa (garden lettuce)
C.Species: Lactuce sativa (garden lettuce)
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C.Accession: T30558
R.Meyers, B.C.; Chin, D.B.; Shen, K.A.; Sivaramakrishnan, S.; Lavelle, D.O.; Zhang, Z.; N Plant Cell 10, 1817-1832, 1998
A.Title: The major resistance gene cluster in lettuce is highly duplicated and spans seve A.Feference number: Z20859; MUID:99030190; PMID:9811791
A.Accession: T30558
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-1847 <MEY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9ZT69; UNIPARC:UPI00000A22B8; EMBL:AF072271; NID:g4139035; i C;Gonetics: 894/3; 1069/3; 1293/3; 1848/3; 1838/3 A;Introns: 894/3; 1068/3; 1293/3; 1548/3; 1838/3
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequa; Ricerence number: A72200; MUID:99287316; PMID:10360571
A;Accession: (772772
A;Status: preliminary
A;Molecule type: DNA
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Cispecies: Neurospora crassa

Cipate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001

Cipate: 07-May-2000 #text_change 17-May-2000 #text_change 16-Feb-2001

Cipate: 05-May-2000 #text_change 17-May-2000 #text_change 16-Feb-2001

Aimolecule type: DNA

Aimolecule type: DNA

Aimolecule 1189 cSGH>

Aimolecule 1180 cSGH
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C7272
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Pred. No. 67;
2; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
24.6%; Score 49.5; DB 2;
Best Local Similarity 35.7%; Pred. No. 4.1e+02;
Matches 10; Conservative 5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 CLPCDYNTTSKKPPRLC 133
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A;Gene: mec-3
A;Introns: 82/3; 106/3; 190/3; 228/3; 300/1
A;Introns: 82/3; 106/3; 190/3; 228/3; 300/1
A;Introns: 82/3; 106/3; 190/3; 228/3; 300/1
C;Superfamily: homeotic protein mec-3; homeobox, homelogy; LIM metal-binding repeat homology cLIM1>
F;99-19/Domain: LIM metal-binding repeat homology cLIM2>
F;99-145/Domain: LIM metal-binding repeat homology cLIM2>
F;91-145/Domain: homeobox homology cHOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-346 <WIL>
A;Cross-references: UNIPARC:UPI0000177DBC; EMBL:281054; PIDN:CAB02885.1; GSPDB:GN00022; C
A;Experimental source: clone F01D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
A;Introns: 26/3; 63/1; 107/2; 131/3; 215/3; 253/3; 325/1
C;Superfamily: homeotic protein mec-3; homeobox homology; LIM metal-binding repeat homolo
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Mateushita, T.; Yamaoka, T.; Otsuka, S.; Moritani, M.; Matsumoto, T.; Itakura, M. Biochem. Biophys. Res. Commun. 242, 176-180, 1998
A; Title: Molecular cloning of mouse paired-box-containing gene (Pax)-4 from an islet bet A; Reference number: JC5827; MUID:98102804; PMID:9439631
A; Accession: JC5828
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cromment: This protein is involved in pancreatic islet development.
C;Comment: This protein is involved in pancreatic islet development.
C;Comment: This protein is involved in pancreatic islet development.
C;Superfamily; paired box transcription factor Pax-4; homeobox homology; paired box homo F;S-129/Domain: paired box nucleus; transcription regulation
F;S-129/Domain: paired box homology ePBH>
F;171-227/Domain: homeobox homology eHOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
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                                                                                                                                                                                                                                                                                                       Query Match

24.4%; Score 49; DB 1; Length 321;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; Score 49; DB 2; Length 346
44.4%; Pred. No. 1.1e+02;
ive 3; Mismatches 7; IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F01D4.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2; 1
Pred. No. 1.1e+02;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T20458
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wild, A. submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paired-box-containing protein Pax-4 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQNEYFDSLLHACIPCQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPCO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 CSQHYYKDHSIHRCAGCK 93
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Best Local Similarity 53.3%;
Matches 8; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4%;
Matches B; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Gene: CESP: F01D4.6
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C;Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Tanglatis (22390, A27662)
C;Accession: S28390, A27662
R;Xue, D.; Finney, M.; Ruvkun, G.; Chalfie, M.
EMBO J. 11, 4969-4979, 1992
A;Title: Regulation of the mec-3 gene by the C. elegans homeoproteins UNC-86 and MEC-3.
A;Recence number: S28390; MUID: 93099872; PMID: 1361171
A;Accession: S28390
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-314 xUNB
A;Residues: 1-314 xUNB
A;Residues: UNIPROT: P09088; UNIPARC: UPI000012EEA8; EMBL: L02877; NID: G156488; PIC
R;Way, J.C.; Chalfie, M.
Cell 54, 5-16, 1998
A;Title: mec-3, a homeobox-containing gene that specifies differentiation of the touch x
A;Reference number: A27662; MUID: 88253425; PMID: 2898300
A;Accession: A27662
A;Molecule type: DNA
A;Residues: 'MPRAHDIWILLY', 20, 'DLLQESS', 28, 'ITASSKNSETIIYFQ', 44-321 xWAY>
A;Cross-references: 'MPRAHDIWILLY', 20, 'DLLQESS', 28, 'ITASSKNSETIIYFQ', 44-321 xWAY>
A;Cross-references: 'MPRAHDIWILLY', 20, 'DLLQESS', 28, 'ITASSKNSETIIYFQ', 44-321 xWAY>
A;Cross-references: 'WINIPARC: UPI000016B90E; GB:MZ0244; NID: 9156363; PIDN: AAA28108.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession B71439
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel P.; Wedler, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71439
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-306 < BEV.>
A;Cross-references: UNIPROT:023551; UNIPARC:UPI00000A5737; GB:Z97342; NID:g2245031; PID:
                      A,Cross-references: UNIPROT:Q9X118, UNIPARC:UPI0000D38D8, GB:AE001784; GB:AE000512; NID A,Experimental source: strain MSB8 C,Genetics: C,Genetics: A,Genetics: C,Superfamily: cell division inhibitor related protein; ferredoxin 2[4Fe-4S] homology
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                                                                                                                                                                                                                                              Score 49, DB 2, Length 283,
Pred. No. 95,
2, Mismatches 8, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Superfamily: Arabidopsis thaliana 33.5K hypothetical protein
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FESLCHGCGACSIMCPVN 112
                                                                                                                                                                                                                                                                                                                                                                                                      FDSLLHACIPCOLRCSSN 24
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity
   A;Residues: 1-283 <ARN>
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hypothetical protein F17J16.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47794
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Le submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24476
A;Reference number: Z24476
A;Reference number: Draiminary
A;Residues: 1-602 - DAN>
A;Residues: 1-602 - DAN>
A;Residues: 1-602 - CDAN>
A;Cross-references: UNIPROT:Q9LYS4; UNIPARC:UP10000046194; EMBL:AL163527
A;Experimental source: cultivar Columbia; BAC clone F17J16
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A;Residues: 1-654 <DUZ>
A;Cross-references: UNIPROT:Q17982; UNIPARC:UPI000017B77E; EMBL:U53141; PIDN:AAA96110.1;
A;Experimental source: strain Bristol N2; clone C14C11
C;Genetics:
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A;Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3
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Cipate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
Cipate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
Cipacession: T30136
Ribu, Z.; Gattung, S.
submitted to the EMBL Data Library, March 1996
AiDescription: The sequence of C. elegans cosmid C14C11.
A;Reference number: Z20742
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.9e+02;
3; Mismatches 7; Indels
    Length 461;
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N;Alternate names: hypothetical protein YKL162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 602;
                                                                        13; Indels
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Query Match
24.4%; Score 49; DB 2; I
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 11; Conservative 5; Mismatches 13.
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24.4%; Score 49; DB 2; 1
Best Local Similarity 37.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 8
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                          1 CSQNE---YFDSLLHACIPCQLRCSSNTPPLTC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SEWF----YRCSICNFFLDFRCARNFPPLTIQ 167
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Local Similarity 42.9%;
Les 12; Conservative
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A; Note: F17J16.170
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                      Pagester TIF9.18 [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004 (C.Accession: A96639) (C.Accession: A96639) (C.A.; Edung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 416-820, 2000 (C.A.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Tallon, A; Tallon, A; Tactus: preliminary A; Tactus: preliminary A; Tallon, A; Tallon, A; Tactus: preliminary A; Tallon, A; Tallon, A; Tallon, A; Tactus: preliminary A; Tallon, A
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C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homold
C;Keywords iglycoprotein; kidney; receptor; transmembrane protein; tumor
C;Keywords iglycoprotein; kidney; receptor; transmembrane protein; tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: NGF receptor repeat homology <NGI>
F;44-184/Domain: NGF receptor repeat homology <NGI>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;31-231/Domain: transmembrane #status predicted <TMM>
F;54-145/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Rolecule type: mRNA
A;Rosesidues: 1-461 «SUT>
A;Cross-references: UNIPROT:P50555; UNIPARC:UPI00001372A9; GB:U19994; NID:g1141752; PIDN
A;Accession: PC4033
A;Rosldues: 1-7 «SU2>
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A,Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A,Reference number: JC4302, MUID:96011645; PMID:7590278
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JG4302; PC4093
R;Suter, B.; Pauli, U.
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Pred. No. 1.4e+02;
5; Mismatches 12; Indels
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A)Experimental source: kidney cell line 15
C;Genetics:
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                                                289 RCLSDTPPKACLKPC 303
20 RCSSNTPPLTCQRYC 34
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Matches 10; Conservative
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text change 05-Oct-2004
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text change 05-Oct-2004
C;Caccession: A6019; S25144; C49175; B46438; A46438; PHI569; S32109
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I A;Reference number: A46019; MUID:93194170; PMID:8449489
A;Accession: A46019
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A; Residues: 1.2531 < DEL.
A; Residues: 1.2531 < DEL.
A; Cross-references: UNIPROT:001705; UNIPARC:UPI000002922B; GB:Z11886; GB:S4722B; NID:g28
A; Cross-references: UNIPROT:001705; UNIPARC:UPI000002922B; GB:Z11886; GB:S4722B; NID:g28
A; Note: sequence extracted from NCBI backbone (NCBIP:127318)
B; Franco del Amo, P.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; is ubmitted to the EMBL Data Library, April 1992
A; Pescription: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggest A; Reference number: S25144
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A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinati
A;Reference number: A46438; MUID:93252998; PMID:8486742
A;Accession: B46438
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                                                                                                  A,Residues: 1-1984 <SCH>
A,Cross-references: UNIPROT:P98163; UNIPARC:UPI0000138879; EMBL:U13637; NID:g535345; PID
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A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: C49175
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Fig. 19-20 (Domain: LDL receptor ligand-binding repeat homology cLDL8)
Fig. 22-26 (Domain: LDL receptor ligand-binding repeat homology cLDL0)
Fig. 26-304 (Domain: LDL receptor ligand-binding repeat homology cLDL2)
Fig. 26-304 (Domain: LDL receptor ligand-binding repeat homology cLDL2)
Fig. 26-306 (Domain: LDL receptor ligand-binding repeat homology cLDL2)
Fig. 119-1109 (Domain: LDL receptor ligand-binding repeat homology cLDL2)
Fig. 119-122 (Domain: LDL receptor ligand-binding repeat homology cLDL9)
Fig. 1199-1217 (Domain: LDL receptor ligand-binding repeat homology cLDL9)
Fig. 1199-1218 (Domain: LDL receptor ligand-binding repeat homology cLDL9)
Fig. 1199-1318 (Domain: LDL receptor ligand-binding repeat homology cLDL9)
Fig. 1199-1318 (Domain: LDL receptor ligand-binding repeat homology cLDL9)
Fig. 1199-1318 (Domain: LDL receptor ligand-binding repeat homology cLDL9)
Fig. 1190-1315 (Domain: LDL receptor ligand-binding repeat homology cLDL9)
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F;90-124/Domain: LDL receptor ligand-binding repeat homology <LD13>
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Note: sequence extracted from NCBI backbone (NCBIP:126159)
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A;Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRA>
A;Cross-references: UNIPARC:UPI0000177461; EMBL:211886
R;Lardelli, M.; Lendahl, U
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A,Molecule type: mRNA
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Pred. No. 5e+02;
7; Mismatches 1
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A;Cross-references: FlyBase:FBgn0004649
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ilarity 33.3%;
Conservative
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N;Alternate names: motch protein
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A; Residues: 1161-1547 < LAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S25144
A; Accession: T13171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrotherical protein Y64G10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
Submitted to the EMBL Data Library, September 1999
A;Reference number: Z20336
A;Accession: T27283
A;Accession: T27283
A;Accession: T27283
A;Accession: U27283
A;Accession: U38471.1;
A;Coss-references: UNIPARC:UPI000017BCB4; EMBL:ALI10498; NID:e1542303; PIDN:CAB54471.1;
A;Coss-references: UNIPARC:UPI000017BCB4; EMBL:ALI10498; NID:e1542303; PIDN:CAB5471.1;
A;Coss-references: UNIPARC:UPI000017BCB4; EMBL:ALI10498; NID:e1542303; PIDN:CAB5471.1;
A;Genetics:
A;Genetics:
A;Genetics: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7
                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1483 <PAS>
A;Cross-references: UNIPROT:P31202; UNIPARC:UPI0000137AD6; GB:S53418; NID:g263497; PIDN:
A;Cross-references: UNIPROT:P31202; UNIPARC:UPI0000137AD6; GB:S53418; NID:g263497; PIDN:
A;Experimental source: strain S288C
R;Boyer, J; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Colleaux, L.; Thierry, A.; Monnie submitted to the Protein Sequence Database, March 1994
A;Reference number: S37813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1483 <BOY>
A;Cross-references: UNIPARC:UPI0000137AD6; EMBL:Z28010; NID:g485992; PIDN:CAA81845.1; PI
A;Experimental source: strain S288C
                                                                                                                                                               Yeast 8, 987-995, 1992
AjTille: The sequence of a 9.3 kb segment located on the left arm of the yeast chromosom
Thosomal protein L10.
A,Reference number: 830013; MUID:93127732; PMID:1481574
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13171
R;Schonbaum, C.P.; Lee, S.; Mahowald, A.P.
Proc. Natl. Acad. Sci. U.S.A. 92, 1485-1489, 1995
A;Title: The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the A;Reference number: Z17627; MUID:95183490; PMID:7878005
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    C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004
C;Accession: S30015; S37821
R;Pascolo, S.; Charvini, M.; Boyer, J.; Colleaux, L.; Thierry, A.; Dujon, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 4.2e+02;
7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2; Length 148
Pred. No. 3.9e+02;
4; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SGD:UFD4
A;Cross-references: SGD:S0001493; MIPS:YKL010c
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Best Local Similarity 34.4%;
Matches 11; Conservative
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S3782.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-474 <WIL>
A;Cros-*references: UNIPROT:Q9XXQ2; UNIPARC:UPI00000783D7; EMBL:AL021503; PIDN:CAA16417.1
A;Experimental source: clone Y68A4A
C;Genetics:
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A;Crosalouse: 1-bub everk.

A;Crosalouse: 1-bub everk.

C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, r mones (weak bonds with these hormones promote their transfer across the membranes), thyrc c;Superfamily: serum albumin; serum albumin repeat homology

C;Superfamily: serum albumin; serum albumin repeat homology

C;Keywords: carrier protein; duplication; plasma estimates

F;11-14/Domain: signal sequence #status predicted <SIG>
F;15-18/Domain: propeptide #status predicted <MAT>

F;13-196/Domain: serum albumin #status predicted <MAT>
F;23-196/Domain: serum albumin repeat homology <SAL>
F;21-390/Domain: serum albumin repeat homology <SAL>
F;21-390/Domain: serum albumin repeat homology <SAL>
F;21-391/Domain: serum albumin repeat homology <SAL>
F;21-30/Domain: serum albu
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DNA Cell Biol. 9, 647-655, 1990

A;Title: Atlantic salmon (Salmo salar) serum albumin: cDNA sequence, evolution, and tiss.

A;Reference number: A36238; MUID:91083837; PMID:2261082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 47/2; 80/3; 145/3; 181/2; 196/3; 238/2; 269/2; 306/3; 342/2; 357/3; 418/3
                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y68A4A.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Salmo salar (Atlantic salmon)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A36238; S13079
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                                                                                                              --- LRCSSNTPPLTCOR 32
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24.1%; Score 48.5; DB 2; Length 474;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 8; Indels
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       26.0%; Pred. No. 8.4e+02;
tive 5; Mismatches 14; Indels
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Bubmitted to the EMBL Data Library, January 1998
A;Reference number: 220340
A;Accession: T27297
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                                                                                                                  1 CSQNEYFDS --- LLHACIPCQ
                                             13; Conservative
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   Best Local Similarity
Matches 13; Conserv
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A;Status: preliminary
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1865-1932, 'RK',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054
A;Cross-references: UNIPARC: UPI0000177463
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C;Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwee decentions:
A;Gene: notch-1
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residues: 1-3635 cMIN>
A, Cross-references: UNIPROT: Q61001; UNIPARC: UP1000004C5E8; EMBL: U37501; NID: 92599231; PI
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C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10039
R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.
B;Date: 1997
A;Reference number: Z16923
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protein; ankyrin repeat homology; EGF homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2531;
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F;1983-2015/Domain: ankyrin repeat homology
F;2016-2048/Domain: ankyrin repeat homology
F;2049-2081/Domain: ankyrin repeat homology
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F;1149-1180/Domain: EGF homology <EG17>
F;1187-1218/Domain: EGF homology <EG18>
F;1233-1264/Domain: EGF homology <EG74>
F;1352-1383/Domain: EGF homology <EG74>
F;1351-1425/Domain: EGF homology <EG79>
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F,795-826/Domain: EGF homology <EG10>
F,813-994/Domain: EGF homology <EG11>
F,911-942/Domain: EGF homology <EG12>
F,949-980/Domain: EGF homology <EG12>
F,949-980/Domain: EGF homology <EG12>
F,987-1018/Domain: EGF homology <EG14>
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Il Similarity 40.7%;
11; Conservative 4
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F.122-254/Domain: EGF hor
F.221-224/Domain: EGF hor
F.339-370/Domain: EGF hor
F.339-370/Domain: EGF hor
F.416-449/Domain: EGF hor
F.456-447/Domain: EGF hor
F.456-447/Domain: EGF hor
F.455-555/Domain: EGF hor
F.532-563/Domain: EGF hor
F.532-563/Domain: EGF hor
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Best Local Similarity
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A,Note: proximal regi
C,Superfamily: notch
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F;757-788/Domain:
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RESULT 67

24.4%; Score 49; DB 2; Length 3635;

Query Match

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C.) Special Transmission of the control of the cont
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C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol.
C;Keywords: serine proteinase inhibitor
F;4-54/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;4-54/13-37,29-50/Disulfide bonds: #status predicted
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Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cipate: 2802 2012-2018
Cipate: 2812 2012-2018, 1998
Ajtitle: Genome sequence of the nematode C. elegans: a platform for investigating biolog Ajtitle: Genome sequence of the nematode C. elegans and waw sanger.ac.uk/Projects/C_elemance: see websites genome.wustl.edu/gss/C_elegans/ and waw sanger.ac.uk/Projects/C_elemance: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and AjAccession: C89946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: JN0380
R;Zykova, T.A.; Vinokurov, L.M.; Markova, L.F.; Kozlovskaya, E.P.; Elyakov, G.B.
Bioorg. Knim. 11, 293-301, 1985
A;Title: Amino-acid sequence of trypsin inhibitor IV from Radiantis macrodactylus.
A;Reference number: JN0380
A;Accession: JN0380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trypsin inhibitor IV - sea anemone (Radianthus macrodactylus)
C;Species: Radianthus macrodactylus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
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24.1%; Score 48.5; DB 2; Length 3034;
Best Local Similarity 25.5%; Pred. No. 8.3e+02;
Matches 12; Conservative 4; Mismatches 18; Indels 13
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even-pass transmembrane receptor protein precursor - mouse; Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPCQL----
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A;Residues: 1-56 <ZYK>
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A,Molecule type: DNA
A,Residues: 1-98 <STO>
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A;Gene: Celsr1
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TABOUT 198

Hypothetical protein P56A6.2 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1399 #text_change 23-Mar-2001
C; Accession: T33079
R; Murray, J; Rohlfing, T; O'Neal, D; Wilson, R.
submitted to the EMBL Data Library, May 1998
A; Description: The sequence of C. elegans cosmid F56A6.
A; Recession: T33079
A; Accession: T3307
A; Accession: T3307
A; Accession: T3307
A; Accession: T3307
A; Constrinental source: strain Bristol N2; clone F56A6
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Recentions induces:

A; Molecule type: mRNA
A; Redidues: 1-608 eBYRA
A; Redidues: 1-608 eBYRA
A; Residues: 1-608 eBYRA
A; Residues: 1-608 eBYRA
A; Residues: 1-608 eBYRA
A; Residues: 1-608 eBYRA
A; Contents: 0.319-320, 1992
A; Title: Sequence analysis of a second cDNA encoding Atlantic salmon (Salmo salar) serum A; Reference number: $30594; MUID: 93013056; PMID: 1398147
A; Contents: annotation
A; Reference number: $30594; MUID: 93013056; PMID: 1398147
A; Contents: annotation
A; Note: only a list of differences from sequence A36238 is shown
C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: carrier protein; duplication; plasma
C; Keywords: carrier protein; duplication; plasma
C; Keywords: serum albumin; serum albumin #status predicted <RIG>
F; 1-14/Domain: signal sequence #status predicted <RIG>
F; 19-608/Product: serum albumin #status predicted <AND>
F; 19-608/Product: serum albumin repeat homology <SAI>
E; 21-196/Domain: SETUM albumin repeat homology SAI>
E; 21-196/Domain repeat homology SAI>
E; 21-196/Doma
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F;411-591/Domain: Berum albumin repeat homology <SA3>
F;26-72,71-80,93-108,107-118,142-187,186-195,218-264,263-271,283-299,298-309,336-381,380
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                                              serum albumin 2 precursor - Atlantic salmon
C;Species: Salmo salar (Atlantic salmon)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A46757; S30594
R;Byrnes, L
Bubmitted to the EMBL Data Library, June 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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1. Similarity 34.4%; Pred. No. 2.1e+02;
11; Conservative 5; Mismatches 9; Indels
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Les 9; Conserv
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Best Local S
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A; Residues: 1-304 < KAM>
A; Cross references: UNIPROT: Q28864; UNIPARC: UPI0000136C90; GB: S73337; NID: 9685016; PIDN: A; Experimental source: 11ver
C; Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI
C; Superfamily: tissue factor pathway inhibitor; asset inhibitor
C; Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
C; Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor homology < BP1>
F; 29-304; Product: tissue factor pathway inhibitor homology < BP2>
F; 29-304; Product: tissue factor pathway inhibitor homology < BP2>
F; 21-104; Domain: animal Kunitz-type proteinase inhibitor homology < BP2>
F; 21-25-175; Domain: animal Kunitz-type proteinase inhibitor homology < BP3>
F; 21-204; G3-87, 79-100, 125-175, 134-189, 150-171, 217-267, 226-250, 242-263/Disulfide bonds: #
F; 64/Inhibitory site: Lys (coagulation factor X) #status predicted
F; 135/Inhibitory site: Arg (coagulation factor X) #status predicted
F; 227/Inhibitory site: Arg (unidentified proteinase) #status predicted
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Lissue factor pathway inhibitor precursor - rhesus macaque

Lissue factor pathway inhibitor precursor - rhesus macaque

Lissue factor pathway inhibitor; lipoprotein-associated coagulation inhib

C;Alecrase: Macaca mulatta (rhesus macaque)

C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JC2264

R;Kamel, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamot

J. Blochem. 115, 708-714, 1994

A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path

A;Reference number: JC2264; MUID:94375417; PMID:8089087
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A;Accession: T27686
A;Accession: T27686
A;Accession: T27686
A;Acteutus: preliminary; translated from GB/EMBL/DDBJ
A;Acteutus: DNA
A;Residues: 1-314 <WIL>
A;Residues: 1-314 <WIL>
A;Cross-references: UNIPROT:023390; UNIPARC:UPI000007D293; EMBL:Z70038; PIDN:CAA93886.1;
C;Genetics:
A;Gene: CESP:ZK1067.7
   H
A;Cross-references: UNIPROT:Q94162; UNIPARC:UPI000007C506; GB:chr_V; PIDN:AAB09171.1; C;Genetics:
C;Genetics:
A;Gene: C;10G8.4
A;Map position: 5
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T27686
Hypotherical protein ZK1067.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27686
S;Thomas, K.
submitted to the EMBL Data Library, March 1996
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                                                                                                                                                                                   Length 98;
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Pred. No. 51;
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Best Local Similarity 40.0
Matches 14; Conservative
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A;Introns: 30/3; 296/2
C;Superfamily: gliadin
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                        protein kinase (EC 2.7.1.37) R-mil - Rous-associated virus (type 1)
N;Alternate names: kinase-related transforming protein R-mil; R-mil proto-oncogene protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A40341
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-450 eFEL>
A;Cross-references: UNIPROT: P27966; UNIPARC: UPI00001342F7; GB:M62407; NID:g210080; PIDN: IC;Comment: This protein is translated as a mil-env polyprotein.
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C,Superfamily: kinase-related transforming protein; protein kinase homology
C,Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase;
F;81-347/Domain: protein kinase homology <KIN>
F;89-97/Region: protein kinase ATP-binding motif
F;109/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rous-associated virus
A;Note: host Gallus gallus (chicken)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40341
R;Felder, M.P.; Eychene, A.; Barnier, J.V.; Calogeraki, I.; Calothy, G.; Marx, M. J. Virol. 65, 353-3540, 1991
A;Title: Common mechanism of retrovirus activation and transduction of c-mil and c-Rmil A;Reference number: A40341; MUID:91251215; PMID:1645786
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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Score 48; DB 2; Length 314; Pred. No. 1.4e+02;
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Pred. No. 1.9e+02;
4; Mismatches 4.
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
   Query Match 23.9%; Score 48; DB 3
Best Local Similarity 38.1%; Pred. No. 1.4e-
Matches 8; Conservative 0; Mismatches
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406 LLVVCLPCLLQCVSSS 421
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Matches 8; Conservative
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09ZUD0_ARATH
09VLT6_DROME
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0181I8_CABEL
0924K7_MERUN
081YJ8_HUMAN
06BJV77_DEBHA
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QBCFA7 MOUSE
Q9D351 MOUSE
Q6P233 MOUSE
Q6P233 MOUSE
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Q81X30_HUMAN
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MEDLINE=93010984; PubMed=1396583;

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Name=TNFRSF17; Synonyms=BCM, BCMA;
Name=TNFRSF17; Synonyms=BCM, BCMA;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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7 HUMAN
OLO223:
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
                                                                                                                                                                                                      05XQY7_9HEPC
061M32_CAEBR
09WDU6_9H1V1
09WDU6_9H1V1
09WDV6_9H1V1
09WDW7_9H1V1
09WDW
ALIGNMENTS
  WCBI_TaxID=9606;
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  TNR17
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1(1) TISSUE=Lymph node, and Peripheral blood leukocyte;

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FUNCTION, AND INTERACTIONS WITH TRAFI AND TRAF3.

MEDLINE=20363816; PubMed=10903733;
Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
Hatzoglou A., Devergne O., Tsapis A.,
TINOUE J.-I., Devergne O., Tsapis A.,
TINF receptor family member ECMA (B cell maturation) associates with
TNF receptor associated factor (TRAF) 1, TRAF2, and TRAF3 and
activates NP-kappa B. elk-1, c-Jun N-terminal kinase, and p38 mitogen-
activated protein kinase.;
J. Immunol. 165:1322-1330(2000).
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NUCLECTIDE SEQUENCE (GENOMIC DNA), AND VARIANTS VAL-54; VAL-65;
UAL-75; ASN-81 AND SER-16J., Chung M.-W., Ritchie T.K., Olson A.N.,
Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
Sherwood J.K., Sherwood A.M., Leithausers B.J., Nickerson D.A.;
"NIEMS-SNPs, environmental genome project, NIEMS ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    MEDLINE-94118235; PubMed-8165126; Laabi Y., Gras M.P., Tsapis A.; Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.; The Star M.P., Decentially expressed during B lymphoid maturation, is bidirectionally transcribed."; Nucleic Acids Res. 22:1147-1154(1994).
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                 Labbi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
Larsen C.-J., Tsapis A.;
"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
by a t(4;16) (q26;p13) translocation in a malignant T cell lymphoma.";
EMBO J. 11:3897-3904(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21419161; PubMed-11528522; DOI-10.1038/sj/gene/6363770; Kawasaki A., Touchiya N., Fukazawa T., Hashimoto H., Tokunaga K. "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid
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MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
Shu H.-B., Johnson H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             [3]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE, AND VARIANT THR-153
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                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                DISEASE: A chromosomal aberration involving TNFRSF17 is found in a pictur of T-cell acute lymphoblastic leukemia (T-ALL). Translocation t (4:16) (q26;p13) with 1L2. SIMILARITY: Contains 1 TNFR-Cys repeat.
cell maturation protein is a receptor for the tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomal translocation, Immune response,
Proto-oncogene, Receptor, Signal-anchor, Transmembrane.
1 S4 Extracellular (Potential).
55 77 Signal-anchor for type III membrane
                                                                                                                                                           O9Y275:TNFSF13B; NDExp=1; IntAct=EB1-519945, EB1-519169; SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.
TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
               family member TALL-1.",

Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).

-!- FUNCTION: Receptor for TNFSF13B/BLPS/BAFF and TNFSF13/APRIL.

Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK.

-!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
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277AF11E2767D932 CRC64;
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S -> N (in dbSNP:373496).
/FTId=VAR_018758.
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Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 214954; CAA78679.1; -; mRNA.

EMBL; 229575; CAA82691.1; -; mRNA.

EMBL; 229574; CAA82690.1; -; Genomic_DNA.

EMBL; U95742; AAB67251.1; -; Genomic_DNA.

EMBL; AY509112; AAB67251.1; -; Genomic_DNA.

EMBL, AY509112; AAR84240.1; -; Genomic_DNA.

PIR; S43486; S43486.

PDB; 10QD; X-ray; K/L/M/N/O/P/Q/R=8-46.

PDB; 1XU2; X-ray; R/S/T=5-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016021; C:integral to membrane; TAS. GO; GO:0004802; C:plasma membrane; TAS. GO; GO:0004072; P:receptor activity; TAS. GO; GO:0000283; P:cell proliferation; TAS. GO; GO:0007275; P:development; TAS. GO; GO:0007165; P:signal transduction; TAS. InterPro; IPR001368; TNFR. GO; PROSITE; PSO0652; TNFR. NGFR. 1; FALSE NEG. PROSITE; PSO0652; TNFR. NGFR. 1; FALSE NEG.
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By similarity.
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Ensembl; ENSG00000048462; Homo sapiens.
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100.0%; Score 201; DB 1; Length 184;

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A MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Bitchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Schaefein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Marian M., Madan A., Schein J.E., Jones S.J.M., Marra M.A.,
B. Chenzation and initial analysis of more than 15,000 full-length human
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28-FEB-2003 (Rel. 41, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
11-MXY-2005 (Rel. 47, Laseptor superfamily member 17 (B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 184;
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                          Indele
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Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058291; AAH58291.1; -; mRNA.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20139 MW; C7ACF9B40FC5531A CRC64;
                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor receptor superfamily, member 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
100.0%; Pred. No. 2.1e-18; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Match 100.0%; Score 201; DB 2; Local Similarity 100.0%; Pred. No. 2.1e-18; Nes 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
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                                                                                34
                                                                                                                                                                                                                                                                                     184 AA
                                                                                                                      8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
                                                                                   1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC
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                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                               QEPE46_HUMAN PRELIMINARY;
                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ведпенсев
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 AA;
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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088472;
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O6PE46 HUMAN
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RY NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RY NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RY NUCLECTION STATE SUB-COlon; RY Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Hala E., Tomaru Y., Hall D.P., Bult C., Hume D.A., Chochand C., Corbanha D.,

RA Baldare J.A., Bradt D., Burdt C., Hume D.A., Chochanha D.A.,

RA Baldare J.A., Fletcher C.P., Torrest A., Frazer K.S.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Balda E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gassterland T., Marchionni L., McKenzie E., Mikh H.,

RA Gassterland T., Numata K., Marchionni L., McKenzie E., Mikh H.,

RA Nagashima T., Numata K., Okido T., Param W.J., Pertea G., Peecle G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Varan C., Sandolin M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Shiraki T., Waki K., Kawai J., Yanagisawa M., Yang I., Yang I.,

RA Shiraki T., Waki K., Kawai J., Alazawa K., Arakawa T., Fohuda S.,

RA Hara A., Hashizume W., Imceni K., Ishing Y., Rogers J.,

RA Hara A., Hashizaki Y.;

RA Shiraki T., Wati K., Kawai J., Shibata K., Shinagawa R.,

Raunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa R.,

Raunishi A., Sakai K., Sasaki D., Shibata K., Lander E.S., Rogers J.,

RA Waunishi A., Soshino M., Waterston R., Lander B., Lander S.,

RA Nature 420:561-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA STREADENING SEQUENCE LLARGE SCALE MRNAJ (ISOFORM 1).

RE STRAATES-STRAINGSTREMENMENTY GLANG;

RA STRAINES-STRAINGSTREMENMENTY GLANG;

RA STRAUBBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pales L. W., McZenna M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pales L. W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakeeley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length human

RA DALL NALL NALL REL., RAMA MARKA M.A.,

RA DALL NALL RAMA MARKA M.A.,

RA Generation and initial analysis of more than 15,000 full-length human
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                              NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
STRNIN=BALB/c; TISSUE=Spleen;
MEDLINE=99061155; PubMed=9846699, DOI=10.1093/intimm/10.11.1693;
MEDLINE=99061155; V. Callebaut I., Roussel J., Hatzoglou A.,
Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
"The characterization of murine BCMA gene defines it as a new member of the tumor necrosis factor receptor superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
  maturation protein).
Name=Tnfrsf17; Synonyms=Bcm, Bcma;
                                    musculus (Mouse)
                                                                                                              NCBI_TaxID=10090;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                  Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK (By similarity). SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom1;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognath1;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                    thymus, bone marrow and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
TISSUE=Stomach;
Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane
FUNCTION: Receptor for INFSF13B/BLyS/BAFF and INFSF13/APRIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q02223; 10QD.
Ensembl; ENSMUSGO000022496; Mus musculus.
MGI:1343050; Thirist of miscard to membrane; TAS.
G0; G0:0016021; C:integral to membrane; TAS.
InterPro; IPR001369; TNFR C6.
PROSITE; PSOSO65; TNFR NGFR 1; FALSE NEG.
PROSITE; PSSO050; TNFR NGFR 2; PALSE NEG.
Alternative splicing; Tmmune response; Receptor; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                                                    similarity).
-!- SUBCELLULAR LOCATION: Type III membrane protein (Probable)
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.7%; Score 136; DB 1; Length 185; 70.6%; Pred. No. 7.4e-10; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor for type III protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8806352B4FD26A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
/FIIG-VSP_006507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                          Isoid=088472-2; Sequence=VSP_006507;
-1-TISSUS SPECIFICITY: Detected in spleen, thymus
heart, and at lower levels in kidney and lung.
-1- SIMILARITY: Contains 1 TNPR-Cys repeat.
                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36
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                                                                                                                                                                                                                             IsoId=088472-1; Sequence=Displayed;
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Name-Muc6; Synonyms-gastric mucin-like;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF061505; AAC23799.1; -; MRNA.
EMBL; AK020247; BAB32038.1; -; MRNA.
EMBL; BC027519; AAH27519.1; -; MRNA.
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088714;
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36
18
32
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91
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                                                                                                                                                                                                           Name=1
                                                                                                                                                                                                                                                        Name=2
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REPEAT
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DISULFID
VARSPLIC
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TRANSMEM
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Q80T03_MOUSE PRELIMINARY;
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NON TER
SEQUENCE
                                                                                                                            Name=Muc6;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72.5; DB 2; Length 1674;
Pred. No. 1.6;
1; Mismatches 7; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.1%; Score 72.5; DB 2; Length 499; Best Local Similarity 48.3%; Pred. No. 0.45; Matches 14; Conservative 1; Mismatches 7; Indels 7
                                                                                               Tomaseric Cini.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AD10752; CAA09343.1; -; mRNA.
HSSP, P56682; ICCV.
Ensembl; ENSMUSG0000048191; Mus musculus.
NG1; MG1: 2566323; Muc6.
InterPro; IPR001846; VWF D.
Pfam; PF001845; VWP D.
Pfam; PF001845; VWD; 1.
SMART; SM00216; VWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1674 AA; 181168 MW; 3BC42CB004476309 CRC64;
                   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                499 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escande F., Bulsine M.P.;
"The mouse secreted gel-forming mucin gene cluster.";
Biochim. Biophys. Acts 1676:240-250(2004).
EMBL, AJS11867; CAD54415.1; -; Genomic DNA.
EMBL, AJS11868; CAD54415.1; -j Genomic DNA.
HSSP; O46162; IKJO.
MGI, MGI-2663233; Muc6.
InterPro; IPR002919; Prot Inh_CR_TIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBOZ18 MOUSE PRELIMINARY; PRT; 1674 AA. 080Z18. 01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Secreted gel-forming mucin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J;
PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 CSQNEYFDHSEGTCVPC-----APPTT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSONEYPDSLLHACIPCOLRCSSNTPPLT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.1%;
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Pfam; PF00094; VWD; 3.
SMART; SM00216; VWD; 3.
NON_TER 1674 1674
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Best Local Similarity
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                                                              NUCLEOTIDE SEQUENCE.
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RESULT 6, Q80T03_MOUSE

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                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desseyn J.-L., Laine A.;

"Characterization of mouse muc6 and evidence of conservation gen-forming mucin gene cluster between human and mouse.";

Genomics 81:433-436 (2003).

EMBL; AY184388; AAO47735.1; -; Genomic_DNA.

EMBL; AY184388; AAO47735.1; JOINED; Genomic_DNA.

EMBL; AY184386; AAO47735.1; JOINED; Genomic_DNA.

EMBL; AY184386; AAO47735.1; JOINED; Genomic_DNA.

HSSP; O46162; IX.0.
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PROSITE; PS01225; CTCK 2; 1.
SEQUENCE 2850 AA; 300398 WW; 9CD95F0845C79C9D CRC64;
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EMBL; ALG46093; CAI25894.1; -; Genomic DNA.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Tumor necrosis factor receptor superfamily, member 13b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 74 74 74 74 74 AA; 8337 MW; DA8A3B06FE191A26 CRC64;
                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PRT; 2850 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSWUSG0000048191; Mus musculus. MGI; MGI:2663233; Muc6.
InterPro; IPR006207; Cys knot_C.
InterPro; IPR002919; Prot_Inh_CR_TIL.
InterPro; IPR001846; VWF_D.
Pfam; PF01826; TIL; 2.
Pfam; PF00094; VWD; 3.
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Name=Tnfrsf13b; ORFNames=RP23-5512.2-002;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSSUB4 MOUSE
ID QSSUB4 MOUSE PRELIMINARY;
AC QSSUB4;
                                                                                                                                                                                                                                                                                                      Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
"Identification of a receptor for BLyS demonstrates a crucial role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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OPETJS; OSDBZ3;
28-FEB-2003 (Rel. 41, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Tumox necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
Name-Tnfrsf13b; Synonyms-Taci;
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                                                                                                                                                                                                                                                                                                                                                          35.6%; Score 71.5; DB 2; Length 140; 35.3%; Pred. No. 0.17; ive 8; Mismatches 13; Indels
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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                           Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                              01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Tunor necrosis factor receptor superfamily, member 13b
                                                                                                                                                                                                                                                                                                                                   140 AA; 15672 MW; 005D8CDF4E8E3D15 CRC64;
                                                                                                                                                                                                                                                                                                                                                             0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                    CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                        CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                                                         140 AA
           CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC
                                                                                                                                                                                                                                                                                     J. AL646093; CAI25895.1; -; Genomic DNA. GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                       Name=Tnfrsf13b; ORFNames=RP23-5512.2-003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muroidea, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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                                                                                         QSSU83 MOUSE PRELIMINARY;
QSSU83;
                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
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NON TER
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Muroidea; Muridae; Murinae; Mus
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Pfam; PF00094; VWD; 3.
SMART; SW00215; VWC_out; 2.
SMART; SW00216; VWD; 3.
NON TER 1569 1569
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       Genomics 83:936-939(2004)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;
Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,
Toribara N.W.;
"The complete genomic organization of the human MUC6 and MUC2 mucin
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71.5; DB 1; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases EMBL; AL646093; CAI25896.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Tumor necrosis factor receptor superfamily, member 13b.
Name=Tnfrsf13b, ORFNames=RP23-5512.2-001;
                                                                                                                                                                                                                                                                                                                                                                CB2F2D61C2931D81 CRC64;
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   Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 (in Ref. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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TNFR-Cys 2.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                   26947 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%;
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QSSU82;
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Q6W4X9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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DT 05-JT
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PCSK5 MOUSE STANDARD, PRT; 1877 AA.

004592; Q62040,

01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)
(Subtilisin-like proprotein convertase 6) (SPC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa T., Murakami K., Nakayama K.;
"Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
FEBS Lett. 327:165-171(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 330-1877 (ISOFORM PC5B).
STRAIN=ICR; TISSUE=Intestine;
MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAYTIAL PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.
MEDLINE=97103178; PubMed=8947550; DOC=10.1083/jcb.135.5.1261;
De Bie I., Marcinklewicz M., Malide D., Lazure C., Nakayama K.,
Bendayan M., Seidah N.G.;
"The isoforms of proprotein convertase PCS are sorted to different Subcellular compartments.";
J. Cell Biol. 135:1261-1275(1996).
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J. Biochem. 113:132-135(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                           Score 68.5; DB 2; Length 1569;
Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                               1569 AA; 168065 MW; 6AEDEE143ECB855B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
EMBL, AY312160, AAQ82434.1; -; mRNA.
InterPro; IPR002919; Prot Inh_CR_TIL.
InterPro; IPR006552; VWC_out.
InterPro; IPR001846; VWF_D.
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MEDLINE=93224489; PubMed=8468318;
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MEDLINE=93342056; PubMed=8341687;
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CARBOHYD
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Isold=00459; Synonyme=Short,

Isold=00459-2; Sequence=VSP 005439, VSP 005439;

Isold=00459-2; Sequence=VSP 005438, VSP 005439;

Intestine, adrenals and lung but not in the brain.

Intestine, adrenals and lung but not in the brain.

Isold=00459-2; SanGE: Weakly expressed throughout the embryo, except in the developing nervous system, the ribs and the liver, but markedly up-regulated at discrete sites during development. At ES-5, intense expression observed in differenciated decidua. At ES-5, intense expression in extraembryonic endoderm, amnion and nascent mesoderm. At ES-5, abundant expression in AER (thickened decidua. At ES-5, abundant expression in AER (thickened ectodermal cells of limb buds). At ES-5, expression in the limbs is confined to the condensing mesenchym surrounding the cartilage. At this stage, strong expression also detected in vertebral and facial cartilage primordia and in the muscle of the intestinal villi. Isoform A is most abundant at all stages but significant levels of isoform B occur at ES-2.

Isoldorm B occur at ES-2.
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                                                                                                                                                                                                                                            can be any amino acid and Yaa is Arg or Lys-1-cad bonds, where Kaa SUBCELLULAR LOCATION: PCSA is secreted through the regulated secretory pathway. PCSB is a type I membrane protein localized to a paranuclear post-Golgi network compartment in communication with ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
               MEDLINE-96293359; PubMed-8698813; DOI=10.1083/jcb.134.1.181; Constam D.B., Calfon M., Robertson B.J.; Christoft, SpCf, and the novel procease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis."; J. Cell Biol. 134:181-191(1996).
                                                                                                                                                                                DEVELOPMENTAL EXPRESSION.
MEDLINE=97436919; PubMed=9291583;
DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of growth factors.
CATALYTIC ACTIVITY: Release of mature proteins from their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the peptidase S8 family. SIMILARITY: Contains 1 homo B/P domain.
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Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PC5B; Synonyms=Long;
IsoId=Q04592-1; Sequence=Displayed;
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EMBL; D12619; BAA02143.1; -; mRNA.
EMBL; L14932; AAA74636.1; -; mRNA.
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PIR; A48225; A48225. PIR; S34583; S34583.

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                                                                                                                                                                                                                                               Alternative splicing; cleared on pair of basic residues;
Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Repeat;
Serine protease; Signal; Transmembrane; Zymogen.
SIGNAL 1 34
PROPEP 35 116
PROPEP 15 1877 Proprotein convertase subtilisin/kexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Сарв
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ATEESWAEGGFCMLVKKNNLCQRKVLQQLCCKTCTFQG
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                                                                                                                                                                                                                                                                                                                                                               type 5.
Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Cys-rich motif)
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Last annotation update)
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MEMORIS 300-706;
MGI; MGI:97515; Pcek5.
MGI; MGI:97515; Pcek5.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR003460; AFP.
InterPro; IPR00209; Pept_S8_SS3.
InterPro; IPR02884; PrprotnConvertsP.
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PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
                                                                                                                       Pfam; PF02420; AFP; 1.
Pfam; PF01481; 1.
Pfam; PF01481; 1.
PR0082; PEptidase S8; 1.
PRINTS; PR00723; SUBTILISIN.
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(Rel. 41, Last sequ
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37.8%;
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ID TR13B HUMAN ST

AC 014836; 0726F5;

DT 28-FEB-2003 (Rel. DT 28-FEB-2003 (Rel. DT 13-SEP-2005 (Rel.
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IsoId=014836-1; Sequence=Displayed;
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Q53F36;
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MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;

Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,

Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,

Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,

Meng S.-Y., Boyle W.J., Hsu H.;

"TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis

factor family member involved in B cell regulation.";

J. Exp. Med. 192:137-143(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
"ARRIL and TALL-I and receptors BCMA and TACI: system for regulating
                                                                                                   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 68-109, AND STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hymowitz S.G., Patel D.R., Wallweber H.J., Runyon S., Yan M., Yin J.,
Shriver S.K., Gordon N.C., Pan B., Skelton N.J., Kelley R.F.,
Starovasnik M.A.;
Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).

Name=TNFRSF13B; Synonyms=TACI;
Homo saplens (Human).
                                                                                                                                                                                                                MEDLINE=97458245; PubMed=9311921; DOI=10.1126/science.278.5335.138; OND Buelow G.-U., Bram R.J.; R.Y. a CAML-interacting member of the tumor necrosis factor receptor superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200; Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., LaFleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.; Thur Carrectosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLyS."; Blol. Chem. 275:35478-35485(2000).
                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O75888 TNFSF13; NbExp=1; IntAct=EBI-519160, EBI-519208; Q927275:TNFSF13B; NbExp=4; IntAct=EBI-519160, EBI-519169; SUBCELLULAR LOCATION: Type III membrane protein. ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15542592; DOI=10.1074/jbc.M411714200;
                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Immunol. 1:252-256(2000)
                                                                                                                                                                                                                                                                                            Science 278:138-141(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             humoral immunity
                                                                                                                                         NCBI_TaxID=9606;
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FUNCTION

FUNCTION

OF 68-109

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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GO; GO:000166; P:celeptor activity; TAS.

GO; GO:000166; P:cell surface receptor linked signal transdu. . .; TAS.

InterPro; IPRO01368; TNFR GG.

PROSITE; PSO0652; TNFR NGFR 1; 1.

PROSITE; PSO0650; TNFR NGFR 2; FALSE NEG.

BO-STICLURE; Alternatīve splicing; Glycoprotein; Immune response;

Receptor; Repeat; Signal-anchor; Transmembrane.

TOPO DOM 1 166 Signal-anchor for type III membrane

TRANSMEM 166 186 Signal-anchor for type III membrane
IsoId=014836-2; Sequence=VSP_013798;
-!- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukcoytes. Expressed in resting B-cells and activated T-cells, but not in resting T-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRT
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAFCR -> W (in isoform 2)
/FIId=VSP_013798.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last senterion update)
Tumor necrosis factor receptor 13B variant (Fragment).
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TWFR-Cys 2.
N-linked (GlcNAc.
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By similarity.
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                                                                                                                  -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ensembl; ENSG0000108516; Homo sapiens.
HGNC; HGNC:18153; TNFRSF13B.
                                                                                                                                                                                                                                                                                                                                             EMBL; AF023614; AAC51790.1; -; MRNA.
EMBL; AY302137; AAP57629.1; -; MRNA.
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TISSUE-Small intestine;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentía; Sciurognathi;
                                                                                                                                                                                                                                                                                          Miller W., Koop B.F.; "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                        STRAIN=129/Sv;
MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
Miller W., Koop B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 5374;
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GO; GO:0016020; C:membrane; IEA.
GO: 00:0007339; P:binding of sperm to zona pellucida; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
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Local Similarity 35.1%; Score 64.5; DB 2; Length 5
Local Similarity 35.1%; Pred. No. 58;
Length 5
Local Similarity 35.1%; Mismatches 16; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         579545 MW; 90D2D8CFE5DE24EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF312033; AAK28824.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3298 CPTNSOFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3334
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InterPro; IPR0013128; Tila_Cysrich
InterPro; IPR001307; WWF_C.
InterPro; IPR001846; WWF_D.
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InterPro; IPR06209; EGF 11ke.
InterPro; IPR001345; Pol N.
InterPro; IPR006210; IEGF.
InterPro; IPR000998; MAM.
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SMART; SM00124; FOLIN; 20.
SMART; SM00124; MAM; 3.
SMART; SM00114; WWC; 18.
SMART; SM00114; WWD; 4.
PROSITE; PS00102; EGF 2; 18.
PROSITE; PS00186; EGF 3; 1.
PROSITE; PS000140; MAM 1; 1.
PROSITE; PS000140; MAM 1; 1.
PROSITE; PS000140; MAM 1; 1.
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Pfam; PF00094; VWD; 4.
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Pfam; PF00629; MAM; 3.
Pfam; PF01826; TIL; 25.
                                                                                                               Muridae; Murinae; Mus.
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                                             Mus musculus (Mouse)
                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
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(Zonadhesin).
                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129/Sv;
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TISSUE-Small intestine;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AK221453; BAD97173.1; -; mRNA.
                                                                                                                                                     Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.; "Construction and characterization of a full length-enriched and a end-enriched cDNA library."; Gene 200:149-156(1997).
                        "Oligo-capping : a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides."; Gene 138:171-174(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
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"Draft sequence of the diardia lamblia genome.";
"Draft sequence of the EMBL/GenBank/DDBJ databases.
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.1%; Score 66.5; DB 2; Length 293; 32.4%; Pred. No. 1.6; ive 8; Mismatches 14; Indels 1
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Giardia lamblia ATCC 50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI_TaxID=184922;
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EMBL, AACB01000001; EAA43000.1; -; Genomic_DNA.
HSSP, Q9S7B3; 1EHD.
INTERPRO: IPR002021, Laminin EGF.
PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN 1.
SEQUENCE 1025 AA; 109044 MW; 36281DF3FEZDDB43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AA; 31846 MW; D9EA2F28B3BF466D CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;
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Extracellular (Potential)
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    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Probably forms covalent oligomers.
SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head.
TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.
DOMAIN: The MAM domains probably mediates sperm adhesion to the cona pellucida.
DOMAIN: During sperm migration through the reproductive tracts, the mucin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.
DOMAIN: The VWFD domain 2 may mediate covalent oligomerization (By
                                                                                                                                                                                                                              TISSUB=Testis;
MEDLINE=97271566; PubMed=9126492; DOI=10.1006/geno.1997.4620;
MEDLINE=97271566; PubMed=9126492; DOI=10.1006/geno.1997.4620;
Gao Z., Haxumi T., Gazbers D.L.;
Chromosome localization of the mouse zonadhesin gene and the human zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).

-I FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or signaling
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                             "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like
                                                                                                    TISSUE=Testis;
MEDLINE=98123114; PubMed=9452463; DOI=10.1074/jbc.273.6.3415;
Gao Z., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U97068; AAC26680.1; -; mRNA.

PIR; T9215; T4215.

HSP; Q90248; 14225.

HSP; Q90248; 14225.

MGI; MGI:106656; Zan.

G0; G0:0005615; C: extracellular space; TAS.

G0; G0:0005615; C: extracellular space; TAS.

InterPro; IPR004153; CXCXC_repeat.

InterPro; IPR004153; CXCXC_repeat.

InterPro; IPR006209; EGF_like.

InterPro; IPR006209; EGF_like.

InterPro; IPR002919; Prot. Inh.

InterPro; IPR002919; Prot.

InterPro; IPR001846; VWF D.

Pfam; PF00308; EGF; 11.

Pfam; PF00308; EGF; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
Similarity: Contains 1 EGF-like domain.
Similarity: Contains 3 MAM domains.
SIMILARITY: Contains 25 VWFD domains.
                                                                                                                                                                         domains.";
J. Biol. Chem. 273:3415-3421(1998).
                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 4864-5376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02345; TIL assoc; 25
Pfam; PF00094; VWD; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00022; EGF 1; 1.
PROSITE: PS01186; EGF 2; 18.
PROSITE: PS0026; EGF 3; 1.
PROSITE: PS00740; MAM 1; 1.
PROSITE; PS50060; MAM 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00629; MAM; 3
Pfam; PF01826; TIL; 2
                                                                                     NUCLEOTIDE SEQUENCE.
                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed
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repeats (approximate)

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(Potential) (Potential)

(Potential) Potential) Potential) Potential)

(Potential) (Potential) (Potential)

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QSOYS1_ENTHI PRELIMINARY;
QSOYS1;
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Best Local Similarity 35.3
Matches 12; Conservative
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                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=294381;
                                                                                                                            NCBI_TaxID=294381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q50Y51
1D Q5
DT 133
DT 133
DT 133
DT 133
DT 0X
DE CX
GSN ED
OX ED
OX EN
RN (11
RR NT
δ
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St
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                                                                                                           2;
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                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Fusarium graminearum genome sequence.";
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibberella zeae PH-1.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
NCBI_TaxID=229533;
                                                     DB 1; Length 5376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64; DB 2; Length 762;
Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                              16; Indels
  579913 MW; 0E44DB77DF2A2620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 762 AA; 84756 MW; 55B25D037F21A35A CRC64;
                                                                                                                                                                                                  3300 CPTWSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
                                                                                                                                                                1 CSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AACM01000370; EAA78173.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                           762 AA.
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                                                     32.1%; Score 64.5; D
35.1%; Pred. No. 58;
ive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ACIPCO---LRCSSNTPPLTCOR----YC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Best Local Similarity 43.3%;
Matches 13; Conservative
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Q50LY7 ENTHI
ID Q50LY7, ENTHI PRELIMINARY;
AC Q50LY7;
DT 13-SEP-2005 (TremBlrel. 31,
DT 13-SEP-2005 (TremBlrel. 31.)
                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                             O4IOYS GIBZE PRELIMINARY;
                                                                                                                13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
ORFNames=FG09123.1;
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        5376 AA;
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                                                                                    Local Similarity
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     SEQUENCE
                                                           Query Match
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10410YS GIBB
10410YS GIBB
10410YB
AC Q410Y
AC Q410Y
AC Q410Y
BDT 13-SE
DT 13-SE
BA BEICH
RA BILLE
RA MAICH
RA SMICH
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STRAIN=HM-1:IMSS;

X PubMed=15729342; DOI=10.1038/nature01291;

PubMed=15729342; DOI=10.1038/nature01291;

A Amedeo B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

A Amedeo B., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

A Bub B., Pop M., Duchene M., Ackers J., Tannich B., Leippe M.,

A Hofer M., Bruchhaus I., Willhoeft U. Bhattacharya A.,

Chilingworth T., Churcher C., Hance Z., Harris B., Harris D.,

A Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

A Guillen N., Glichrist C., Stroup S.E., Bhattacharya S., Lohla A.,

Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,

BI-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,

Rraser C.M., Hall N.;

"The genome of the protist parasite Entamoeba histolytica.";

"The genome of the protist parasite Entamoeba histolytica.";

"The square 433 s65-868 (2005).

EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.

--- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AAFBO1001427; EAL42605.1; --; Genomic_DNA.

GO; GO: 0016301; Fixinase activity; IEA.

InterPro; IPR006212; Purin repeat.

InterPro; IPR000219; Prot_Kinase.

InterPro; IPR00221; Ser Ehr pkin AS.

InterPro; IPR002290; Ser thr pkinase.

InterPro; IPR001245; Tyr pkinase.
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Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update) Protein Kinase, putative (Fragment). ORFNames=e50.t00003. Entamoeba histolytica HM-1:IMSS. Bukaryota; Entamoebidae; Entamoeba.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; Pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_Kinase; 1.
SWART; SW00261; FU; 4.
SWART; SW00220; S. TKC; 1.
SWART; SW00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63.5; I Pred. No. 11;
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STRAIN=HM-1:IMSS;
PubMed=15729342; DOI=10.1038/nature03291;
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Eukaryota; Entamoebidae; Entamoeba
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Paramecium
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SEQUENCE
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Q6BFG4 PAR
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X PubMed=15729342; DOI=10.1038/nature03291;

X Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

A Anderson I., Davies R., Alsmark U.C., Samuelson J.,

A medeo P., Roncaglia P., Berriama M., Hirt R.P., Mann B.J., Nozaki T.,

A by P. R., Duchene M., Ackers J., Tannich E., Leippe M.,

A hofer M., Bruchhaus I., Willhoeft U., Bhatracharya A.,

RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,

RA Jagels K., Moule S., Mangall K., Ormond D., Squares R., Whitehead S.,

RA Quail M.A., Rabbinowitech E., Norbertczak H., Price C., Wang Z.,

Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohla A.,

RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,

RA Fraser C.M., Hall N.,

RT Frae genome of the protist parasite Entamoeba histolytica.";

RT The genome of the protist parasite Entamoeba histolytica.";

RA Fraser C.M., The sequence shown here is derived from an EBBI/Gensank/DDBJ whole genome shotgun (WGS) entry which is
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A medeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T., A Bub B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M., Hofer M., Duchene M., Ackers J., Tannich E., Leippe M., Hofer M., Burchhaug I., Willhoeft U., Bhattacharya A., Hofer M., Burchhaug I., Willhoeft U., Bhattacharya A., Harris D., Chillingworth T., Churcher C., Hance Z., Harris B., Harris D., Quail M.A., Rabbinowitch E., Norbertczak H., Price C., Wang Z., Guillen M., Rabbinowitch E., Norbertczak H., Price C., Wang Z., Guillen M., Rabbinowitch E., Norbertczak H., Price C., Wang Z., Guillen M., Rober P.G., Singh U., Mukherjee C., Rrser C.M., Hall M., Clark C.G., Embley T.M., Barrell B., Fraser C.M., Hall N., Clark C.G., Embley T.M., Barrell B., Nature 433:865-868(2005).

In Ature 433:865-868(2005).

EMBL, AAPBOIO00471; EAL46536.1; -, Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%; Score 63.5; DB 2; Length 802; 35.3%; Pred. No. 11; tive 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.3%; Score 63; DB 2; Length 1150; 36.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1150 AA; 128938 MW; 0DBE7051D4B4E286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          802 AA; 90126 MW; 1425BF8514DED237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         654 CQDNYYYDKELQSCVGCSSECLTCSNKDICFTCK 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAFB01000933; EAL43605.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSQNEYFDSLLHACIPCQ---LRCSSNTPPLTCQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Entamoeba histolytica HM-1:IMSS.
Eukaryota, Entamoebidae, Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor protein kinase, putative. ORFNames=359.t00009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q50PT4 ENTHI PRELIMINARY;
Q50PT4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=294381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative surface protein with EGF domains and furin-like repeats.
ORFNames=PTMB.409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paramecium tetraurelia.
Eukaryota, Alveolata; Ciliophora, Oligohymenophorea, Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.

EMBL; AAB01008803; EAA05574.2; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
GO; GO:0008865; F:protein transporter activity; IEA.
GO; GO:0006886; P:intracellular protein transport; IEA.
Interpro; IPR0020860; Glyco_hydro_BNR.
Interpro; IPR002172; LDL_receptor_A.
Interpro; IPR002012; LDL_receptor_rep.
Interpro; IPR00033; Ldl_receptor_rep.
Ffam; PF02012; BNR; 6.
Ffam; PF02012; BNR; 6.
Ffam; PF00085; Ldl_recept_a; 7.
Ffam; PF00085; Ldl_recept_b; 4.
FFAM; FR00085; Ldl_recept_b; 7.
FFAM; FR00085; FR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1294 1294
1294 AA; 146748 MW; 10C251750A3F0586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1131 CKADEFRCNVTNACLPNÓWRCDTEKDCPDGSTPPRRKDRTC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQNEYFDSLLHACIPCOLRCSS-----NTPPLTCQRYC 34
                                                                                                                                                                                                     Last annotation update)
                                                                                                                                                            Last sequence update)
     PRT; 1294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI; 3005 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.1%; Score 62.5; I
31.7%; Pred. No. 25;
tive 8; Mismatches
                                                                                                          Created)
                                                                                                                                                                                                                                                  ENSANGP0000012534 (Fragment) ORFNames=ENSANGG00000010045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWART; SW00181; Edfs; 3.
SWART; SW00192; LDEs; 7.
SWART; SW00135; LY; 5.
SWART; SW00602; VBS10; LDERA 1; 5.
PROSITE; PS01209; LDLRA 1; 5.
PROSITE; PS50068; LDLRA 2; 5.
                                                                                           01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae str. PEST
Eukaryota; Metazoa; Arthrop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEBFG4 PARTE PRELIMINARY;
QEBFG4;
Q7QGV0_ANOGA PRELIMINARY;
Q7QGV0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 31.7 es 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00181; EGF; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=180454;
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Gaps

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10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Proprotein convertaes subtilisin/kexin type 5 (Fragment).
Name=PCSK5; ORFNames=RP11-422N19.4-002;
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.3%; Score 61; DB 2; Length 1560;
                                                                                                                                                                                                                                          DB 2; Length 966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1560 AA; 173890 MW; 7211FBC127A8A08C CRC64;
               Pfam; PF01667; CBM 14; 2.
Pfam; PF01683; EB; 1.
SMART; SM00181; EB; 1.
PROSITE; SM00289; WRI; 12.
PROSITE; PS00205; B KETOACYL SYNTHASE; UNKNOWN 1.
Complete Proteome; Hypothetical protein.
SEQUENCE 966 AA; 102461 MW; B565A3CDD25216D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
Mashreghi-Mohammadi M.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AL391689, CA140675.11, -; Genomic_DNA.
EMBL, AL393673, CA1406090.11, -; Genomic_DNA.
EMBL, AL353607; CA140675.11, -; Genomic_DNA.
EMBL, AL353607; CA140675.11, JOINED, Genomic_DNA.
EMBL, AL353607; CA140690.1; JOINED, Genomic_DNA.
EMBL, AL3936893, CA140809.1; JOINED, Genomic_DNA.
EMBL, AL391868; CA140809.1; JOINED, Genomic_DNA.
EMBL, AL391868; CA141234.1; JOINED, Genomic_DNA.
EMBL, AL589653; CA141234.1; JOINED, Genomic_DNA.
EMBL, AL589653; CA141234.1; JOINED; Genomic_DNA.
GO, GO:0004589; F: subtlass activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCOLR--CSSNTPPLTC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1560 AA
                                                                                                                                                                                                                                          Query Match 30.3%; Score 61; DB 2
Best Local Similarity 37.5%; Pred. No. 29;
Matches 12; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR002884; Prproinconvertep. Pfam; PF0240; APF; 1. Pfam; PF0340; DUP326; 2. Pfam; PF03860; DUP326; 2. Pfam; PF03860; DUP326; 2. Prodom; PD000717; PrproinconverteP; 1. SMART; SM00181; EGF; 16. SMART; SM00261; PU; 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006212; Purin_repeat.
InterPro; IPR006210; IEGF.
InterPro; IPR000209; Pept_S8_53;
InterPro; IPR002884; PrprotnoonvertsP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00138; SUBTILASE_SER; 1.
InterPro; IPR006150; Worm_repeat_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUF326.
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QSJSG7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003460; AFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pelan S
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Q5JSG7_HUM
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                               STRAIN=Stock d4-2;
PubMed=15296759; DOI=10.1016/j.cub.2004.07.029;
Zagulaki M., Nowak J.K., Le Mouel A., Nowacki M., Migdalaki A.,
Gromadak R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
Cohen J., Mayer E., Sperling L.;
"High Coding Density on the Largest Paramecium tetraurelia Somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 3005;
                                                                                                                                                                                                                                                                                                                                           Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;

Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;

"Paramecium megabase sequencing project.";

Submitted (UUL-2004) to the EMBL/GenBank/DBJ databases.

EMBL, CR548612, CR403606.1; -; Genomic_DNA.

InterPro; IPR006208; EGF like.

InterPro; IPR006210; EGF like.

InterPro; IPR006210; EGF.

SMART; SM00181; EGF, 22.

SMART; SM00181; EGF, 22.

SMART; SM00261; FU; 29.

R PROSITE; PS01106; EGF 2; 12.

R PROSITE; PS01106; EGF 2; 12.

S PROSITE; PS01106; EGF 2; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology.";
Science 282:2012-2018(1998).
EMBL; U39644; AAA80360.2; -; Genomic_DNA.
PIR; T16840; T16840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
NDI-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T10E10.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 YFDSLLHACIPCOLRCSSNTPPLTCQ---RYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            966 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 30.6%; Score 61.5; D
Best Local Similarity 40.6%; Pred. No. 80;
Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ensembl; T10E10.4; Caenorhabditis elegans. Wormbase; WBGene00020421; T10E10.4. WormPep; T10E10.4; CE25989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR000794; Ketoacyl_synth.
Interpro; IPR003571; Snake_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                    Curr. Biol. 14:1397-1404(2004).
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                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                 STRAIN=Stock d4-2
          NCBI_TaxID=5888;
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CQ22378
CQ22378
AC Q2237
AC Q2237
DT 01-NC
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SSPO BOVIN
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                                                                                  P98167;
                  KESULT 27
SSPO_BOVIN
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                                                                      Maucoli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maucoli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A. Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
II. Nature 431:946-957(2004).
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                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigraviridis (Green puffer).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterrygii, Neopterrygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterrygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                              | | : | | : | | | | | : | | CSPSEYWDEDAPGCKPCHVKCFHCMGPAEDQCQTCPMNSLLLINTTCVKDC 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                         14; Indels 16;
                                                                    1 CSQNEYFDSLLHACIPCQLRC-----SSNTPPL-----TCQRYC 34
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29.9%; Score 60; DB 2; Length 830;
Best Local Similarity 24.1%; Pred. No. 34;
Matches 14; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 12 SCAP14996, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91073 MW; 94415DC15C27B26A CRC64;
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InterPro; IPR000742; BGF 2.
InterPro; IPR006209; BGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; Laminin EGF.
PRam; PR00053; Laminin EGF.
PRINTS; PR00011; EGFLAMININ.
SWART; SM00181; EGFLAMININ.
SWART; SM00180; EGF 17.
SROSITE; PS00022; EGF 17.
PROSITE; PS01186; EGF 2; 4.
PROSITE; PS01066; EGF 2; 4.
Laminin EGF-like domain.
                                                                                                                                                                                                                               830 AA
  28.0%; Pred. No. 47; ive 6; Mismatches
                                                                                                                                                                                                                               PRT;
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ORFNames=GSTENG00029038001;
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Q4RTY8;
                         14; Conservative
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Best Local Similarity
Matches 14; Conserv
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SEGO BOOTH STANDARD, PRT, 867 AM.

10.007-1996 (Rel. 34, Created)

10.007-1996 (Rel. 34, Last sequence update)

10.007-1996 (Rel. 34, Last sequence update)
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Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5146;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.9%; Score 60; DB 2; Le 42.9%; Pred. No. 2.2e+02; tive 3; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01285; FA58C 1; UNKNOWN 1.
PROSITE; PS01286; FA58C 1; 1.
PROSITE; PS00226; PA58C 3; 1.
PROSITE; PS00261; GLYCO HORMONE BETA 1; 2.
PROSITE; PS00261; LDLRA 1; 7.
PROSITE; PS50068; LDLRA 2; 9.
PROSITE; PS50068; LDLRA 2; 9.
PROSITE; PS50089; VWFC 1; UNKNOWN 1.
              InterPro; IPR006209; Cyg_knot.
InterPro; IPR006207; Cyg_knot_C.
InterPro; IPR011499; EMI_
InterPro; IPR001421; FAS9 C.
InterPro; IPR001545; GIY, hormoneB.
InterPro; IPR002172; LDL_receptor A.
InterPro; IPR002919; Proc_Inh_CR_TIL.
InterPro; IPR002919; Proc_Inh_CR_TIL.
P:cell adhesion; IEA
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1814 VFHACVPCPLTCDDISGQATC 1834
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LdI recept_a; 1
Pacifastin_I; 1
                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00094; VWD; 3.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR01705; TSPIREPEAT.
                                                                                                                                                                 InterPro; IPR008085; TSP_1.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
Pfam; PF00007; Cys knot; 1.
Pfam; PF07546; EMI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8SZ58;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBSZ58_DROME PRELIMINARY;
                                                                                                                                      InterPro; IPR008037; Prot
InterPro; IPR000884; TSP1
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              FA58C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDLa; 10.
TSP1; 25.
                                                                                                                                                                                                                                                                                         Pfam; PF05375; Pacīfast
Pfam; PF01826; TIL; 10.
Pfam; PF00090; TSP_1; 2
Pfam; PF00093; VWC; 1.
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STRAIN=Berkeley;
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SMART; SM00192; I
SMART; SM00209; T
SMART; SM00214; V
GO:0007155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=8cO-spondin;
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                    ..) (Potential)...) (Potential)...)
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MEDLINE=20465125; PubMed=11008217;
DOI=10.1002/1098-1136(200011)32:2<177::AID-GLIA70>3.0.CO;2-V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.9%; Score 60; DB 1; Length 867; 42.9%; Pred. No. 35;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJG57; CAC94914.1; -; mRNA.
HSSP; P98162; 1K7B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91817 MW; 9538F2108E787B49 CRC64;
                               LDL-receptor class A 1.
LDL-receptor class A 2.
LDL-receptor class A 3.
TSP type-1 3.
TSP type-1 4.
N-linked (GLONAC. ..) (F
N-linked (GLONAC. ..)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GO:0005179; F:hormone activity; IEA.
GO:0030414; F:protease inhibitor activity; IEA.
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   VWFC.
F5/8 type C.
LDL-receptor c
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3; Mismatches
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TISSUE=Subcommissural organ;
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QBSPM4 BOVIN PRELIMINARY;
QBSPM4;
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690
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Glia 32:177-191(2000)
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867 AA;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                            344
508
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527
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Barandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C. Baldwin D.,

RA Ballew R.M., Basu A., Bascendale J., Bhandari D., Bolshakov S.,

RA Ballew R.M., Basu A., Bascendale J., Brokstein P., Bolshakov S.,

RA Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Deckher A., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

R Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

R Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

R Hortin D., Houston K.A., Heynand T.J., Wei M.-H., Ibegwam C.,

RA Hortin D., Houston K.A., Heynand T.J., Wei M.-H., Ibegwam C.,

RA Hortin D., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harke P., Lei Y., Leviteky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Harke P., Lei Y., Leviteky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Halzzolo M., Pittman G.S., Pan Murphy L., Murphy D., Murphy D., Murphy B., Murphy D., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Sunder R., Shen H.,

RA Rainert K., Remington K., Saunders R., Poller F., Sanith T.,

RA Palazzolo M., Pittman G.S., Pan B., Sunder S., Sund R., Shen H.,

Shier E., Spiden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Stirskas R., Tector C., Turner R., Wohler E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG7348-PA.

Name=CG7348; ORFNames=CG7348;

Drosophila melanogaerer (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 CSVGNYFDPARRACLPVAISAAHQCSCVLPDNATLANPSDCETY 162
                                                                                                                                                                                                                                                                                                                                                                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQNEYFDSLLHACIPCQL----RCSSNTP-----PLTCQRY 33
                      Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                       GO, GO:0005576; C:extracellular region, IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0008061; P:chitin binding; IEA.
InterPro; IFRQ02557; Chitin metabolism; IEA.
Pfam; PF01607; CBM 14; 4.
SMART; SM00494; ChEBD2; 3.
PROSITE; PS0940; CHIT BIND II; 4.
SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FF9921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13, Last sequence update)
25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 AA
                                                                                                                                                                                                                                                                                                                                                                  29.6%; Score 59.5; D
31.8%; Pred. No. 16;
iive 4; Mismatches
                                                                    EMBL, AY071103, AAL48725.1, -; mRNA.
Ensembl, CG7348; Drosophila melanogaster.
FlyBase; FBgn0036940; CG7348.
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.8*
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Q9VW81;
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090W81 DRO
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MEDLINE=22426070; PubMed=12537573;

Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Fribe E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.,

"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                  MUCLEOTIDE SEQUENCE.
MEDLINE=22426665; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Meeler D.A., Kronmiller B., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Paciel J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Rollers B., Strokas R., Tabor P.E., Wan K., Stapleron M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shocqun: release 3 of the Drosophila melanogaster euchromatic genome sequence.",
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
MEDLINE=22426069; PubMed=12537572;
Mrista S., Croeby M.A., Kamingall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Evosophila melanogaster."; Science 287:2185-2195(2000).
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 29.6%; Score 59.5; DB 2; Length 353; Local Similarity 31.8%; Pred. No. 16; les 14; Conservative 4; Mismatches 15; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 CSVGNYFDPARRACLPVAISAAHQCSCVLPDNATLANPSDCETY 162
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:000861; F:chitin binding; IEA.
GO; GO:0008031; P:chitin metabolism; IEA.
InterPro; IFR002557; Chitin bind PerA.
PEam; PF01607; CBM 14; 4.
SMART; SM00444; ChEBD2; 3.
PROSITE; PSG0940; CHIT BIND II; 4.
SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Ensembl; CG7348; Drosophila melanogaster.
Flybase; FBgn0036940; CG7348.
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Pubmed-14702039; DOI-10.1038/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A kakamateu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Iranka T., Ishii S.,

A sekine M., Obayashi M., Nishi T., Shibahara T., Ishii S.,

A mamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,

A shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,

A wazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

Rusano J., Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O.,

Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

Nomura Y., Masshino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

Nomura Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ34691.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (FRB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, CR936873; CAIS97851; -; -; -; InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.6%; Score 59.5; DB 2; Length 484; 28.9%; Pred. No. 22; tive 5; Mismatches 9; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 AA; 53895 MW; 8895A663E9DB369C CRC64;
                                                                                   Hypothetical protein DKFZp686D20108 (Fragment)
Name=DKFZp686D20108,
Homo sapiens (Human).
Bukaryota; Metarro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 CSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 278
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                                                      484 AA
                                                      PRT;
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Pfam; PF07699; GCC2 GCC3; 3.
SMART; SM00042; CUB; 1.
PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal kidney;
The German cDNA Consortium;
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                                             QSCZ68 HUMAN PRELIMINARY;
QSCZ68;
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NCBI_TaxID=9606;
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Matches
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QBNAVB HUM
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Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhiní; Hominidae;
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tarigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kawabani T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komateu T., Oyama M., Hata H., Watanabe M., Komateu T., Okamoto S., Okumura K., Nagase T., Nomura N., Takuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Tomplete sequencing and characterization of 21,243 full-length human
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0004889; F:calcium ion binding; IEA.

GO; GO:0004889; F:transmembrane receptor activity; IEA.

GO; GO:0004889; F:transmembrane receptor activity; IEA.

GO; GO:0007596; P:blood coagulation; IEA.

InterPro; IPR000152; Asx. hydroxyl_S.

InterPro; IPR001432; EGF_2.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR001891; EGF_Ca.

InterPro; IPR001601; GGC_2 GCC3.

InterPro; IPR001491; Thrmbomoduln.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PP00431; CUB; 1.
Pfam; PP07699; GCC2 GCC3; 3.
SMART; SMO0042; CUB; 1.
PROSITE; PS01180; CUB; 1.
SEQUENCE 581 AA; 64343 MW; D17BC28CDA1E4EE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp686B1223 (Fragment)
Name=DKFZp686B123;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 CSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSONEYFDSLLHACIPCOL------RCSSNT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59.5; DE Pred. No. 27; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNAB.;
Nat. Genet. 36:40-45(2004).
BMBL; AKO92010; BAC03789.1; -; mRNA.
InterPro; IPR000859; CUB.
InterPro; IPR011641; GCC2_GCC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Pfam; PF00008; EGF; 5.
Pfam; PF07645; EGF CA; 1.
Pfam; PF07699; GCCZ_GCC3; 3.
PRINTS; PR00907; THEMBOMODULN.
SMART; SM00042; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.6%;
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AC 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TREMBLrel.) (TREMBLR).

AND MADE OF TAXIDES (Human).

AND GOTON (Human).

AND TAXIDES (H
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nes 11; Conserv
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Rakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Schine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Rayamacro J. I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
Rayawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
Rayamara Y., Abe K., Kamihara K., Yasuda N., Sato K., Tanikawa M.,
Rayamaraki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
Raibida S., Ono Y., Takahashi-Fujii A., Hara H., Murakawa K.,
Raibida S., Ono Y., Takahashi-Fujii A., Hara H., Tanase T.-O.,
Rayamara Y., Nantennawa H., Ichihara T., Shiohata N., Sano S.,
Nomiyama H., Satoh N., Takami R., Tarashima Y., Sazuki O.,
Rayagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Rayamasaki M., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y.,
Rayamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Rayamazaki M., Watanabe T., Sugiyama A., Takemoto M., Rawakami T.,
Rayamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Rayabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Rayabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Rayabata A., Hikiji T., Kobatake N., Inagaki H., Matanabe M., Kawabatu T.,
Rayabhima Y., Nakajima Y., Monuro T., Morinaga M., Saaski M.,
Rogashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Rayabhima Sugano J., Satoh T., Shitaal Y., Rayabahi Y., Nakajama Y., Makai M., Matanabe T., Nomura N., Kikuchi H., Masaubo S.;
Rayachima K., Nadaemura N., Nikuchi H., Masaubo S.;
Rayachima M., Yada T., Nakamura N., Chara O., Isogai T., Sugano S.;
Rayachima M., Rayacterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0005509; C: membrane; IEA.
GO; GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0007599; P: blood coagulation; IEA.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR00059; CUB.
InterPro; IPR00059; CUB.
InterPro; IPR0001891; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR01641; GCC_GCG.
InterPro; IPR001491; ThrmDomoduln.
Pfam; PF00411; CUB; 1.
Pfam; PF07649; EGF_A; 2.
Pfam; PF07649; EGF_A; 2.
Pfam; PF07649; GCC_GCG; 3.
Pfam; PF07649; GCC_GCG; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01186; EGF 2; 5.
PROSITE; PS5026; EGF 2; 3, 3.
PROSITE; PS01187; EGF CA; 3.
SEQUENCE 880 AA, 97239 MW; FOBDE6E85266FD60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSONEYFDSLLHACIPCOL------RCSSNT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.
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Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         985 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 36:40-45(2004).
EMBL; AK092062: BAC03798.1; -; mRNA.
HSSP; P35555; 1LMJ.
Ensembl; ENSG00000146197; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00179; EGF_CA; 3.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS01180; CUB; 1.
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Query Match
Best Local Similarity 28.79,
Conservative
The Conservative
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QBIZO6 HUMAN PRELIMINARY;
QBIZO6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC; HGNC:13655; SCUBE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00042; CUB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
Q81Z06 HUM
1D Q81Z0
AC Q81Z0
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptococcus neoformans var. neoformans B-3501A.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                      9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
EMBL; AAEY01000041; EAL19380.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 861 AA; 93346 MW; 8745729FBD869366 CRC64;
                                                                                                                                                                                                   852 AA; 93812 MW; 514918C0D126C7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FL034743.
                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQL------RCSSNT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 CSSGLYYDSSTSSCESCSPACSTCTGPGTSDCLSC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRCSSNTPP----LTC 30
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                                                                                                                                                                                                                                                                                      5; Mismatches
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Pred. No. 40;
                                              PROSITE; PSOUND ASX HYDROXYL; 3. PROSITE; PSOUND; CUB; 1. PROSITE; PSOUNDS; EGF 2; 4. PROSITE; PSOUNDS; EGF 3; 3. PROSITE; PSOUNDS; EGF A; 3. EGF 11ke domain; Hypothetical protein. NON TER. SEQÜENCE 852 AA; 93812 MW; 514918COD
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PubMed=14702039; DOI=10.1038/ng1285;
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                                EGF CA; 4
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                                                                                                                                                                                                                                                                                      11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
ORFNames=CNBH0730;
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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          SMART; SM00181;
SMART; SM00179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=B-3501A;
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RESULT 35
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Matches
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                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubbMed=12477932; DOI=10.1073/pnas.242603899;
StraubDerg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butcaffield Y.S.N., Krzywinski M.I., Skalska U., Smills D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smills D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smills D.E.,
Butterfield Schein J.E., Jones B.J.M., Marra M.A.,
Butterfield Schein J.E., Jones S.J.M., Marra M.A.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; . .
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.6%; Score 59.5; DB 2; Length 985; 21.6%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032835; AAH32835.1; -; mENA. Ensembl; ENSG00000164953; Homo sapiens. InterPro; IPR000150; Hypothet cof. PROSITE; PG01228; COF 1; UNIXCÓWN 1. SEQUENCE 985 AA; 110872 MM; 971B5526C726B3B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein MGC26979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 985 AA
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  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.6%;
Matches 11, Conservative
  23,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7Z5T8 HUMAN PRELIMINARY;
Q7Z5T8;
                    01-MAR-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                MGC26979 protein.
Name=MGC26979;
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                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jozeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Distchench D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Distchench D., Warusina K.B., Farmer A.A., Rubin G.M., Hong L.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.B., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Monton and initial analysis of more than 15,000 full-length human
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Alterbul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carainer T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Radesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 29.6%; Score 59.5; DB 2; Length 985; Local Similarity 21.6%; Pred. No. 46; 11; Conservative 9; Mismatches 12; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPC------QLRCSSNTPPLTCOR 32
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Strauberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054389, AAH54338.1; -; mRNA.
InterPro; IPR000150; Hypothet cof.
InterPro; PS01228; COF_1; UNKNÖWN_1.
Hypothetical protein.
EQUENCE 985 AA; 110858 WW; 711109F095C12E89 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal peptide, CUB domain, EGF-like 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Q8GUZ9;
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QSHYA8 HUMAN PRELIMINARY;
QSHYA8;
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nes 11; Conservative
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   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOUENCE
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QSHYA8 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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Matches
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DRAPA
DR
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfarr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R., Hankeln T., Winterpacht A.; Hankeln T., Winterpacht A.; "Novel human gene family (CEGF) encoding mosaic proteins with EGF-like, STT2R and a CUB module: cloning and expression analysis."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15234972; DOI=10.1074/jbc.M405912200; Wu B.T., Su Y.H., Tasi M.T., Wasserman S.M., Topper J.N., Yang R.B.; "A novel secreted, cell-surface glycoprotein containing multiple epidermal growth factor-like repeats and one CUB domain is highly expressed in primary osteoblasts and bones.";
J. Biol. Chem. 279:37485-37490(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBIX30;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
CUB and EGF containing protein (Signal peptide, CUB and EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 992;
                                                                                                                                                                                                            Straubberg R. S. Straubberg R. S. Straubberg R. Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BOS25263; AAH52263.2; -; mRNA. HSSP; P3555; IEMN. GO; GO:0005509; F:calcium ion binding; IEA. InterPro; IPR000152; Asx_hydroxyl_S. InterPro; IPR000459; CUB. InterPro; IPR001891; EGF 2. InterPro; IPR001891; EGF 2. InterPro; IPR00509; EGF 2. InterPro; IPR006209; EGF 2. InterPro; IPR006209; EGF 2. InterPro; IPR006210; IEGF 2. InterPro; IPR006210; IEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF 2; 7.
PROSITE; PS50026; EGF 2; 7.
PROSITE; PS50016; EGF 2; 6.
SEQUENCE 992 AA; 109165 MW; 24093050738932E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain containing protein 3 precursor) (OTTHUMP00000018) Name=SCUBE3; Synonyms=CEGF3; ORFNames=RP3-329A5.4-001; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 785
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                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59.5; D
Pred. No. 47;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Pfam; PP00009; EGF; 5.
Pfam; PP07645; EGF_CA; 4.
Pfam; PP07699; GCCZ GCC3; 3.
SWART; SW00042; CUB; 1.
SWART; SW001181; EGF; 10.
PROSITE; PS00010; ASX_HYDROXYL; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.6%;
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QBIX30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 28.9
tes 11, Conservative
                                                           and mouse cDNA sequences.
                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                            FISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX648768; CAI45999.1; -; mRNA.
InterPro; IRR000150; Hypothet cof.
PROSITE; PSO1228; COF_1; UNKNÖNN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.6%; Score 59.5; DB 2; Length 993; 28.9%; Pred. No. 47; ive 5; Mismatches 9; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.6%; Score 59.5; DB 2; Length 995; Best Local Similarity 21.6%; Pred. No. 47; Matches 11; Conservative 9; Mismatches 12; Indels 1:
Williams S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AF452494; AAN76808.1; -; mRNA.
EMBL; AF439608; AAU08347.1; -; mRNA.
EMBL; Z97832; CA120187.1; -; Genomic_DNA.
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995 Aa; 111730 MW; AEBD4A6B84F759A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109282 MW; 19BBE0E5627EEAF4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHACIPCQL------RCSSNT 25
                                                                                                                                                                                 HGNC; HGNC:13655; SCUBEZ;
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000189; CUB.
InterPro; IPR0001891; EGF_Z.
InterPro; IPR0001891; EGF_Z.
InterPro; IPR001891; EGF_Z.
InterPro; IPR011641; GCCZ_GCG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             995 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSQNEYFDSLLHACIPC-------
                                                                                                                                                                 Ensembl; ENSG0000146197; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMARY; SMULLY; ESS. M., C., PROSITE; PS0010; ASX HYDROXYL; PROSITE; PS01186; EGF 2; 7. PROSITE; PS50026; EGF 3; 6. PROSITE; PS01187; EGF GA; 6.
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00451; CUB; 1.
Pfam; PF00009; EGF; 6.
Pfam; PF07659; EGF CA; 3.
SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 6.
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49 CDNNQYFDISALSCVPCGANQRQDARGTSCVCLPGFQMISNNGGPAIICKK 99

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MUCLEOTIDE SEQUENCE.

A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Dubrat S., Brottier P., Coutanceau J.P., Gouzy J.,
Biemont C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Arlis M., Volff J.M., Guigo R., Zody M.C., Mesirov J.,
A. Kellis M., Volff J.V., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
III Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
0RFNames=C23G10.8;
Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                         Tetracdon nigroviridis (Green puffer).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Eukaryota, Metozoa, Chordata, Craniata, Vertebrata; Neoteleostei,

Actinopterydii, Neoperygii, Teleostei, Euteleostei, Neoteleostei,

Acanthomorpha, Acanthopterygii, Percomorpha, Tetracdontiformes,

Tetradontoidea, Tetracdontidae, Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; CAABC1014738; CAG04379.1; -; Genomic_DNA.
SEQUENCE 184 AA; 19133 MW; 3B2167E5E4FB1BB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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nome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
29.4%; Score 59; DB 2; Length 184;
Best Local Similarity 27.3%; Pred. No. 9.7;
Matches 9; Conservative 10; Mismatches 4; Indels
                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 2 SCAF14738, whole genome shotgun sequence.
CRFNames=GSTENG00024082001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 CSSSEFWNSDVDVCVPCE-----SCKKY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          937 AA
                                                                   184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                   PRT;
                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGGYRS CAEEL PRELIMINARY;
OGGYRS;
                                                        Q4S4Q3_TETNG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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"Genome
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                                         TETNG
                                                                                                             048403
RESULT 41

104840

AC 04840

DT 13-SE
SS BLEAR

RA MAUCLE
RA LAUGE
RA LAUG
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                                                                                              O45080:C17H12.9; NbExp=1; IntAct=EBI-312175, EBI-312180; P41829:nhr-6; NbExp=1; IntAct=EBI-312175, EBI-314469; EMBL; U39811; AAF99879.1; -; Genomic_DNA. PIR; T15577, T15577. Ensembl; C23G10.8; Caenorhabditis elegans. WormBase; WaGene00016015; C23G10.8. WormPep; C23G10.8; C25784. Gomplete proteome; Hypothetical protein. SEQUENCE 937 AA; 106669 MW; 1C140595DFD3ACE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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InterPro; IPR06212; F.Kinase activity; IEA.
InterPro; IPR06212; F.Urin repeat.
InterPro; IPR01641; GCCZ-GCC3.
InterPro; IPR006210; IEGF.
InterPro; IPR004094; Prot_inh_antistn.
InterPro; IPR004094; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR001369; TNFR_C6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.4%; Score 59; DB 42.9%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=10.t00040;
Entamoeba histolytica HM-1:IMSS.
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|: | | ::|||: |||
439 ESVFHPLYPAEIRCSADGPPL 459
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ProDom; PD000001; Prot kinase; 1.
SMART; SM00181; EGF; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001245; Tyr Dkinase.
Pfam; PF02822; Antistasin; I.
Pfam; PF07699; GCC2_GCC3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 DSLLHACIPCQLRCSSNTPPL 28
investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43
QSIED6 ENTHI
ID QSIED6_ENTHI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein kinase, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=294381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=HM-1:IMSS;
                                                                          -!- INTERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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        S K B B B B B C C C C F F
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninol P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Ahramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skaløka U., Smallus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58.5; DB 2; Length 827;
Pred. No. 53;
5; Mismatches 9; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Signal peptide, CUB and EGF-like domain containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN-CS7BL/6; TISSUE-Brain;
Director MGC PROJECt;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079849; AAH79849.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        827 AA; 90870 MW; DF6BB3337B4CE91D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611 CSPGHYYNTSIHRCIRCAVGSYQPDFRQNFCTRCPGNT 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               993 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI; MGI:3045253; Scube3.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx_hydroxyl_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-0cT-2004 (TrEMBLrel. 28, Created)
25-0cT-2004 (TrEMBLrel. 28, Last seq
25-0cT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000859; CUB.
InterPro; IPR000142; EGF 2.
InterPro; IPR000142; EGF 2.
InterPro; IPR0005109; EGF like.
InterPro; IPR0065109; EGF like.
InterPro; IPR006510; IEGF.
Pfam; PF004011; CUB; 1.
Pfam; PF000008; EGF; 5.
Pfam; PF001699; EGF CA; 3.
Pfam; PF07649; EGF CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00042; CUB; 1.
SMART; SM00181; EGF; 9.
SMART; SW00179; EGF (A; 7.
PROSITE; PS00110; ASX HYDROXYL;
PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Scube3; Synonyms=SCUBE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01186; EGF 2; 6. PROSITE; PS50026; EGF 3; 4. PROSITE; PS01187; EGF CA; 4. EGF LIKe domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QG6PY1 MOUSE PRELIMINARY;
Q66PY1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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Q66PY1_MOU
                RAPARA RA
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10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
Schistosoma japonicum (Blood fluke).
Bukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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STRAIN=CSTBL/6; ITSUE=Brain;
STRAIN=CSTBL/6; ITSUE=Brain;
MEDIJINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Colling F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The full-length cDNA sequences of Schistosoma japonicum genes.";
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY814458; AAW26130.1; -; mRNA.
InterPro; PRN06212; Furin_repeat.
SWART; SM0261; FU; 2.
Hypothetical protein.
SEQUENCE 248 AA; 27756 MW; F8D8EBD4F5DD2EEB CRC64;
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                                                                                                                                                                                                                                                                                                                                    Score 59; DB 2; Length 1917;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                     SEQUENCE 1917 AA; 212684 MW; 4AD7144F6A3CF30D CRC64;
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Last annotation update)
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4; Mismatches
      SMART; SM00261; FU; 17.

SMART; SM00219; S_TKc; 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00101; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; TNFR NGFR 2; 1.
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les 11; Conservative
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Q68FG9;
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NCBI_TaxID=10090;
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OSD DBG SC DB
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CSTRAIN=C57BL/6;

Rubmed=15234972; DOI=10.1074/jbc.M405912200;

Rubmed=15234972; DOI=10.1074/jbc.M405912200;

Rubmed=15234972; DOI=10.1074/jbc.M405912200;

Rubmed=15234972; DOI=10.1074/jbc.M405912200;

Rubmed=15234972; DOI=10.1074/jbc.M405912200;

Rubmed=15234972; DOI=10.1074/jbc.M405910;

Rubmed=15234972; DOI=10.1074/jbc.M405910;

Rubmed=15234972; Doi=10.1074/jbc.M405910;

Rubmed=15234972; Doi=10.1074/jbc.M405910;

Rubmed=15234972; Doi=10.1074/jbc.M405910;

Rubmed=15234972; Doi=10.1074/jbc.M40591;

Rubmed=15234972; Doi=10.1074/jbc.M40591;

Rubmed=1524972; Doi=10.1074/jbc.M40591;

Rubmed=1524972; Doi=10.1074/jbc.M40591;

Rubmed=1524972; Doi=10.1074/jbc.M40591;

Rubmed=1524972; Doi=10.1074/jbc.M40591;

Rubmed=1524972; Doi=10.1074/jbc.M40591;

Rubmed=1524972; Doi=10.1074/jbc.M40591;

Rubmed=1524972;

Rubmed=1624972;

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Rubmed=1624973;

Rubmed=16249
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230316E19 product:hypothetical protein, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
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993 AA; 108983 MW; E43989ACACCC345F CRC64;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58.5; DE Pred. No. 63; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.1%;
28.9%;
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QBBR19;
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Nes 11; Conserv
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NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSTB=Corpora quadrigemina;

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Adachi J., Aizawa K., Akimura T., Arakawa T., Hashizume W.,

Bukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

An Hayashida K., Imotani K., Ishin Y., Kondo S., Konno H., Kowia S.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Katoh H., Kawai J., Kojima Y., Myazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksazui Y.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2001) to the EmBlal/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina; MEDLINE=20499314; PubMed=110421159; DOZI-10.1101/gr.145100; Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.; Shibata K., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrin L.M., Staubli F., Suruki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Staubli F., Suruki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Eluruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodzinguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Winghaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 YFNSLLFLSLFCIFKRILTLRCTSHPPPSPPPPPPPHSHSLACGYFC
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101 AA; 11571 MW; E899420B6F215D23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.9%; Score 58; DB 2;
31.9%; Pred. No. 7.1;
cive 5; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 31.9%;
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEOUENCE.
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18798 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal-anchor;
                                                                                                                                                                          Name=1;
                                                                                                                                                                                                           Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 49
Q8R4W8 MOU
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RADINES-2354681; PubMed-12466851; DOI=10.038/nature01266;

RADINES-2354681; PubMed-12466851; DOI=10.038/nature01266;

RADINES-2354681; PubMed-12466851; DOI=10.038/nature01266;

RADINES-2354681; PubMed-12466851; DOI=10.038/nature01266;

RADINES-2354681; PubMed-12466851; Rondon S.,

RADINES-2354681; PubMed-12466851; Rondon S.,

RADINES-2354681; PubMed-12466851; Rondon S.,

RADINES-2354681; PubMed-12466851; Rondon S.,

RADINES-2354681; PubMed-1246851; Rondon S.,

RADINES-2354681; Rondon S.,

RADINES-2364681; Rondon S.,

RADINES-2364681; Rondon S.,

RADINES-2364681; Rondon S.,

RADINES-2364681; Rondon S.,

RADICA D.R., Radinas R.,

RADINES-256861; Rondon S.,

RADICA D.R.,

RADINAS RADINA
                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yan M., Brady J.R., Chan B., Lee W.P., Hgu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.; "Identification of a novel receptor for Blymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency."; Curr. Biol. 11:1547-1552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21475520; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                    "BAFF-R, a newly identified TNF receptor that specifically interacts with \mathsf{BAFF}...\,,
                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/C; TISSUE=B-cell lymphoma; MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965; Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORM 1), AND DISEASE.
                                                   175 AA.
                                                                                                                                                                                       Name=Tnfrsf13c; Synonyms=Baffr, Bcmd, Br3;
                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 293:2108-2111(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNAB.";
                                                                                                                                                                        (B-cell maturation defect)
                                                   STANDARD;
                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A/J;
                                                                                                                                                                                                                                                                                                                                                                                                                         Ambrose C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION
                               TR13C MOUSE
ID TR13C MOI
AC Q9D8D0;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute, There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MGI: MGI:1919299; Thfrefl3c.

MGI: MGI:1919299; Thereflace of plasma membrane; IDA.

GO; GO:0011296; P:B cell costimulation; IDA.

GO; GO:001782; P:B cell homeostasis; IMP.

GO; GO:001782; P:Positive regulation of E cell proliferation; IDA.

GO; GO:001295; P:positive regulation of interferon-gamma bio. . ; IMP.

GO; GO:001295; P:regulation of immune response; IMP.

GO; GO:001295; P:Tegulation of immune response; IMP.

InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: Highly expressed in spleen and testis; detected at lower levels in lung and thymus.
-i- DISEASE: Defects in Thfrefila are a cause of severe B-cell deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion in the BAFFR gene leading to an altered C-terminus. The mutant RNA is not detectable. B-cells in wmbhopiesis is normal, but the life span of peripheral B-cells is much reduced.
-i- SIMILARITY: Contains I TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
TNFR-Cys (incomplete).
N-linked (GlcNAc. . .) (Potential).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
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PROSITE; PSS0050; TNFR NGFR 2; FALSE NEG.
Alternative splicing; Glycoprotein; Immune response; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.9%; Score 58; DB 1; Length 175; 47.4%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal-anchor for type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28BC7C1A02FB87EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 2). /FIId=VSP 006506.
                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             [80Id=09D8D0-2; Sequence=VSP_006506;
                                                                                                                                                                                                                                                                                                                                                 IsoId=09D8D0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBR4W8 MOUSE PRELIMINARY; PRT; QBR4W8; 01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF373847; AAK91827.1; -; mRNA.
EMBL; AK008142; BAB25490.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSONEYFDSLLHACIPCOL 19
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MEDLINE-84255715; PubMed=6564898;
Babin D.R., Peanasky R.J., Goos S.M.;
"The isoinhibitors of chymotrypsin/elastase from Ascaris lumbricoides:
                                                                                                                                                                                                                                                                                                    Spodoptera frugiperda (Fall armyworm).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea,
Noctuidae, Amphipyrinae, Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P07851; 077419; 01-AUG-198 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 01-AUG-1988 (Rel. 08, Last sequence update) Chymotrypsin/elastase isoinhibitor 1 (C/B-1 inhibitor) (AsC/E-1). Ascaris suum (Fig roundworm) (Ascaris lumbricoides). Bukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO: GO:0016C01; C:membrane; IEA.
GO: GO:0005524; F:ATP binding; IEA.
GO: GO:0005524; F:ATP binding; IEA.
GO: GO:0008239; F:peptidase activity; IEA.
GO: GO:00044289; F:subtilase activity; IEA.
GO: GO:00044289; F:subtilase activity; IEA.
GO: GO:0004714; F:transmembrane receptor protein tyrosine kin.
GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
GO: GO:000169; P:transmembrane receptor protein tyrosine kin.
InterPro; IRR006212; Puttin repeat.
InterPro; IRR002894; PryctinConvert8P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Sf9;
Cieplik M., Klenk H.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z68888; CAA93116.1; -; mRNA.
PIR; T43251; T43251.
                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Endoprotease FURIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch. Biochem. Biophys. 232:143-161(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01483; P. proprotein; 1. Pfam; PF00082; Peptidase S8; 1. PRINTS; PR00723; SUBTILISIN. SMART; SM00261; FU; 10. PROSITE; PS00136; SUBTILASE ASP; UN PROSITE; PS00137; SUBTILASE HIS; 1. PROSITE; PS00138; SUBTILASE HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 37.1%;
ses 13; Conservative
                               39 SPOFR
QZ6489 SPOFR PRELIMINARY;
Q26489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the primary structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6253;
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ICEL ASCSU
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Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
"Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
                                                                                                              Name-Tnfrsfläc;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Lymphocystis disease virus - isolate China.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
NCBI_TaxID=256729;
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GO; GO:0009997; C:external side of plasma membrane; IDA.

GO; GO:00019097; C:external side of plasma membrane; IDA.

GO; GO:0001782; P:B-cell homeostanis; IMP.

GO; GO:001782; P:B-cell homeostanis; IMP.

GO; GO:0045078; P:positive regulation of B-cell proliferation; IDA.

GO; GO:0045078; P:positive regulation of interferon-gamma bio. .;

GO; GO:0042102; P:positive regulation of Interferon-gamma bio. .;

GO; GO:0042102; P:positive regulation of interferon-gamma bio. .;

GO; GO:0050776; P:regulation of immune response; IMP.

SEQUENCE 175 AA; 18846 MW; B64EFF4B52EB93B1 CRC64;
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28.9%; Score 58; DB 2; Length 289;
Best Local Similarity 37.5%; Pred. No. 21;
Matches 12; Conservative 1; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.9%; Score 58; DB 2; Length 175; 47.4%; Pred. No. 12;
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Mizuno K., Irie S., Sato T.-A.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF53c0257; AAL83914.1; -; mRNA.
HSSP; Q96RJJ; 10QE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ll protein. _ _ 2686114D4D5D6C3F CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
   Last sequence update)
Last annotation update)
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GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001369; INFR c6.
Ffam; PF00020; TNFR c6; 2.
SWART; SW0208; TNFR; 4.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 3.
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J. Virol. 78:6982-6994(2004).
   21,
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Q678B7;
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01-JUN-2002 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel.
                                                                               TRAF3 binding protein.
                                                                                                                                                                                                                                                                Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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NUCLEOTIDE SEQUENCE (ISOFORM D).
STRAIN=ISO-1, Oregon-R, and Tuebingen;
MEDLINES=22381035; PubMed=1512259;
REDINES-2A.G.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
"Cloning and functional expression of Dfurin2, a subtilisin-like
proproctin processing enzyme of Drosophila melanogaster with multiple
repeats of a cystein emotif.";
J. Biol. Chem. 267:17208-17215(1992).
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MEDLINE=95186060; PubMed=7880443;
Rebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
Nan de Ven W.J.M.;
"The Dfurz gene of Drosophila melanogaster: genetic organization,
expression during embryogenesis, and pro-protein processing activity
of its translational product Dfurin2.";
DNA Cell Biol. 14:223-234(1995).
                                                                                                                         Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J., Park S., Wan K., Yu C., Rubin G.M., Celniker S.; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, BT021414, AAX33562.1, -; mRNA.

InterPro; IPR010980; Cyt C.b562.

InterPro; IPR011029; DEATH_like.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IRRO02884; PrprotnconverteP.
InterPro; IRR008891; Retrov capsid_N.
Pfam; PF01483; P proprotein; 1.
SMART; SM00181; FGF; 8.
SMART; SM00261; FU; 10.
PROSITE; PS01188; SUBTILASE_SER; 1.
SEQUENCE 1061 AA; 115699 WW; 4E7F1FC5388FF229 CRC64;
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                                                                                                                                                                                                                                                                          InterPro; IPR006212; Furin repeat.
InterPro; IPR011025; GproteinA insert.
InterPro; IPR012287; Homeodomain-rel.
                                                                                                                                                                                                                                                                                                                                      Interpro; IPR006210; IEGF.
Interpro; IPR0015013; LT-IIB.
Interpro; IPR0010503; LT-IIB.
Interpro; IPR000070; Pectinesterase.
Interpro; IPR0000209; Pept S8 533.
Interpro; IPR004094; Prot inf antistn.
Interpro; IPR004094; Prot-inf antistn.
Interpro; IPR002884; Pror-chnconvertsP.
                                                                                                                                                                                                                                                           nterPro; IPR012286; Fcc3 N_cyt.
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                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                               STRAIN=Berkeley
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        MEDLINE=98297373; PubMed=9635450; DOI=10.1006/expr.1998.4284;
Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
"Anisakis simplex: mutational bursts in the reactive site centers of
serine protease inhibitors from an ascarid nematode.";
Exp. Parasitol. 89:257-261(1998).
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                                                                                                                                                      MEDINE-55006335; PubMed-922044;
Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;
"The molecular structure of the complex of Ascaris
chymotrypsin/elastase inhibitor with porcine elastase.";
                                                                                                                                                                                                                                      Structure 2:679-689(1994).
-1- FUNCTION: Defends the organism against the host's proteinases.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Contains 1 TIL (trypsin inhibitory-like) domain.
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                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Pred. No. 5.
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PDB; 1EA1; X-ray; C/D=1-61.
InterPro; IPRO2919; Prot_Inh_CR_TIL.
Pfam; PF01826; TIL; 1.
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Q5B110 DROME PRELIMINARY;
Q5B110;
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Best Local Similarity
Local 13; Conserve
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Q9W4G3:CG15470; NbExp=1; IntAct=EBI-496684, EBI-162037; Q94524:Dlc90F; NbExp=1; IntAct=EBI-496684, EBI-158251; ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named lsoforms=2;

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RX TATALNESERVALEY,

RXATN=REBERVALEY,

RATALN=REBERVALEY,

RADARDINES_20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RADARDINES_20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RADARDINES_20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RADARDINES_20196006; PubMed=10731132; DAID STAND, Galle R.F.

RADARDINES_CONSTRUCTOR,

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STRAIN=Berkeley; TISSUB=Embryo;

MEDLINE=22426066; PubMed=12537569;

SEQUENOM M., CATLESON U., Broketein P., Yu C., Champe M.,

SEAPLEOON M., CATLESON U., Broketein P., Yu C., Champe M.,

Replecon M., Calland U., Krommiller B., Pacleb J.M., Park S., Wan K.H.,

Rubin G.M., Celniker S.E.; DN Essentin D., Yu C., Champe M.,

Rubin G.M., Celniker S.E.; DN Essentin D., Pacleb J.M., Park S., Wan K.H.,

Rubin G.M., Celniker S.E.; Drosophia full-length CDNA resource.;

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).

- I- FUNCTION: Furin is likely to represent the ubiquitous endoprotease activity within constitutive secretory pathways and capable of activity within constitution of activity within constitution of activity within constitution of activity within constitution of ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 MEDLINE=22426069; PubMed=1253757; Mistra S., Campbell K.S., Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Mistadecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., NJ., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
          [3]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   systematic review.";
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                     Note=No experimental confirmation available; TISSUE SPECIFICITY: Transient expression in a subset of central nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic

    development.
    -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
    -!- SIMILARITY: Belongs to the peptidase S8 family. Furin subfamily.

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Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
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PROSITE; PS00137; SUBTILASE H1S; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Alternative splicing; Glycoprotein; Hydrolase; Multigene family;
Protease; Repat; Serine protease; Signal; Transmembrane; Zymogen. SIGNAL
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Cytoplasmic (Potential)
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EMBL; L3381; AAA69860.1; -; Genomic DNA.
EMBL; AE003502; AAF48596.2; -; Genomic_DNA.
EMBL; AE003502; AAN69400.1; -; Genomic_DNA.
EMBL; AX070553; AAL48024.1; ALT_INIT; mRNA.
PIR; A43434; A43434.
HSSP; P23188; 1P8J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; SOB.049; -.
Ensembl; CG18734; Drosophila melanogaster.
FlyBase; FB900004598; Furz.
InterPro, 1000476; F:furin activity; IDA.
InterPro; IPR006212; Furin repeat.
InterPro; IPR006210; IEGF.
Name=D; Synonyms=E;
Isold=P10432-1; Sequence=Displayed;
Name=A; Synonyms=B;
Isold=P30432-2; Sequence=VSP_009365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PRO0723; SUBTILISIN.
PRODOMS, PRO00717; ProprofinconverteP; 1.
SMART; SM00181; EGF; 1.
SMART; SM00261; FU; 10.
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InterPro; IPR002884; PrprotnconvertsP.
Pfam; PF01483; P. Proprotein; 2.
Pfam; PF00082; Peptidase_S8; 1.
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X PubMed=15729342; DOI=10.1038/nature03291;

X Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

A Amedeo P., Roncaqlia P., Berriama M., Hirr R.D., Mann B.J., Nozaki T.,

RA Buchhaus I., Willhoeft U., Bhattacharya A.,

RA Hoffer M., Burchhaus I., Willhoeft U., Bhattacharya A.,

RA Jagels K., Moule S., Murgall K., Ormond D., Squares R., Whitehead S.,

RA Quail M.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z.,

Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,

RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,

RA Fraser C.M., Hall N.,

RA Fraser C.M., Hall N.,

RT Fraegenome of the protist parasite Entamoeba histolytica.";

RA Fraese C.M., Pall N.,

RT RTHE Genome of sequence shown here is derived from an embly densamk DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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                                                                                                                                                                                                                                                                                                                                    Score 57.5; DB 1; Length 1679;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.4%; Score 57; DB 2; Length 304; 29.2%; Pred. No. 30; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSONEYFDSLLHACIPCQ------LRCSS----NTPPLTC
                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches 17; Indels
                                                                                                                                                                                                                                   Missing (In Ref. 1).

V -> F (in Ref. 1).

V -> VOL (in Ref. 1).

MW, 3F9E749F0B021CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preliminary data.
EMBL; AAFB01000134; EAL49926.1; -; Genomic_DNA.
SEQUENCE 304 AA; 34236 MW; 4A32F0137B3869A8 CRC64;
                                                                                                                                                                                           L -> LVSK (in isoform A) /FIId=VSP 009365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSIAP47
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSESEYYSQVEGQCRPCHASCGSCNGPADTSCTSC 1232
                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSQNEYFDSLLHACIPCQLRCSS-NTPPLTCQRYC 34
                                                                          N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
                                       (GlcNAc.
                                                       (GlcNAc.
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                                                                                                                                    By similarity.
By similarity.
By similarity.
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                N-linked
N-linked
N-linked
N-linked
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Entamoeba histolytica HM-1:IMSS.
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                 183370
                                                                                                                                                                                                                                                                                                                                        28.6%;
                                                                                                                                                                                                                                                                                                                                                          34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSIAP4 ENTHI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          Local Similarity 34.3
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 29.2
les 14; Conservative
                    927
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1679 AA;
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480
927
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1181
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1277
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CONFLICT
SEQUENCE
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CARBOHYD
CARBOHYD
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CARBOHYD
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Q9MAMO_ARP
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PRT;

Q9MAMO_ARATH PRELIMINARY;

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Dunn P., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B. Lee J., Lanz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Thayen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chao O., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Len C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sparmatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The C.briggsae Sequencing Consortium; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL; CAACO1000022; CAE61236.1; -; Genomic_DNA. GO; GO:0005576; C:extracellular region; IEA. GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007323; AAF26467.1; -; Genomic_DNA.
HSSP; P54274; 1ITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR001005; Myb DNA bd.
InterPro; IPR001965; Zif_PHD.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG05036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  919 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 HACIVCDIADDGVVPCSGNECPLAVHRKC 91
                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50090; MYB 3; 1.
PROSITE; PS01359; ZF PHD 1; UNKNOWN 1.
Nuclear protein; Repeat.
SEQUENCE 321 AA; 36644 MW; F3411A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTOLAY CAEBR
1D 061V24 CAEBR PRELIMINARY;
DT 25-OCT-2004 (TrEWBLrel. 28,
DT 25-OCT-2004 (TrEWBLrel. 28,
DT 25-OCT-2004 (TrEWBLrel. 28,
DT 25-OCT-2004 (TrEWBLrel. 28,
DF 25-OCT-2004 (TrEWBLrel. 28,
DF 25-OCT-2004 (TrEWBLrel. 28,
DF 4YPOCHECICAL PROTEIN BY
DC 25-OCT-2004 (TrEWBLrel. 28,
DF 4YPOCHECICAL PROTEIN BY
DC CAEBROSO36,
CENARATOCIA METAZOA; Nematoda
OC Rhabditidae, MetaZoa; Nematoda
OC Rhabditidae, Peloderinae; CS
NCBI_TAXID=6238;
NN 11
RP NUCLEOTIDE SEQUENCE.
RG The C.briggaes Sequencing CC
RL Submitted (SEP-2003) to the
DR GO; GO:0005576; C:extracellub
DR GO; GO:0016021; C:integral L
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MEDLINE=21625102; PubMed=11752452; DOI=10.1073/pnas.261477698;
King N., Carroll S.B.,
"A receptor tyrosine Kinase from choanoflagellates: molecular insights into early animal evolution.";
Proc. Natl. Acad. Sci. U.S.A. 98:15032-15037(2001).
            Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea, Strigeidida,
Schistosomatoidea, Schistosomatidae, Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Сарв
                                                                                                                    STRAIN=Puerto Rican;
MEDLINE=92365727; PubMed=1501637; DOI=10.1016/0166-6851(92)90003-3;
Shoemaker C.B., Ramachandran H., Landa A., dos Reis M.G., Stein L.;
Alternative splicing of the Schistosoma mansoni gene encoding a homologue of epidermal growth factor receptor.";
Mol. Biochem. Parasitol. 53:17-32(1992).
EMBL, M86396; AAA29866.1; -; mRNA.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                     GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006463; F:receptor activity; IEA.
GO; GO:0006469; P:preceptor activity; IEA.
GO; GO:0006469; P:prensmembrane receptor protein tyrosine kin.
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CHAIN 20 1717 epidermal growth factor receptor.
SEQUENCE 1717 AA; 192303 MW; 1101A338C1653D8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monosiga brevicollis.
Eukaryota, Choanoflagellida, Codonosigidae, Monosiga.
NCBI_TaxID=81824;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000494; EGRR L.
InterPro; IPR006211; Furin-like.
InterPro; IPR006211; Furin-like.
InterPro; IPR006129; Purin repeat.
InterPro; IPR000129; Purin repeat.
InterPro; IPR0001245; Tyr_Dkinase.
InterPro; IPR000366; Tyr_Dkinase.
InterPro; IPR000366; Tyr_Dkinase.
InterPro; IPR000366; Tyr_Dkinase.
Pfam; PP00757; Furin-like; 2.
Primis, PR001039; Recep_L domain; 2.
PRINTS; PR00109; TYRKINASE.
SMART; SM00241; FU; 6.
SMART; SM00241; FU; 6.
PROSITE; PS00109; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TRR; 1.
PROSITE; PS00109; PROTEIN KINASE_TRR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.4%; Score 57; DB 2; L 40.9%; Pred. No. 1.8e+02; ative 2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1476 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSONEYFDSLLHACIPCOLRCS 22
Schistosoma mansoni (Blood fluke)
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Best Local Similarity 40...
Best Local 9; Conservative
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QBWRF4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor tyrosine kinase.
Name=MBRTK1;
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STRAIN=ATCC 50154;
                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Signal.
                                                          NCBI_TaxID=6183;
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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen G.J., Sogin M.L.,
"Draft sequence of the Giardia lamblia genome.";
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL, AACE01000029; EAA41074.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLP 447 64408 57776.
Giardia lamblīa ATCC 50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                                           Query Match
28.4%; Score 57; DB 2; Length 919;
Best Local Similarity 34.4%; Pred. No. 92;
Matches 11; Conservative 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1210 AA; 132501 MW; 0AC83EEA78ASD726 CRC64;
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                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 919 AA; 96816 MW; BE3EFC096CE53DFD CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Epidermal growth factor receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                          PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                              164 CSQSTVFNAELSVCVPLAIQNSCDSSTQQPVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1210 AA.
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GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
INCEPPO: IPR002557; Chitin bind_PerA.
INCEPPO: IPR00149; BE region.
INCEPPO: IPR000794; KeCoacyl_gynth.
INCEPPO: IPR001571; Snake toxin.
InterPro: IPR00150; Worm_repeat_1.
Pfam; PF01607; CBM 14; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P25963; 11KN.
InterPro; IPR002110; ANK.
Pfam; PF00023; Ank; 20.
PRINTS; PR01415; ANK/RIN.
PROSITE; PS50297; ANK_REP_REGION; 2.
PROSITE; PS50088; ANK_REPERT; 1.
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Q26566 SCHMA PRELIMINARY;
Q26566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7R165 GIALA PRELIMINARY;
Q7R165;
                                                                                                                                                                                         SMART; SM00289; WR1; 14.
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RESULT 59

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026566 1D 022 AC 022 DT 011 DT 011 DE EP

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1 CSQNEYFDSLLHACIP-CQLRCSSNTPPLTCQRYC 34
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Q60WC9;
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         SOUR REPRESENTATION OF THE PROPERTY OF THE PRO
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PubMed-15729342; DOI=10.1038/nature03291;
Loftus B., Anderson I., Davies R., Alemark U.C., Samuelson J.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.
Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.
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MEDLINE=22752268; PubMed=12869759; DOI=10.1126/science.1083853;
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;
                             King N., Hittinger C.T., Carroll S.B., "Evolution of key cell signaling and adhesion protein families
                                                                                                                                                                                                       R HSSP; POBSB1; RIM.

GO; GO: 0005524; F:ATP binding; IEA.

GO; GO: 0005524; F:ATP binding; IEA.

GO; GO: 0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO: 0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO: 0004872; F:receptor activity; IEA.

GO; GO: 000488; P:protein amino acid phosphorylation; IEA.

INTERPO: IPR00152; ABX hydroxyl_S.

INTERPO: IPR00152; ABX hydroxyl_S.

INTERPO: IPR00152; BGF_1;

R INTERPO: IPR00152; BGF_1;

R INTERPO: IPR00159; BGF_1;

R INTERPO: IPR00159; Prot Kinase.

R INTERPO: IPR00159; Prot Kinase.

R INTERPO: IPR00159; BGF Z;

R Ffam; PF00008; BGF; 2.

R Ffam; PF00008; BGF; 2.

R Ffam; PF00164; Subh; 1.

R PROSITE; PR00109; TYRKINASE.

R PROSITE; PR00109; TYRKINASE AFP; UNKNOWN 1.

R PROSITE; PR00109; PROTEIN KINASE TYR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1476 AA; 157129 MW; BEF0A03DDC3AD897 CRC64;
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13-SEP-2005 (TrEWBLrel. 31, Last annotation update)
Protein kinase, putative.
Protein kinase, putative.
Entames=10.t00023.
Entameba histolytica HM-1:IMSS.
Eukaryota; Entamoebidae; Entamoeba.
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                                                                         predates animal origins.";
Science 301:361-363 (2003).
EMBL; AF440359; AAL33602.2; -; mRNA.
HSSP; P08581; 1RIW.
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QSIEF3;
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0518F3 ENT
10 0518F
AC 0518F
DT 13-SE
DT 13-SE
DT 13-SE
DT 13-SE
DT 13-SE
CO NORN
OC BURAZ
OC NORN
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
Quail M.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A., Foster P.G., Siroheritz-Ponten T., Weber C., Singh U., Mukherjee C., Bl-Sayed M.M., Petri W.A., Clark C.G., Embley T.M., Barrell B., Fraser C.M., Hall N.; Rithe genome of the protist parasite Entamoeba histolytica."; Nature 433:865-868(2005).

Nature 433:865-868(2005).

BMBL/GenBank_JDBJ whole genome shotgun (WGS) entry which is EmBL/GenBank_JDBJ whole genome shotgun (WGS) entry which is
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 27.9%; Score 56; DB 2; Length 135; Local Similarity 37.1%; Pred. No. 17; Local 13; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indele
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG19174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.1%; Score 56.5; DB 2; Best Local Similarity 39.4%; Pred. No. 2e+02; Matches 13; Conservative 3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.

EMBL; CAACO1000099; CAE72086.1; -; Genomic_DNA.
InterPro; IPR0005209; EGF_like.

Pfam; PF01826; TIL; 2.

PROSTTE; PS01186; EGF 2; UNKNOWN_2.

HYDOCHELICAL protein.

SEQUENCE 135 AA; 14981 MW; 74B21060EAF539B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      754 YFEEHKFSCITCSDGLFINNCSSSINVLYCOSY 786
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NUCLEOTIDE SEQUENCE
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NUCLEOTIDE
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=In vitro fertilized eggs;
MEDINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/Sv x C57BL; TISSUE=Testis;
MEDINE=2239718; PubMed=12351194; DOI=10.1016/S0925-4773(02)00258-7;
YAD W., Burns K.H., Ma L., Marzuk M.M.;
"Identification of Zfp393, a germ cell-specific gene encoding a novel
                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus in vitro fertilized eggs cDNA, RIKEN full-length in vitro fertilized eggs cDNA, RIKEN full-length in Library, clone:7420700M05 product:weakly similar to DJ675G8.1
ZINC FINGER PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; POS0201; ANALOGO 11, MANALOGO 12, MANALOGO 13, MANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Germ cell specific zinc finger protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%; Score 56; DB 2; Len
29.4%; Pred. No. 45;
tive 7; Mismatches 17;
80 CPQNEQFRGCGTACEPTCE----NPKPMACTKQC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  zinc finger protein.";
Mech. Dev. 118:233-239(2002).
EMBL; AF508984; AAN31656.1; -; mRNA.
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                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9D351 MOUSE PRELIMINARY;
Q9D351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 29.4 nes 10; Conservative
                                                                                                             QBCFA7 MOUSE PRELIMINARY;
QBCFA7;
                                                                                                                                                                                                                                                                                                  Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                MOUSE
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1 CSONEYFDSLLHACIPCOL-----RC-----SSNTPPLTCQ 31
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
075-1ike transmembrane protein fullback (Neurotrophin receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=15258592; DOI=10.1038/ncb1158;
Sasai N., Nakazawa Y., Haraguchi T., Sasai Y.;
"The neurotrophin-receptor-related protein NRH1 is essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.9%; Score 56; DB 2; Length 387; 25.4%; Pred. No. 51;
                                              27.9%; Score 56; DB 2; Length 341; 29.4%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42066 MW; 1A386A239C7C8A82 CRC64;
341 AA; 38046 MW; 62BB8F5059125A2B CRC64;
                                                                                                                                                                                        60 CNEREWESQLIRSLPEHGVRCPSQLAPIPFQNYC 93
                                                                                                                                                        1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                                                                                                                                                                                                                                                                                                                           387 AA
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                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 51;
6; Mismatches
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Pfam; PP0020; TNFR_c6; 3.
SWART; SM00209; TNFR; 1.
SMART; SM00209; TNFR; 4.
PROSITE; PS50017; DEATH DOWAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     convergent extension movements.";
Nat. Cell Biol. 6:741-748(2004).
EMBL, AF131890; AAD$4072.1; -; mRNA.
ESMBL; AB162703; BAD36761.1; -; mRNA.
HSSP; P07174; INGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000488; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus; Xenopus
                                                Query Match 27.9%;
Best Local Similarity 29.4%;
Matches 10; Conservative
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                        Q9PVD4_XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 RYC 34
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SEQUENCE
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Q4KLX7_XENLA
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Matches
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KX STRAIN-C57BL/64; TISSUE-Unfertilized egg;

KX STRAIN-C57BL/64; TISSUE-Unfertilized egg;

KX STRAIN-C57BL/64; TISSUE-Unfertilized egg;

KX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KAlausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A Detchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.M., Krzzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzzywinski M.I., Skalska U., Smailus D.E.,

B. Butterfield Y.S.M., Krzzywinski M.I., Skalska U., Smailus D.E.,

B. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinee; Mus.
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                                                                                                                                                                                                                                                                 27.9%; Score 56; DB 2; Length 341;
                                                                                                                                                                                                                                                                                                                7; Mismatches 17; Indels
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GO; GO:0007276; P:gametogenesis; IDA.
InterPro; IRR007087; Znf C2H2.
Promon; Promono3; Znf C2H2; 3.
PROSTE; PROMO03; Znf C2H2; 3.
PROSITE; PSOMO28; ZINC FINGER C2H2 1; 3.
PROSITE; PSSOMO37; ZNC_FINGER_C2H2 2; 3.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFFC CRC64;
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Last sequence update)
Last annotation update)
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PROSITE; PS50157; ZINC FINGER C2H2 2; 3.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                    CNEREWESQLIRSLPEHGVRCPSQLAPIPFQNYC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 AA
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STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                       29.48;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
2inc finger protein 393.
Name=ZEp393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEP233 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                  10; Conservative
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                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA
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LOC398134 protein (Fragment).
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Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 CPERQYLDS-NGICLPCQLCSKGHGVVSQCTHNKNTVCQLCSSGFYSEVKSSESPCLPCR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSQNEYFDSLLHACIPCQL------RC-----SNTPPLTCQ 31
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                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Skaryvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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25.4%; Pred. No. 51;
tive 6; Mismatches 11; Indels
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Submitted (JUL-2005).
EMBL, BC098955; AA498955.1; -; mRNA.
SEQUENCE 387 AA, 42040 WW; DA256A239C61BA8B CRC64;
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                                                                                                Last sequence update)
Last annotation update)
         387 AA.
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                                                                                                13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
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Q6NUF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 25.4 Matches 16, Conservative
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      Q4KLX7 XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                               LOC398134 protein.
Name=LOC398134;
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
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                                                                     13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     initiative.
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TISSUE=Embryo;

X Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Altsuberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Habth F.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., McKernan K.J., Marek J.A., Gunaratne P.H.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Nilalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Rad Mniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Mniting M., Achunt J.W., Green E.D., Dickson M.C.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

X Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
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Klain S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
Name=LOC398134;
Name=LOC398134;
Name=LOC398134;
Nanopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 52;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00531; Death; 1.
Pfam; PF00020; TNFR_c6; 3.
SNART; SN00005; DEATH; 1.
SNART; SN00208; TNFR; 4.
PROSITE; PS50017; DEATH DOWAIN; 1.
PROSITE; PS00652; TNFR NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.98;
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Klein S., Strausberg R.;
Submitted (APR-2004) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 RYC 34
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Pfam;
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                                                                                                                                               PIR; T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 823-830; 859-872; 883-890; 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1668-1,77-1795 AND 1914-1921.
STRAIN=Meishan; TISSUE=Testis; MEDLINE=96064659; Pubmed=7592795; DOI=10.1074/jbc.270.44.26025;
                                                                                                    Caenorhabditis briggsae.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zona pellucida.
DOMAIN: During sperm migration through the reproductive tracts, the mucin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.
                                                                                                                                                        The C.briggaae Sequencing Consortium; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                  27.9%; Score 56; DB 2; Length 938; 38.1%; Pred. No. 1.3e+02; ive 6; Mismatches 7; Indels
                                                                                                                                                                                         preliminary data.
EMBL: CAACO1000266; CAE56536.1; -; Genomic_DNA.
Hypothetical protein:
SEQUENCE 938 AA; 106775 MW; A57E19A356BF605D CRC64;
                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                          938 AA
                                                                                                                                                                                                                                                                                                                                 PRT; 2476 AA.
                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
Hypothetical protein CBG24263.
                                                                                                                                                                                                                                                                                8 DSLLHACIPCQLRCSSNTPPL 28
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                                         QGOK18 CAEBR PRELIMINARY;
QGOK18;
                                                                                                                                                                                                                                            Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           Zonadhesin precursor.
                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig)
                                                                                             Name=CBG24263;
                                                                                                                                                                                                                                    Query Match
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028983;
                                    CAEBR
                          RESULT
Q60K18
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
DOMAIN: The VWFD domains 2 and 3 may mediate covalent oligomerization (By similarity to human intestinal mucin MUC2). PTM: The MAM domains and the mucin-like domains are missing from the zonadhesin that binds to the egg extracellular matrix. Processing might occur during sperm maturation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 X approximate heptapeptide repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00181; EGF; 1.

SMART; SM00137; MAM; 1.

SMART; SM00137; MAM; 1.

SMART; SM00214; VWC; 2.

SMART; SM00214; VWC; 2.

SMART; SM00216; VWD; 4.

PROSITE; PS00026; EGF 1; 1.

PROSITE; PS00740; MAM 1; 1.

PROSITE; PS00060; MAM 1; 1.

Cell adheaton; Direct protein sequencing; EGF-like domain; Glycoprotein; Repeat; Signal; Transfemembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular (Potential)
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N-linked (GlCNAc. .
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(GlcNAc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (partial)
                                                                                                               -!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 2 MAM domains.
-!- SIMILARITY: Contains 5 VWFD domains.
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF_.
InterPro; IPR006210; IEGF..
InterPro; IPR002919; Prot_Inh_CR_III.
InterPro; IPR003328; TIL.
InterPro; IPR001007; VWF_C.
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N-linked
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EGF-like.
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VWFD 2.
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                                                                                                                                                                                                                                                                                                           EMBL; U40024; AAC48486.1; -; mRNA.
PIR; T34022; T34022.
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Pfam; PF01826; TIL; 5.
Pfam; PF02345; TIL_assoc;
Pfam; PF00094; VWD; 4.
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687
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Pfam; PF00629; MAM; 2.
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InterPro; IPR000742;
                                                                                                     capacitation.
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NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinzawa H., Shao L., Jiang Q., Togashi H., Zhang X., Ishibashi Hatanabe H., Saito T., Takahashi T., Ohba K., Mizokami M.; Submitted (Aud-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB030968; BABLI770.1; -; Genomic RNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
Interpro; IPR002519; HCV env.
FEan; PF01539; HCV env.
Fran; PF01539; HCV env.
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                C -> V (in Ref. 1; AA sequence).
S -> Y (in Ref. 1; AA sequence).
W -> Y (in Ref. 1; AA sequence).
S -> K (in Ref. 1; AA sequence).
Mw; A13B690375A6548C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.6%; Score 55.5; DB 2; Length 146; 31.8%; Pred. No. 22; ive 6; Mismatches 13; Indels 11
                                                                                                                                                                                                                                      Length 2476;
                                                                                                                                                                                                                                                     Pred. No. 3.4e+02;
8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQN----EYFDSLLH--ACIPCQ-----LRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 CSNNSITWQLTDAVLHLPGCVPCESDNGTLRCWIQVTPNVAVKY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AA; 15763 MW; 9C67046FD8507C30 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
CG7714-PA (RH2498Bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHACIP-CQ---LRCSSNTPPLTCQRYC 34
                                 (GlcNAc.
(GlcNAc.
                                                                                                                                                                                                                      27.9%; Score 56; DB 1;
Best Local Similarity 31.6%; Pred. No. 3.4e+02;
Matches 12; Conservative 8; Mismarcher
                    CNAC.
                                                                N-linked (GlCNAC
By similarity.
By similarity.
C -> V (in Ref.
S -> Y (in Ref.
W -> Y (in Ref.
S -> K (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                           146 AA.
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                 N-linked
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Q9VE40;
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Best Local Similarity 31.8<sup>1</sup>
*****hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Q9EP28, 9HEPC PRELIMINARY;
Q9EP28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyprotein (Fragment).
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                                                                  2359
2381
2390
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                                                                                                                                                                                                      2476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus
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OGSEP28 9HE
OGSEP28 9HE
DT 01-MP
DT 01
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preliminary data.
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096DN2 HUMAN
1D 096DN2 HT
AC 096DN2 HT
DT 01-DEC-20
DT 01-MEC-20
DT 01-MEC-20
DT HYPOCHMEL
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Matches
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A Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
A Arachchi H.M., Barna N., Bagein V., Bloom T., Boguslavkiy L.,
A Arachchi H.M., Barna N., Calvo S.E., Camarata J., Chang J.,
A Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
A Boukhgalter B., Dodge S., Cook A., Cooke P., Corum B., DeArellano K.,
A Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
A Erickson J., Farreira P., FitzGerald M., Gage D., Galagan J.,
A Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
A Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
A Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
A Anaffe D., Mabbitt R., Macclean C., Mandord P., Mandord J., Manning J.,
A Matthews C., Mauceli E., McCartry M., Menderim J., Menders L.,
A Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                       Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
NCBI_TaxID=229533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AE003723; AAF55589.1; -; Genomic_DNA. EMBL; AY071711; AAL49333.1; -; MRNA. Ensembl; CG7714; Drosophila melanogaster. FlyBase; FBgn0038645; CG7714.
                                                                                                                                                                                         "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                             Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01607; CBM 14; 1. _ _ SEQUENCE 225 AA; 22568 MW; E6EA7C3E301CBE30 CRC64;
Bystematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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Pred. No. 34;
6; Mismatches 13;
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GO:0008061; F:chitin binding; IEA.
GO:0006030; P:chitin metabolism; IEA.
erPro; IPR002557; Chitin_bind_PerA.
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13-SEP-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, Le
Hypothetical protein.
ORFNames=FG03892.1;
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31.4%;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                        "Fusarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Liam Z., Liu J., Li L., Li X., Tufan S.N.L., Clayton M., Wu I wang H., Arbuthnot P., Kew M., Feitelson M.A.;
Lubaited (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY205235, AA047660.
EMBL, AY205235, AA0476051.
ENSGRONOUS FOR INCORD SAPIENS.
R InterPro; IPR001304; Lectin_C.
R InterPro; IPR001304; Lectin_C.
R Ffam; PF000093; VWF_C.
R Pfam; PF000093; VWF_C.
R PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN 1.
R PROSITE; PS01208; VWFC_1; UNKNOWN 5.
R PROSITE; PS01208; VWFC_1; UNKNOWN 5.
R PROSITE; PS01208; VWFC_1; UNKNOWN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 436;
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                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AACM01000168; EAA73360.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 436 AA; 49023 WW; 23722102A0B89CF9 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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37.5%; Pred. No. 1.1e+02;
ive 4; Mismatches 11;
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36.4%; Pred. No. 68;
tive 6; Mismatches
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es 12; Conservative
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QBGWKB HUMAN PRELIMINARY;
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PURCECOIDE SEQUENCE.

AMERIAGEA A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

AMERIAGEA A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

AS Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Rekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Amamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,

Angahari K., Murakami K., Xawai Y., Isono Y., Nakamura Y.,

Angahari K., Murakami K., Kawai Y., Isono Y., Nakamura Y.,

Angahari K., Murakami T., Kaku Y., Kodaira H., Kondo H.,

Andra Y., Abe K., Kamhara K., Kateuta N., Sato K., Tanikawa M.,

Andra Y., Abe K., Takiahashi T., Yamashita H., Murakawa K.,

Anjimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

Ishida S., Ono Y., Takiahashi T., Yamashita H., Murakawa K.,

Anjimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

Ishida S., Ono Y., Takiahashi T., Yamashita H., Murakawa K.,

Anjida S., Musashino K., Yuuki H., Ooshima A., Satoki N., Sano S.,

Nomura Y., Matsunawa H., Ichhara T., Shiohata N., Sano S.,

Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

Anjimori Y., Komiyama H., Ishipara M., Takama S., Pukuzumi Y.,

Anjimori Y., Komiyama M., Tashiro H., Taniagami A., Takamami B.,

Amazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y.,

Anjimori Y., Komiyama M., Tashiro H., Taniagami A., Takamata T.,

Anjimori Y., Komiyama M., Tashiro H., Taniagami A., Takamata Y., Sana K.,

Anjimori Y., Komiyama M., Tashiro H., Taniagami A., Takamata T.,

Anjimori Y., Komiyama M., Hata H., Watanabe M., Komatu T.,

Anjimori Y., Wadaima Y., Mulatanabe M., Komatu T.,

Anjimori Y., Wadaima M., Hata H., Watanabe M., Komatu T.,

Anjahan M., Wadamura Y., Manjama M., Hata H., Watanabe M., Komatu T.,

Anjahan M., Yada T., Nomura N., Chara O., Isogai T., Sugano S.,

Anakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

Andra M., Andra 
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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E; PSO0615; C TYPE LECTIN 1; UNKNOWN_1.
E; PSO0625; EGF_1; UNKNOWN_1.
E; PSO1186; EGF_2; 2.
E; PSO1187; EGF_3; 3.
E; PSO1187; EGF_CA; 3.
E; PSO1187; WFC_1; 1, UNKNOWN_5.
E; PSO1184; VWFC_2; 5.
E; PSO1184; WWFC_2; 5.
E; PSO3184; WWFC_2; 5.
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InterPro; IPR000152; Aax hydroxyl_S.
InterPro; IPR000142; EGF_Ca.
InterPro; IPR001841; EGF_Ca.
InterPro; IPR001304; Lecfin_C.
InterPro; IPR001304; Lecfin_C.
InterPro; IPR001304; Lecfin_C.
InterPro; IPR001007; WWF_C.
Pfam; PF07645; EGF_CA; 3.
FAMRT; SM00179; EGF_CA; 3.
SMART; SM00179; EGF_CA; 3.
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EMBL; AKO56571; BAB71219.1; -; mRNA.

TKSP; P00743; LCCF.

Ensembl; ENSG0000167992; Homo gapiens.
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Best Local Similarity 37.5
Matches 12; Conservative
sapiens (Human)
                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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66, Appl
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15.7 354 7 US-11-090-439-62 Sequence 62, 15.7 2333 7 US-11-096-281-13 Sequence 13, 15.7 2339 7 US-11-096-281-13 Sequence 11, 15.5 146 6 US-10-131-826A-408 Sequence 11, 15.5 215 7 US-11-116-144-297 Sequence 297 15.5 236 6 US-10-467-657-8082 Sequence 297 15.5 236 6 US-10-793-667-657-8082 Sequence 297 15.5 437 6 US-10-131-826A-466 Sequence 466 15.5 497 6 US-10-41-678-55 Sequence 55, 15.5 497 6 US-10-454-437-410 Sequence 21 15.5 500 7 US-11-067-577-2	44 15.5 504 6 US-10-763-712A-78 Sequence 228, Appl. 44 15.5 514 7 US-11-186-284-28 Sequence 228, Appl. 44 15.5 514 7 US-11-029-003-8 Sequence 9, Appl. 44 15.5 1028 7 US-11-029-003-8 Sequence 9, Appl. 44 15.5 1028 7 US-11-029-003-8 Sequence 142, Appl. 44 15.5 1036 6 US-10-131-826A-142 Sequence 142, Appl. 44 15.5 1255 7 US-11-022-562-213 Sequence 213, Appl. 44 15.5 1255 7 US-11-132-262-213 Sequence 213, Appl. 5125 7 US-11-132-262-213 Sequence 10, Appl. 5125 7 US-11-132-262-213 Sequence 10, Appl. 515.4 304 7 US-11-087-177-4 Sequence 4, Appl. 525.5 1255 7 US-11-087-177-4	15.4 305 7 US-11-080-091-2 Sequence 15.4 305 7 US-11-0807-177-7 Sequence 15.4 305 7 US-11-087-177-7 Sequence 15.4 305 7 US-11-067-121-16 Sequence 15.4 757 7 US-11-186-284-41 Sequence 15.4 1018 7 US-11-667-121-17 Sequence 15.2 42 6 US-10-467-657-6806 Sequence 15.2 42 6 US-10-467-657-470 Sequence 15.2 331 7 US-11-078-733-33 Sequence 15.2 331 7 US-11-078-735-33 Sequence 15.2 331 7 US-11-078-735-33 Sequence	15.2 35.7 0.8-11-070-735-35 Sequence 15.2 397 6 0.8-10-985-554-189 Sequence 15.2 397 6 0.8-10-985-561-928 Sequence 15.2 397 6 0.8-10-985-561-928 Sequence 15.2 484 7 0.8-10-990-276-3 Sequence 15.2 723 6 0.8-10-985-561-929 Sequence 15.2 723 6 0.8-10-98-286-346 Sequence 15.2 723 7 0.8-11-078-735-17 Sequence 15.2 1113 7 0.8-11-067-811-4 Sequence 15.2 1210 7 0.8-11-11-202-6 Sequence 15.2 1210 7 0.8-11-145-566-1 Sequence 15.2 1210 7 0.8-110-995-561-538 Sequence	3 15.2 1367 7 US-11-113-202-18 Sequence 3 15.2 1368 US-11-113-424-53 Sequence 3 15.2 1368 US-11-113-424-52 Sequence 5 15.0 160 US-11-113-424-52 Sequence 15.0 338 US-10-632-12 Sequence 15.0 338 VUS-11-073-457-12 Sequence 15.0 338 VUS-11-073-457-12 Sequence 15.0 526 US-10-606-302-5 Sequence 15.0 755 VUS-11-067-302-5 Sequence 15.0 86 US-10-606-302-7 Sequence 15.0 125 VUS-11-1390 Sequence 15.0 121 VUS-11-1390 Sequence 15.0 121 VUS-11-137-1390 Sequence 15.0 1159 VUS-11-113-751-27 Sequence 15.0 1159 VUS-11-113-751-27 Sequence 14.8 18 US-11-113-751-27 Sequence <tr< td=""><td>14.8 184 6 US-10-96-527A-5 Sequence 14.8 235 7 US-11-126-126-16 Sequence 14.8 235 7 US-11-126-126-16 Sequence 14.8 323 6 US-10-910-388-119 Sequence 14.8 344 7 US-11-128-26A-308 Sequence 14.8 444 7 US-11-13-285-6 Sequence 14.8 461 7 US-11-13-285-6 Sequence 14.8 461 7 US-11-13-285-6 Sequence 14.8 461 7 US-11-13-246-4 Sequence 14.8 461 7 US-11-13-246-4 Sequence 14.8 461 7 US-11-147-047-31 Sequence 14.8 264 6 US-10-770-726-45 Sequence 14.7 395 7 US-11-0770-726-45 Sequence 14.7 830 6 US-10-995-561-899 Sequence 14.7 830 6 US-10-995-561-899 Sequence 14.7 842 6 US-10-645-441-2 Sequence</td></tr<>	14.8 184 6 US-10-96-527A-5 Sequence 14.8 235 7 US-11-126-126-16 Sequence 14.8 235 7 US-11-126-126-16 Sequence 14.8 323 6 US-10-910-388-119 Sequence 14.8 344 7 US-11-128-26A-308 Sequence 14.8 444 7 US-11-13-285-6 Sequence 14.8 461 7 US-11-13-285-6 Sequence 14.8 461 7 US-11-13-285-6 Sequence 14.8 461 7 US-11-13-246-4 Sequence 14.8 461 7 US-11-13-246-4 Sequence 14.8 461 7 US-11-147-047-31 Sequence 14.8 264 6 US-10-770-726-45 Sequence 14.7 395 7 US-11-0770-726-45 Sequence 14.7 830 6 US-10-995-561-899 Sequence 14.7 830 6 US-10-995-561-899 Sequence 14.7 842 6 US-10-645-441-2 Sequence

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100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.8e-29;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.8e-29;
Matches 51; Conservative 0; Mismatches 0; Indels
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Sequence 9, Application US/10967527A

Publication No. US2005256041A1

GENERAL INFORMATION:

APPLICANT: HOLloway, James L.

APPLICANT: HOLloway, James L.

TILLE OF INVENTION: Receptor

TILLE OF INVENTION: Receptor

TILLE OF INVENTION: Receptor

CURRENT APPLICATION NUMBER: US/10/967,527A

CURRENT FILING DATE: 2004-10-18

PRIOR APPLICATION NUMBER: 60/511,698

PRIOR PILING DATE: 2003-10-16

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10967527A

Sequence 8, Application US/10967527A

Bublication No. US2005056041A1

GENERAL INFORMATION:

APPLICANT: Fox, Brian A.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: Zenfr14, A Tumor Necrosis Factor

TITLE OF INVENTION: Zenfr14, A Tumor Necrosis File Reference: 03-17

CURRENT APPLICATION NUMBER: US/10/967,527A

CURRENT APPLICATION NUMBER: 60/511,698

PRIOR FILING DATE: 2003-10-16

PRIOR FILING DATE: 2003-10-16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 184
CURRENT APPLICATION NUMBER: US/10/742,634
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US 60/435,262
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 60/467,198
PRIOR PILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9: 17
SEQ ID NO 9: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: homo sapiens
                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-742-634-9
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US-10-967-527A-8
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                                                                                                                                                     LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Sequence 9, Application US/10742634
Sequence 9, Application No. US20050249671A9
Sequence 9, Control of Co
      Sequence 38, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 15, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 31, Appli
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Sequence 278, Appli
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Sequence 27, Appli
Sequence 27, Appli
Sequence 26, Appli
Sequence 5, Appli
Sequence 688, Ap
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Sequence 5, Appl
Sequence 1067, Appl
Sequence 124, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 310, Appl
Sequence 310, Appl
Sequence 219, Appl
Sequence 219, Appl
Sequence 269, Appl
Sequence 11, Appl
Sequence 269, Appl
Sequence 11, Appl
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118, App
15, App
19, App
20, App
79, App
11, Appli
310, App
65, Appl
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Sequence 5
Sequence 8
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Sequence 1
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Sequence 6
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Sequence 9
Sequence 1
Sequence 2
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Sequence
        US-10-454-437-38

US-11-057-047-2

US-11-057-047-2

US-11-01-034-1034

US-10-645-441-15

US-11-191-374-12

US-11-191-375-12

US-11-191-375-12

US-11-044-051-73

US-11-046-051-73

US-11-06-50-80

US-11-07-364-34

US-11-051-267-29

US-11-051-267-29

US-11-051-267-29

US-11-051-285-2

US-11-051-285-2

US-11-132-285-2

US-11-132-285-2

US-11-132-285-2

US-11-132-285-2

US-11-192-374-5

US-10-961-388-110

US-10-961-388-110

US-10-192-374-5

US-10-193-626-264

US-10-621-344-952

US-11-055-812-644

US-11-055-812-64-11

US-11-077-386-19

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US-10-31-926A-310
US-10-878-556A-65
US-11-167-856-30
US-11-108-172-1067
US-10-131-826A-324
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US-11-022-562-217
US-11-109-157A-10
US-11-132-285-40
US-11-132-285-40
US-10-131-826A-318
US-10-131-826A-219
US-11-109-157A-9
US-11-109-157A-9
US-11-123-896-269
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US-11-132-285-2
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TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                                                                                                               Query Match

81.3%; Score 230; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 9.4e-23;
Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-10-967-527A-21

Sequence 21, Application US/10967527A

Publication No. US20050256041A1

GENERAL INFORMATION:

APPLICANT: Pox, Brian A.

APPLICANT: Holloway, James L.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor

TITLE OF INVENTION: Receptor

TITLE OF INVENTION: Receptor

CURRENT APPLICATION NUMBER: US/10/967,527A

CURRENT FILING DATE: 2004-10-18

PRIOR APPLICATION NUMBER: 60/511,698

PRIOR PILING DATE: 2003-10-16

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-967-527A-10
| Sequence 10, Application US/10967527A
| Sequence 10, Application US/10967527A
| Sequence 10, Application US/10967527A
| Publication No. US20050256041A1
| GENERAL INFORMATION:
| APPLICANT: Fox, Brian A. |
| APPLICANT: Sheppard, Paul O. |
| TITLE OF INVENTION: Znifil4, A Tumor Necrosis Factor |
| TITLE OF INVENTION: Receptor |
| TITLE OF INVENTION: Receptor |
| FILE REFERENCE: 00-17 |
| CURRENT FILING DATE: 2004-10-18 |
| PRIOR PILING DATE: 2004-10-18 |
| PRIOR FILING DATE: 2003-10-16 |
| NUMBER OF SEQ ID NOS: 51 |
| SOFTWARE FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                       1 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 40
                                                                                                                                                                                                                                                                                               6 GOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASV 45
                                                                                                           ; LOCATION: (1)...(40)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-9
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Best Local Similarity 70.8<sup>3</sup>
Matches 34; Conservative
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CORGANISM: mus musculus
US-10-967-527A-10
              TYPE: PRT
ORGANISM: homo sapiens
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NAME/KEY: DOMAIN
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LENGTH: 185
LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapв
                                                       Gaps
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Query Match 25.3%; Score 71.5; DB 6; Length 249; Best Local Similarity 35.3%; Pred. No. 0.025; Matches 12; Conservative 8; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
23.9%; Score 67.5; DB 6; Length 48; Best Local Similarity 30.6%; Pred. No. 0.018; Matches 11; Conservative 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.9%; Score 67.5; DB 6; Length 2 30.6%; Pred. No. 0.092; tive 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/10967527A
Sequence 19, Application US/10967527A
Publication No. US2000256041A1
GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
TITLE OF INVENTION: Anes L.
TITLE OF INVENTION: Receptor
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR FILING DATE: 2003-10-16
PRIOR FILING DATE: 2003-10-16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03.17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT APPLICATION NUMBER: 60/511,698
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
                                                                                                       8 CSQNEYFDSLLHACIPCOLRCSSNTPPLICORYC 41
                                                                                                                                                  6 CPKDOYWDSSRKSCVSCALTCSORS-ORICTDFC 38
                                                                                                                                                                                                                                                                                    Sequence 20, Application US/10967527A Publication No. US20050256041A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)...(48)
OTHER INFORMATION: cysteine rich
US-10-967-527A-20
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Best Local Similarity 30.65
Matches 11; Conservative
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                           9; Indels
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Sequence 7, Application US/10967527A;
Publication No. US20050256041A1
GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zthfr14, A Tumor Necrosis Factor;
TITLE OF INVENTION: Receptor;
FILE REFERENCE: 03-17;
CURRENT APPLICATION NUMBER: US/10/967,527A;
CURRENT FILING DATE: 2004-10-18
CURRENT FILING DATE: 2003-10-16
NUMBER: OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 175
                                                                                                      652 QCSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 OCSONEYPDSLLHACIPCOL------RCSSNT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.8%; Score 64.5; DB 7; Best Local Similarity 30.8%; Pred. No. 0.67; Matches 12; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 QCSQNEYFDSLLHACIPCOL------RCSSNT
Best Local Similarity 30.8%; Pred. No. 0.61;
Matches 12; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                      APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Smirh, Randall, F.
APPLICANT: Kabnick, Karen
TILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-22
PRIOR PILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PARESEQ for Windows Version 3.0
SERNGTH: 993
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Publication No. US20050255558A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-11-137-465-36
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US-10-967-527A-7
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US-10-967-527A-7
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APPLICANT: Hilbert, Olga
APPLICANT: Hilbert, David
APPLICANT: Hosen, Craig A.
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses Th
FILE REFERENCE: 1488.181003.12-22
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/467,198
PRIOR PILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 7
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       34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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US-11-137-465-35
Sequence 35, Application US/11137465
Sequence 35, Application US/11137465
Publication No. US2005025558A1
GENERAL INFORMATION:
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Kanick, Rareall, F.
APPLICANT: Saith, Randall, F.
APPLICANT: Solutoch, Rareall, F.
APPLICANT: Saith, Randall, F.
APPLICANT: GENOIG
FILE REFERENCE: GF50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT APPLICATION NUMBER: US/10/239,663
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR APPLICATION NUMBER: G0/192,158
PRIOR PILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 35
LENGALL SST
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                                                                                                                                              Sequence 7, Application US/10742634; Publication No. US20050249671A9; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 11; Conserva
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ORGANISM:
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Query Match

DB 6, Length 175;

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Sequence 1076, Application US/10821234

Sequence 1076, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

TILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT PILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SEQ ID NO 1076

SEQ ID NO 1076
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                                                                                               Sequence 1015, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CARDITONASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FREESE FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1845 ECAPGFYRDVKGLFLGRCVPCQCHGHSDRCLPGSGVCVDCQHNTEGAHCER-CQAGFVSS 1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 OCSQNEYFD---SLLHACIPCQ------LRCSSNTPPLTCQRYCNASVTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 QCSQNEYFD---SLLHACIPCQ-------LRCSSNTPPLTCQRYCNASVTNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 3714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels
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Publication No. US20050260177A1
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APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.7%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-995-561-1015
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Best Local Similarity
Matches 16; Conserval
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                                                                               US-10-995-561-1015
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US-11-108-172-1116
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LENGTH: 3714
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Sequence 1016, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: LO101559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 1016
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                                                       Gaps
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                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Demoner, Jeroen
APPLICANT: Hall, Claire
APPLICANT: Norriss, Michael Geoffrey
APPLICANT: Norriss, Michael Geoffrey
APPLICANT: Sallsbury, Keith Martin
TITLE OF INVENTION: Compositions Isolated from Forage
TITLE OF INVENTION: Grasses and methods for their use.
FILE REFERENCE: 11000.1074Uc1
CURRENT APPLICATION NUMBER: US/11/110,082
CURRENT PRILIG DATE: 2005-04-19
PRIOR FILING DATE: 2004-04-20
PRIOR FILING DATE: 2003-09-05
PRIOR FILING DATE: 2003-09-05
PRIOR FILING DATE: 2002-09-05
NUMBER: OF SEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     632 FDSYVLAAV-CALSCELQLFPILCKNVTKSNIKDSIK 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 FDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVK 50
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26.7%; Pred. No. 29;
tive 6; Mismatches
Query Match 22.3%; Score 63; DB Best Local Similarity 50.0%; Pred. No. 0.21 Matches 10; Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                             Sequence 30, Application US/11110082
Publication No. US20050266558A1
GENERAL INFORMATION:
                                                                                                      7 OCSONEYFDSLLHACIPCOL 26
                                                                                                                                                      21 ÓCNÓTECFDPLVRNCVSCEL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Festuca arundinacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19.6
Best Local Similarity 29.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.7
Matches 16; Conservative
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US-10-995-561-1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-995-561-1016
                                                                                                                                                                                                                                                          US-11-110-082-30
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19;

48

Gaps

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APPLICANT: Allettuala, Seppo
APPLICANT: Hiltunen, Mikko O
APPLICANT: Jellech, Marku M
APPLICANT: Jellech, Marku M
APPLICANT: Jellech, Marc G
TITLE OF INVENTION: Use of VEGF-C or VEGF-D Gene or Protein to Prevent Restenosis
FILE REFREENCE: 2896/135601A
CURRENT APPLICATION NUMBER: US/01/1064,769
CURRENT APPLICATION NUMBER: US/09/427,657
PRIOR APPLICATION NUMBER: US 60/105,587
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 18
SECTION NOS: 18
SECTION NOS: 18
SEQ ID NO 2
LENGTH: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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Best Local Similarity 35.0%; Pred. No. 4.5;
Matches 14; Conservative 2; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indela
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                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/11/153,880 FILING DATE: 16-jun-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
19.3%; Score 54.5; DB 7;
Best Local Similarity 35.0%; Pred. No. 5.3;
Matches 14; Conservative 2; Mismatches 21;
                                                                                                                                                             FILING DATE: 15 Jun 2030
CLASSIFICATION: DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/219,442
FILING DATE: 23-DEC-1998
CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/999,811
FILING DATE: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/999,811
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION: NAME: MARKOWICZ, KAREN R. REFERENCE/POCKET NUMBER: 1488.1000004
TELECOMMUNICATION: NUMBER: 1488.1000004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-064-769-2

Sequence 2, Application US/11064769

Publication No. US20050256075A1

GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202)371-2600
TELEFRAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 350 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-11-153-880-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-064-769-2
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                                                                                                                                                                                                                                                                                             APPLICANT: Carter, Darrick TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE FILE CURRENT FILING DATE: 2005-04-15 CURRENT FILING DATE: 2005-04-15 PRIOR FILING DATE: 2001-12-19 PRIOR PILING DATE: 2001-04-10 PRIOR PELICATION NUMBER: US 09/922,217 PRIOR PELICATION NUMBER: US 09/649,811 PRIOR PELICATION NUMBER: US 09/649,629 PRIOR PELICATION NUMBER: US 09/640,629 PRIOR PELICATION NUMBER: US 09/480,321 PRIOR PELICATION NUMBER: US 09/480,321 PRIOR PELICATION NUMBER: US 09/480,321 PRIOR PELICATION NUMBER: US 09/476,296 PRIOR PELICATION PERIOR PELICATION PERIOR PELICATION PERIOR PELICATION PERIOR PELICATION PERIOR PELICATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/11153880

Publication No. US20050256050A1

GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN CRAIG A.
APPLICANT: ROSEN CRAIG A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2.
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 QCSQNEYFDSLLHACI-PCQLRCSSNTPPLTCQRYC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                King, Gordon E.
Wang, Aijun
Clapper, Jonathan D.
Skeiky, Yasir A. W.
Fanger, Gary R.
Vedvick Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                      Carole L.
Stolk, John A.
Wang, Tongtong
Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ LD NO 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-153-880-4
                                                                                                                                                                                                                                                                             APPLICANT
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TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/11/113,424

CURRENT APPLICATION NUMBER: US/211/113,424

PRIOR APPLICATION NUMBER: 60/256,704

PRIOR FILING DATE: 2000-20-19

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-12-20

PRIOR PLING DATE: 2000-12-20

PRIOR PLING DATE: 2000-12-20

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-09-29

PRIOR PLING DATE: 2001-07-24

PRIOR PLING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR PLING DATE: 2001-05-02

NUMBER OF SEQ ID NOS: 190

SOFTWARE: PATENTIN VUMBER: 60/294

SEQ ID NO 37

LENGTH: 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
19.3%; Score 54.5; DB 7; Length 419;
Best Local Similarity 35.0%; Pred. No. 5.3;
Matches 14; Conservative 2; Mismatches 21; Indels
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28.2%; Pred. No. 12;
ative 4; Mismatches
PRIOR APPLICATION NUMBER: 09/795,006
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/205,331
PRIOR APPLICATION NUMBER: US 60/185,205
PRIOR PILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 1212
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 QCSQNEYFDSLLHACIPCQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/11113424 Publication No. US20050260713A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-774A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus
US-11-113-424-37
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Matches 11; Conserva
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US-11-110-082-29
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                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                       327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 ÓCGANREPDENTCOCV-CKRTCPRNOPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 16-jun-2005
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/219,442
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/999,811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
19.3%; Score 54.5; DE
Best Local Similarity 35.0%; Pred. No. 5.3;
Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE:
PROR APPLICATION DATA:
PAPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTONNEY CAGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    Sequence 2, Application US/11153880 Publication No. US20050256050A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 419 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-11-153-880-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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APPLICANT: Millennium Fharmaceuticals, inc.
APPLICANT: Millente Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Manahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: HERGER, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2005-07-21
PRIOR FILING DATE: 2005-07-21
PRIOR FILING DATE: 2001-112-10
PRIOR FILING DATE: 2001-112-10
PRIOR FILING DATE: 2001-112-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 371
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APPLICANT: Guilemette, Tracy L.
APPLICANT: Guilemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Hibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: THIBOT THERAPY OF COLON CANCER TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION: MEMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 53; DB 7; Length 371; 31.0%; Pred. No. 7.3; tive 5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 OFCGPCLRNRYGEEVRDALLDPNWHC----PP--CRGICNCS 330
                                  3 OMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNAS 44
8 CSQNE---YFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVT 46
                                                                                                                                                                                                                          Sequence 16, Application US/11186284; Publication No. US20050266493A1; GENERAL INFORMATION: APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.0%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-186-284-14
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| Sequence 2. Application No. US200525069641
| GENERAL INFORMATION:
| APPLICANT: Fisher F., Eric
| APPLICANT: Edwards K., Carl
| APPLICANT: Kief L., Gary
| TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I Repeticant: Prince OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I Repeticant: No NUMBER: US/11/126,126
| CURRENT PELIANG DATE: 2000-06-10
| FILE REFERENCE: 02-006-N
| CURRENT PELIANG DATE: 2001-06-15
| PRIOR APPLICATION NUMBER: 09/214, 613
| PRIOR FILING DATE: 1997-07-09
| PRIOR PELICATION NUMBER: 60/039,314
| PRIOR FILING DATE: 1997-01-23
| PRIOR APPLICATION NUMBER: 60/032,534
| PRIOR FILING DATE: 1996-01-06
| PRIOR PELING DATE: 1996-07-09
| PRIOR APPLICATION NUMBER: 60/032,534
| PRIOR PELING DATE: 1996-07-09
| PRIOR PELING DATE: 1997-07-09
| PRIOR PELING DATE: 1996-07-09
| PRIOR PELING DATE: 1997-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%; Score 54.5; DB 7; Length 1
29.7%; Pred. No. 13;
tive 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
                                                       APPLICANT: Native Mattin Andrew APPLICANT: Native Martin APPLICANT: Saulsbury, Keith Martin APPLICANT: Saulsbury, Keith Martin TITLE OF INVENTION: Compositions Isolated from Forage TITLE OF INVENTION: Grasses and methods for their use. FILE REFRENCE: 11000.10740c1 CURRENT APPLICATION NUMBER: US/11/110,082 CURRENT FILING DATE: 2005-04-19 PRIOR APPLICATION NUMBER: 60/563,723 PRIOR APPLICATION NUMBER: 60/563,723 PRIOR APPLICATION NUMBER: 60/408,782 PRIOR APPLICATION NUMBER: 60/408,782 PRIOR APPLICATION NUMBER: 60/408,782 PRIOR SEQ ID NOS: 40 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 29 LENGTH 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               631 FDSYVLAAV-CALSCELQLFPILCKNVTKTNIKDSIK 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.7
Best Local Similarity 33.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 29.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Lolium perenne
US-11-110-082-29
          APPLICANT: Demmer, Jeroen
APPLICANT: Hall, Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 23
US-11-126-126-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
18.7%; Score 53; DB 7; Length 909;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 CRKNQYRHYWSENLFQCFNCSL-CLNGTVHLSCQEKQNTVCT 165
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GENERAL INFOGRATION:
APPLICANT: Murdoch, Paul R.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Kabnick, Karen
TILE CAINVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PABLES OF WINDOWS Version 3.0
SERIOTH: 1062
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                      PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1998-01-27
PRIOR PELING DATE: 1998-05-06
PRIOR PELING DATE: 1999-05-06
PRIOR PILING DATE: 1999-05-06
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR PELING DATE: 2000-09-30
PRIOR PELING DATE: 2002-09-37
PRIOR APPLICATION NUMBER: 60/413,861
PRIOR APPLICATION NUMBER: 60/413,861
PRIOR PILING DATE: 2002-09-77
PRIOR PILING DATE: 2003-08-77
PRIOR PILING DATE: 2003-08-77
PRIOR PILING DATE: 2004-09-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN NUMBER: 60/608,469
PRIOR FILING DATE: 2004-09-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN ON UMBER: 60/608,469
PRIOR PILING DATE: 2004-09-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN ON OFFICE TOWARTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 43, Application US/11137465; Publication No. US20050255558A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                             DB 7; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.7%; Score 53; DB 7; Length 455; Best Local Similarity 33.3%; Pred. No. 8.8; Matches 14; Conservative 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 QFCGPCLRNRYGEEVRDALLDPNWHC----PP--CRGICNCS 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/11182946

| Sequence 3, Application US/11182946
| Publication No. US20050255100A1
| Publication No. US20050255100A1
| Publication No. US20050255100A1
| APPLICANT: Wei, Ying-Fei
| APPLICANT: Wei, Jian
| APPLICANT: Ruben, Steven
| TILLE OF INVENTION: Tumor Necrosis Factor Receptor 5
| FILE REFERENCE: 1448.1280004
| CURRENT APPLICATION NUMBER: US/00/67
| CURRENT FILING DATE: 2002-07-18
| PRIOR APPLICATION NUMBER: US/09/573,986
| PRIOR PLING DATE: 2000-05-18
| NUMBER OF SEQ ID NOS: 27
| SEQ ID NO 3
| SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CSONE---YFDSLLHACIPCOLRCSSNTPPLTCORYCNASVT 46
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APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Ban, James G
APPLICANT: Gentz, Reiner L
APPLICANT: Dixit, Vishva M
TITLE OF INVENTION: Death Domain Containing Receptor-4
FILE REFERENCE: PF35593
                                                                                                                                                                                                                                                                                                                          Query Match
18.7%; Score 53; DB 7
Best Local Similarity 31.0%; Pred. No. 8.7;
Matches 13; Conservative 5; Mismatches
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: 60/035,722
PRIOR FILING DATE: 1997-01-28
PRIOR APPLICATION NUMBER: 60/037,829
PRIOR FILING DATE: 1997-02-05
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Publication No. US20050244857A1
GENERAL INFORMATION:
                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo Sapiene
US-11-186-284-14
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US-11-182-946-3
                                                                                                                                                             SEQ ID NO 14
LENGTH: 450
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Ying-Fei
APPLICANT: Roben, Steven
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
CURRENT APPLICATION NUMBER: US/11/182,946
CURRENT APPLICATION NUMBER: US/10/186,643
PRIOR FILING DATE: 2002-07-02
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
                                          ---LRCSSNT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 17.5%; Score 49.5; I. Similarity 36.1%; Pred. No. 19; 13; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
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US-10-131-826A-82
US-10-131-826A-82
; Sequence 82, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR PLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR PILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
                                                                                                                                                            RESULT 31
US-11-182-946-13
Sequence 13, Application US/11182946
; Publication No. US20050255100A1
7 QCSQNEYFDSLLHACIPCQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumas, Daniel
Watanabe, Colin K
Wood, William
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers, Luc
Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney, Austin L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-182-946-13
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US-11-080-991-50

Sequence 50, Application US/11080991

Publication No. US20050266437A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST

TITLE OF INVENTION: AND OVARIAN CANCER

TITLE OF INVENTION: AND OVARIAN CANCER

FILE REFERENCE: MRI-039

CURRENT APPLICATION NUMBER: US/11/080,991

CURRENT FILING DATE: 2005-03-11

PRIOR APPLICATION NUMBER: US/10/176,847

PRIOR FILING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 50

LENGTH: 997

TYPE: PRT
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US-11-13-424
US-11-13-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.2%; Score 51.5; DB 7; Length 997; 25.6%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 QCSQNEYFDSLLHACIPCQ------LRCSSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.63
Matches 10; Conservative
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ORGANISM: Homo sapiens
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Matches 10, Conserv
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RESULT 35
US-10-967-527A-18
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US-11-132-285-61
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Publication No. US20050272054A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1559

CURRENT FILIAGO ANTE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SEQ ID NO: 85702

SEQ ID NO 1033

FERMANE: FASELSE OF Windows Version 4.0
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENETIC INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARRILL, MICHAEL OF INVENTION: CARRILL, MICHAEL OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995, 561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059127
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PILING DATE: 1997-09-19
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26.8%; Pred. No. 84;
vative 4; Mismatches
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Best Local Similarity 34.3%; Pred. No. 22;
Matches 12; Conservative 5; Mismatches
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Best Local Similarity 26.8
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-1033
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo Sapien
US-10-131-826A-82
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publication No. US20050244876A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
FILE REFERENCE: PF511P1
CURRENT APPLICATION NUMBER: US/11/132,285
CURRENT FILING DATE: 2005-05-19
PRIOR APPLICATION NUMBER: US/10/046,433
PRIOR APPLICATION NUMBER: 05/261,960
PRIOR APPLICATION NUMBER: 09/619,570
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 60/149,450
PRIOR PILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
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                                                                                                                                                 Length 1798;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT PILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR APPLICATION NUMBER: 60/511,698
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                       DB 6;
                                                                                                                                                 17.5%; Score 49.5; D
26.8%; Pred. No. 84;
tive 4; Mismatches
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                                                                                                                                               Query Match 17.5
Best Local Similarity 26.8
Matches 15; Conservative
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Matches 10; Conservative
; SEQ ID NO 1034
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1034
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ORGANISM: homo sapiens
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Score 49; DB 7; Length 1238; Pred. No. 69; 8; Mismatches 18; Indels

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PRIOR APPLICATION NUMBER: GB 0220912.0
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: GB 0220913.8
PRIOR PILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 21
LENGTH: 1238
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.6%;
Matches 11; Conservative
                                                                                                                                                                                     TYPE: PRT
GORGANISM: Homo sapiens
US-11-078-735-21
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US-10-995-561-827
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publication No. U320050261477A1

GENERAL INCORMATION:
APPLICANT: CHAMPION, BILAN ROBERT
APPLICANT: CHAMPION, BILAN ROBERT
APPLICANT: LENARED, ANDREW CHRISTOPHER
APPLICANT: LENARED, ANDREW CHRISTOPHER
APPLICANT: TUGAL, TAMARA CHRISTOPHER
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 674525-2010
CURRENT FILING DATE: 2005-09-09
PRIOR APPLICATION NUMBER: PCT/GB03/03908
PRIOR PLLING DATE: 2003-09-09
PRIOR PLLING DATE: 2003-09-09
PRIOR PPLING DATE: 2003-04-04
PRIOR PLLING DATE: 2003-01-07
PRIOR PLLING DATE: 2003-01-07
PRIOR PPLING DATE: 2003-11-13
PRIOR PPLING DATE: 2002-11-13
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                                                                                                                                               Length 231;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10967527A

Sequence 17, Application US/20050256041A1

GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
TILLE OF INVENTION: Zantla, A Tumor Necrosis Factor
TILLE OF INVENTION: Receptor
TILLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR PILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 297
                                                                                                                                             Query Match 17.3%; Score 49; DB 7; Best Local Similarity 47.6%; Pred. No. 15; Matches 10; Conservative 3; Mismatches (
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: homo sapiens
           SEQ ID NO 61
LENGTH: 231
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-967-527A-17
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US-11-078-735-21
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TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST TITLE OF INVENTION: AND OVARIAN CANCER CURRENT APPLICATION NUMBER: US/11/080,991 CURRENT FILING DATE: 2005-03-11 PRIOR APPLICATION NUMBER: US/10/176,847 PRIOR FILING DATE: 2002-06-21 NUMBER OF SEQ ID NOS: 112 SOFTWARE FASESEQ for Windows Version 4.0 SEQ ID NO 94 ILBUGTH: 2214
                                                                                                                                                                                                    Sequence 827, Application US/10995561
; Publication No. US2005272054A1
; Publication No. US2005272054A1
; GENERAL INFORMATION:
; APPLICATE CARGILL, Michele et al.
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: PESTEREO for Windows Version 4.0
; SEQ ID NO 827
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.3%; Score 49; DB 6; Length 2107; Best Local Similarity 34.1%; Pred. No. 1.1e+02; Matches 14; Conservative 4; Mismatches 9; Indels
                                    169 AGMINPEDRWKSLHFSGHVAHLELQIRVRCDENYYSATCNKFC 211
5 AGOCSONEYFDSL-----LHACIPCOLRCSSNTPPLTCQRYC 41
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28 GKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTNTQCTPCASDTFTSRNNHLPACLSCN 87
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Pred. No. 25;
3; Mismatches 15; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 350;
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Sequence 14, Application US/11182946

Publication No. US20050255100A1

GENERAL INFORMATION:

APPLICANT: Wei, Ying-Fei

APPLICANT: Wei, Ying-Fei

APPLICANT: Ruben, Steven

TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

FILE REPERENCE: 1448-1280004

CURRENT APPLICATION NUMBER: US/11/182,946

CURRENT FILING DATE: 2005-07-18

PRIOR PILING DATE: 2005-07-18

PRIOR PLING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 14

LENGTH: 355
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22.8%; Pred. No. 25;
tive 3; Mismatches
FILE REFERENCE: PF511P1
CURRENT APPLICATION NUMBER: US/11/132,285
CURRENT FILING DATE: 2005-05-19
PRIOR PILING DATE: 2005-05-16
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-17
PRIOR FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-08-20
PRIOR PILING DATE: 1999-08-20
PRIOR PILING DATE: 1999-08-20
PRIOR PILING DATE: 1999-09-10
SEQ ID NO 41
LENGTH: 350
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Best Local Similarity 22.8
Matches 18; Conservative
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Best Local Similarity 22.8
Matches 18; Conservative
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US-11-182-946-14
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRAEKSEQ for Windows Version 4.0
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Fublication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DEFECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 826
LENGTH: 3116
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; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
                                         Gaps
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Best Local Similarity 34.1%; Pred. No. 1.6e+02;
Matches 14; Conservative 4; Mismatches 9; Indels
                                            Indels
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                 Pred. No. 1.2e+02;
5; Mismatches 8;
                                                                                                                   1211 CIPQRWACDGDTDCQDGSDEDPVNCEKKCN 1240
                                                                                     21 CIPCQLRCSSNT-----PPLTCQRYCN 42
                 Best Local Similarity 30.0%;
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-995-561-826
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US-10-995-561-826
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US-10-995-561-825
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LENGTH: 2480
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43; Gaps

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Sequence 1388, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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CORGANISM: homo sapiens
US-10-967-527A-14
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CORGANISM: Homo sapiens
US-10-821-234-1388
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Best Local Similarity
....hes 9; Conserv?
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; Sequence 1540. Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Tabat, Tabat,
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17.0%; Score 48; DB 6; Length 49;
Best Local Similarity 30.0%; Pred. No. 4.8;
Matches 9; Conservative 4; Mismatches 17; Indels
                                                                                                                                                       Sequence 15, Application US/10967527A

Sequence 15, Application US/10967527A

Publication No. US20050256041A1

GENERAL INFORMATION:

APPLICANT: Fox, Brian A.

APPLICANT: Fox, Brian A.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: Zenfr14, A Tumor Necrosis Factor

TITLE OF INVENTION: Receptor

TITLE OF INVENTION: Receptor

CURRENT APPLICATION UNBER: US/10/967,527A

CURRENT FILING DATE: 2004-10-18

PRIOR APPLICATION NUMBER: 6/511,698

PRIOR APPLICATION NUMBER: 6/511,698

PRIOR FILING DATE: 2003-10-16

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15
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                       GRCDSNOVE --- TRSCNTT 103
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// OTHER INFORMATION: cysteine rich
US-10-967-527A-15
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Best Local Similarity
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US-10-821-234-1540
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                       88
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RESULT 47 US-10-821-234-1388

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Sequence 556, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CLO01559

CURRENT APPLICATION NUMBER: US/10/995,561
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT PAPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1388
LENGTH: 317
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Best Local Similarity 39.1%; Pred. No. 26;
Matches 18; Conservative 6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LOMAGOCSONEYFDSLLHA-CIPCOLRCSSNTP-PLTCORYCNASV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 48; DB 6; Length 447; 30.0%; Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zenfr14, A Tumor Necrosis Factor
FILLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 447
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383 ECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCS--CSVGFRLSVDG 436
Score 47.5; DB 6; Length 703;
Pred. No. 63;
6; Mismatches 25; Indels 13; Gaps
                                                                                                                 7 OCSQNEYFDSLLHACIP------CQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.6%; Score 47; DB 7; Length 427; Best Local Similarity 30.0%; Pred. No. 46; Matches 12; Conservative 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . DB 7; Length 595;
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16.6%; Score 47; DB 7; Length 595;
Best Local Similarity 29.1%; Pred. No. 62;
Matches 16; Conservative 6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/11182946

Sequence 9, Application US/11182946

Publication No. US20050255100A1

GENERAL INFORMATION:

APPLICANT: Wei, Ying-Fei

APPLICANT: Wei, Jian

TITLE OF INVENTION: Teaher,

APPLICANT: Ruben, Steven

TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

FILE REFERENCE: 1488.1280004

CURRENT FILING DATE: 2005-07-18

PRIOR APPLICATION NUMBER: US/11/182,946

CURRENT FILING DATE: 2002-07-02

PRIOR PILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-02

PRIOR PILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN VEY: 2.1

SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wi, Jian
APPLICANT: Wi, Jian
APPLICANT: Wi, Jian
APPLICANT: Gentz. Reiner
APPLICANT: Gentz. Reiner
FILE REPRENCE: 1488.1280004
CURRENT APPLICATION NUMBER: US/11/182,946
CURRENT FILING DATE: 2005-07-18
FRIOR PILING DATE: 2005-07-02
FRIOR PILING DATE: 2000-05-18
FRIOR PILING DATE: 2000-05-18
FRIOR FILING DATE: 2000-05-18
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                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/11182946
Publication No. US20050255100A1
GENERAL INFORMATION:
  Query Match
Best Local Similarity 21.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 1412, Application US/10821234

Sequence 1412, Application US/10821234

Sequence 1412, Application W. US20050255114A1

SEGUENCAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Applicant, Susan
APPLICANT: Tang, Y. Tom
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt_SEQ_genes Version 1.0

SEQ ID NO 1412

LENGTH: 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT PILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR RILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1504
LENGTH: 419
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                                                                                                                                                                                                                                                                                                                                                                                                       2 LOMAG-----OCSQNEYFDSLLHACIPCQLRC-----SSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                18; Indels 14;
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16.8%; Score 47.5; DB 6; Length 4:
Best Local Similarity 37.0%; Pred. No. 39;
Matches 17; Conservative 3; Mismatches 17; Indels
     CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 556
LENGTH: 4655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-821-234-1504; Sequence 1504, Application US/10821234; Publication No. US20050255114A1
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CRGANISM: Homo sapiens
US-10-821-234-1504
                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-995-561-556
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; ORGANISM: Homo sapiens
US-10-821-234-1412
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 1042
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CURRENT PELICATION NUMBER: US/10/131,826A
CURRENT PILLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/05914
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILLING DATE: 1997-09-18
PRIOR FILLING DATE: 1997-09-19
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243 QCEPDYYLDEAGRCTACVSCSRDDLVEKTPCAMNS-SRTCECRPGMICATSATNS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550
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                                                                                   RESULT 54
US-10-131-826A-60
; Sequence 60, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baresini, Maureen
; APPLICANT: DeForge.Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 ---PLTCQRYCNASVTN 47
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Best Local Similarity 28.6
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-131-826A-60
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LENGTH: 724
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APPLICANT:
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RESULT 55

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Sequence 670, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION:

FILE REFERENCE: CLO01559

CURRENT APPLICATION NUMBER: US/10/995,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Sequence 340, Application US/11022562
| Sequence 340, Application US/11022562
| Publication No. US20050249742A1
| GENERAL INFORMATION:
| APPLICANT: Ruprecht, Ruth M. |
| APPLICANT: Ruprecht, Ruth M. |
| APPLICANT: Shisong, Jiang
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
| TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
| TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
| TITLE OF INVENTION NUMBER: US/11/022,562
| CURRENT FILING DATE: 2003-06-27
| PRIOR FILING DATE: 2003-06-27
| PRIOR FILING DATE: 2003-06-27
| PRIOR FILING DATE: 2003-06-27
| NUMBER OF SEQ ID NOS: 340
| SEQ ID NO 340
| LENGTH: 879
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16.6%; Score 47; DB 7; Length 1042;
Best Local Similarity 28.2%; Pred. No. 1e+02;
Matches 11; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/11067811
Publication No. US2050260688A1
GENERAL INFORMATION:
APPLICANT: Morgan, Bruce A
APPLICANT: Brashall-Scijffers, David
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
FILE REFERENCE: 10287-083001
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: US/11/067,811
CURRENT FILING DATE: 2005-02-28
PRIOR PILING DATE: 2004-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
16.6%; Score 47; DB 7; Length 879;
Best Local Similarity 28.9%; Pred. No. 89;
Matches 11; Conservative 6; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||:||:||:||430 VPCHIRQIINTWHKVGKNVYLPPREGDLTCNSTVTSLI 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 IPCQLRCSSNT------PPLTCQRYCNASVTNSV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.3 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 4
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242 CSPGHHYNTTTHRCIRCPVGTYQPEFGQNHCITCPGNT 279
                                                                                                                                                                                                                                                                                                                                                                            8 CSQNEYFDSLLHACIPCQ-----LRCSSNT 32
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16.4%; Score 46.5; DB 6;
Best Local Similarity 28.6%; Pred. No. 85;
Matches 12; Conservative 11; Mismatches 12;
                                                                                                                                                                                                                                                                          Query Match
16.4%; Score 46.5; D
Best Local Similarity 23.7%; Pred. No. 60;
Matches 9; Conservative 5; Mismatches
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-770-726-57
; Sequence 57, Application US/10770726
; Publication No. US/0050266409A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-770-726-66

"Sequence 66, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-770-726-66
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CORGANISM: Homo sapiens
US-10-770-726-57
                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-11-147-047-50
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wyeth
                                                                                                                                                                             TYPE: PRT
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERBERS: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
RUGHER PAPLICATION NUMBER: US 60/462,047
RUGHER OF SEQ ID NOS: 1704
SEQ ID NOS: 1704
SEQ ID NOS: 1704
SEQ ID NO 1155
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                                                                                                                                                                                                                           Length 4347;
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                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                           Query Match 16.6%; Score 47; DB 6; Best Local Similarity 36.4%; Pred. No. 3.9e+02; Matches 8; Conservative 3; Mismatches 11
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FULLICANT: Agarwal, Pankaj

APPLICANT: Murdock, Paul R.

APPLICANT: Smith, Randall F.

APPLICANT: Smith, Randall F.

APPLICANT: Xiang, Zhaoying

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REPERENCE: GPSOO16

CURRENT APPLICATION NUMBER: US/11/147, 047

CURRENT PILING DATE: 2002-06-07

PRIOR PILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US/10/221,097

PRIOR APPLICATION NUMBER: 60/187,107

PRIOR APPLICATION NUMBER: 60/187,107

PRIOR PILING DATE: 2000-03-06

URRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQTYBARE: FastSEQ for Windows Version 4.0
LENGTH: 4347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1155, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          456 QRAGPCPDGHFYLEHSAACLPC 477
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528 QRAGPCPDGHFYLEHSAACLPC 549
                                                                                                                                                                                                                                                                                                                              3 OMAGQCSQNEYFDSLLHACIPC 24
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; Sequence 50, Application US/11147047
; Publication No. US20050260668A1
                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-995-561-670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1155
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APPLICANT: Myeur, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031895-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARES PALENCETIN VERSION 3.2
SEQ ID NO 57
LENGTH: 883
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wyeth
APPLICANT: Busines
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 66
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DB 7; Length 487;
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Sequence 2, Application US/11113424

Publication No. US20050260713A1

GENERAL INFORMATION:
FOR INVENTION: Polypeptides and Nucleic Acids Encoding Same
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REPERENCE: 2402-225

CURRENT APPLICATION NUMBER: US/11/113,424

CURRENT FILING DATE: 2005-04-21

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-19

PRIOR PILING DATE: 2001-08-29

PRIOR PILING DATE: 2001-08-29

PRIOR PILING DATE: 2001-07-24

PRIOR PILING DATE: 2001-07-24

PRIOR PILING DATE: 2001-05-29

PRIOR PILING DATE: 2001-05-29

PRIOR PILING DATE: 2001-05-29

PRIOR PILING DATE: 2001-05-29

PRIOR PILING DATE: 2001-05-02

NUMBER: OF SEQ ID NOS: 190

SEQTHWARE: PATENTING DATE: 2001-05-02

NUMBER: OF SEQ ID NOS: 190

SEQTHWARE: PATENTING DATE: 2001-05-02

LENGTHRE DATE: 2001-05-02
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16.4%; Score 46.5; DB 7; Length 965;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
Matches 9; Conservative 5; Mismatches 11; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                             Score 46.5; DB 7; Length 964;
Pred. No. 1.1e+02;
5; Mismatches 11; Indels 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CSQNEYFDSLLHACIPCQ------LRCSSNT 32
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: 984 SEQ 10 NOS: 66
SOFTWARE: 985 SEQ 10 NOS: 66
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Publication No. US20050260668A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdock, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.7%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens US-11-137-465-58
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US-11-113-424-35
is Sequence 35, Application US/11113424
j Publication No. US20050260713A1
is GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polyeptides and Nucleic Acids Encoding Same FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR APPLICATION NUMBER: 60/215,50
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR PLING DATE: 2001-08-20
PRIOR PLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR APPLICATION NUMBER: 60/204,075
PRIOR PILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-15
PRIOR PILING DATE: 2001-09-16
PRIOR PILING DATE: 2001-09-10
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Pred. No. 1.1e+02;
5; Mismatches 11; Indels 1:
                              Indels
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                          3; Mismatches 17;
                                                                                                                                                   235 CLDTVHFGRQASKCLECOVMCHPKCSTCLPATC 267
                                                                                      8 CSQNEYFDSLLHACIPCQLRC---SSNTPPLTC 37
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PUBLICATION NO. US2005025558A1

GENERAL INPORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Smitch, Randall, F.
APPLICANT: Smitch, Randall, F.
APPLICANT: Smitch, Randall, F.
APPLICANT: Kanny, Zhaoying
APPLICANT: Kabnick, Karen
TILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT APPLICATION NUMBER: US/10/219,663
PRIOR PLING DATE: 2002-09-24
PRIOR PLING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: PCT/US01/09226
PRIOR APPLICATION NUMBER: PCT/US01/09226
PRIOR APPLICATION NUMBER: 2001-03-22
PRIOR APPLICATION NUMBER: 2001-03-22
PRIOR APPLICATION NUMBER: 2001-03-22
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Best Local Similarity 23.7%;
Matches 9; Conservative
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                                 10; Conservative
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US-11-113-424-35
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US-11-137-465-58
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                                 Matches
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US-11-078-735-13
US-11-
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                                                                                                                                                                                                                                                             Query Match 16.4%; Score 46.5; DB 7; Length 1 Best Local Similarity 30.4%; Pred. No. 1.2e+02; Matches 14; Conservative 9; Mismatches 22; Indels
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                                                        ; LENGTH: 1045
; TYPE: RRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 HACIPCQLRCSSNTPPLTCQRYC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-078-735-12
                     SEQ ID NO 100
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NUMBER OF SEQ ID NOS: 1158
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Sequence 100, Application US/11055822

Publication No. US20050260707A1

GENERAL INFORMATION:
APPLICANT: Propelus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: APPLICANTON: GORARA
APPLICANT: APPLICANTON: GORARA
APPLICANT: Hartwig
APPLICANT: APPLICANTON: CONTNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPN
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 06/141,031
PRIOR PILING DATE: 1999-06-25
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-03
PRIOR PELING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   743 CSPGHHYNTTTHRCIRCPVGTYQPEFGQNHCITCPGNT 780
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APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
FILE ALTE OF INVERTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS0016
CURRENT APPLICATION NUMBER: US/11/147,047
CURRENT APPLICATION NUMBER: US/10/221,097
PRIOR APPLICATION NUMBER: US/10/221,097
PRIOR APPLICATION NUMBER: DCT/US01/07143
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-11-147-047-51
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LENGTH: 965
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US-11-078-73-15

Publication No. US20050261477A1

Sequence 15, Application US/11078735

Publication No. US20050261477A1

APPLICANT: CHAMPION:

APPLICANT: CHAMPION:

BRIDAR APPLICANT: LENNARD, ANDREW CHRISTOPHER

APPLICANT: LENNARD, ANDREW CHRISTOPHER

APPLICANT: HORGAL, TAWARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND PROTEINS

FILE REPERBORCE: 674525-2019

CURRENT FILING DATE: 2005-03-109

PRIOR FILING DATE: 2005-03-09

PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-010

NUMBER OF SEQ ID NOS: 51

TENGARDADE CATEON OF SEQ ID NOS: 51

TENGARDADE CATEON OF SEQ ID NOS: 51

TENGARDADE CATEON OF SEQ ID NOS: 51
Query Match 16.3%; Score 46; DB 7; Length 63; Best Local Similarity 30.4%; Pred. No. 11; Astches 7; Conservative 5; Mismatches 11; Indels
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16.3%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 11; Indels
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                                                                                                                                                                 19 HACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                   12 HLELQIRVRCDENYYSATCNKFC 34
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherwood, Steven
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 71
US-10-131-826A-296
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US-11-078-735-15
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16.3%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 11; Indels
FILE KEFEKENCE: 8,4925-2013.
CURRENT PELLING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US/11/078,735
CURRENT PELING DATE: 2005-03-10
PRIOR FILING DATE: 2003-09-09
PRIOR PELLING DATE: 2003-09-01
PRIOR PELLING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-01-07
PRIOR PELLING DATE: 2003-01-07
PRIOR PELLING DATE: 2002-11-13
PRIOR PELLOATION NUMBER: PCT/GB02/05137
PRIOR PELLING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/GB02/05137
PRIOR PELLING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: GB 0220912.0
PRIOR FILING DATE: 2002-09-10
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; ORGANISM: Rattus norvegicus
US-11-078-735-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-11-078-735-13
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LENGTH: 63
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Score 46;
Pred. No. 6
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Publication No. US20050277172A1
GENERAL INFORMATION:
APPLICANT: Goedegebuur, Frits
APPLICANT: Gualfetti, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Trichomonas vaginalis
Query Match
Best Local Similarity 36.6%;
Matches 15; Conservative
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Neefe, Paulien
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US-10-763-712A-104
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APPLICANT:
APPLICANT:
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Sequence 21, Application US/10763712A

Publication No. US20850266541A1

Sequence 21, Application WS/10763712A

Publication No. US20850266541A1

GENERAL INFORMATION:
APPLICANT: Solazyme, Inc.
APPLICANT: Dillon, Harrison F.

TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen

TITLE OF INVENTION: Production
FILIE REPRENEER: H2042101.—CIP

CURRENT APPLICATION NUMBER: US/10/763,712A

CURRENT FILING DATE: 2004-01-21

FRIOR FILING DATE: 2002-11-04

FRIOR FILING DATE: 2003-11-04

FRIOR FILING DATE: 2003-11-04

FRIOR FILING DATE: 2003-04-12

FRIOR FILING DATE: 2003-09-03

NUMBER OF SEQ ID NOS: 184

SEQ ID NO 21

LENGTH: 449
                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT APPLICATION NUMBER: 06/049911
PRIOR APPLICATION NUMBER: 60/05914
PRIOR PILING DATE: 1997-06-18
PRIOR PLING DATE: 1997-06-26
PRIOR PLING DATE: 1997-06-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 397-09-19
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      Stewart, Timothy A.
Tumas, Daniel
                                                                 Watanabe, Colin K
Wood, William
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US-10-131-826A-296
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Sequence 104, Application US/10763712A

Sequence 104, Application US/10763712A

Sequence 104, Application US/2005056541A1

GENERAL INFORMATION:

APPLICANT: Solazyme, Inc.;

APPLICANT: Dillon, Harrison F.

TITLE OF INVENTION: Production

TITLE OF INVENTION: Production

FILE REFERENCE: H2042101-CIP

CURRENT FILING DATE: 2004-01-21

PRIOR PELICATION NUMBER: US/10/763,712A

CURRENT FILING DATE: 2002-11-04

PRIOR FILING DATE: 2003-14-12

PRIOR FILING DATE: 2003-04-12

PRIOR PILING DATE: 2003-04-12

PRIOR PILING DATE: 2003-04-12

PRIOR FILING DATE: 2003-04-12

PRIOR FILING DATE: 2003-04-12

SECTION NUMBER: US 60/500,032

NUMBER OF SEC ID NOS: 184

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16.3%; Score 46; DB 6; Length 449;
Best Local Similarity 36.6%; Pred. No. 64;
Matches 15; Conservative 1; Mismatches 9; Indels
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APPLICANT: Shaw, Andrew
APPLICANT: Stalberg, Maces
APPLICANT: Stalberg, Jerry
APPLICANT: Stalberg, Jerry
TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
TITLE OF INVENTION: Cellulases
FILE REFRENCE: GC772-3
FILE REPRENCE: GC772-3
CURRENT APPLICATION NUMBER: US/10/641,678
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: US 60/458,696
PRIOR FILING DATE: 2003-03-27
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/456,368
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: US 60/404,063
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
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PRIOR FILING DATE: 2002-08-16
DB 6; Length 449;
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16.3%; Score 46; DB 7; Length 938;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches: 8; Conservative 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                             RESULT 75
US-11-109-157A-18
Squence 18, Application US/11109157A
Publication No. US20050277175A1
GENERAL INFORMATION:
TITLE OF INVENTION: TRUNCATED ADAMTS MOLECULES
FILE REFERENCE: 01997.030500.
CURRENT APPLICATION NUMBER: US/11/109,157A
CURRENT APPLICATION NUMBER: 60/562,685
PRIOR PILING DATE: 2004-04-18
PRIOR FILING DATE: 2004-04-18
SOFTWARE: PAPELICATION NUMBER: 60/562,685
NUMBER OF SEQ ID NOS: 44
SSEQ ID NO 18
LENGTH: 938
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; SEQ ID NO 54
; LENGTH: 514
; TYPE: PRT
; ORGANISM: FUSATIUM OXYSPORUM
US-10-641-678-54
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US-11-109-157A-18
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US-10-107-782-4
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	1037-17-12 Sequence 1-104-047-2834 Sequence 1-239-663-35 Sequence 1-470-390A-12 Sequence 1-450-73-5668 Sequence	239-663-36 Sequence -4819-446-14 Sequence -239-663-36 Sequence	406-073-8 Sequence 0-406-073-15 Sequence 1-480-172-21 Sequence 0-930-512-18 Sequence	-898-570-16 Sequence -839-446-16 Sequence -480-172-20 Sequence	0-861-049-49 Sequence (-021-874-49 Sequence (-021-874-147 Sequence (0-380-703-14 Sequence 0-008-063-13 Sequence 0-380-703-9 Sequence	0-469-420-1 0-485-489-18 0-861-049-35 Sequence Sequence	1-021-874-35 Sequence 1-861-049-1 Sequence 1-021-874-1 Sequence)-473-451-10)-108-260A-2874 Sequence)-369-493-5671 Sequence	0-369-493-5672 Sequence 5672 0-424-599-251720 Sequence 2517 3-950-933A-82 Sequence 82,	1-097-143-41457 Sequence 4146 1-097-143-26277 Sequence 2627 1-626-914-14 Sequence 14.	1-861-049-53 Sequence 53,	7-485-489-14 Sequence 14, 3-825-751A-77 Sequence 77, 3-851-438-77 Sequence 77,	9-737-149-25 Sequence 25, 9-737-149-30 Sequence 30,	J-131-409-70 Sequence 70, J-139-854-70 Sequence 52, Sequence 52,)-150-813-70 Sequence 70,	0-701-283-25 Sequence 0-701-283-30 Sequence 0-473-576-14 Sequence)-094-749-2652 Sequence	3-425-115-353168 Sequence 3-779-050A-46 Sequence	-021-874-150 Sequence -021-874-151 Sequence -380-703-17 Sequence	380-703-17 380-703-18 36quence 3-425-115-296079 36quence 3-45-4-599-15639	J-424-599-150539 Sequence 150539 J-767-701-61450 Sequence 61450
675 4 US-10-028-248A-2 Sequence 675 4 US-10-107-782-2 Sequence 418 3 US-09-886-429-2 Sequence 418 4 US-10-162-435-21 Sequence 581 4 US-10-104-047-2804 Sequence 735 3 US-09-898-570-10 Sequence 845 3 US-09-898-570-12 Sequence 845 3 US-09-898-570-12 Sequence 846 3 US-09-898-446-10 Sequence	4 US-10-104-047-2834 Sequence 4 US-10-239-663-35 Sequence 4 US-10-239-663-35 Sequence 5 US-10-470-390A-12 Sequence 1 US-10-450-753-36668 Sequence	1 US-10-480-172-22 Sequence 3 US-09-898-570-14 Sequence 3 US-09-839-446-14 Sequence 4 US-10-239-663-36 Sequence	993 4 US-10-406-073-8 Sequence 1993 4 US-10-406-073-15 Sequence 1993 4 US-10-480-172-21 Sequence 106 3 US-09-930-512-18 Sequence	009 3 US-09-898-570-16 Sequence 009 3 US-09-839-446-16 Sequence 009 4 US-10-480-172-20 Sequence	175 5 US-10-861-049-49 Sequence 4 US-11-021-874-49 Sequence 6 US-11-021-874-147 Sequence	4 US-10-380-703-14 Sequence 4 US-10-008-063-13 Sequence 4 US-10-380-703-9 Sequence	4 US-10-469-420-1 Sequence 5 US-10-485-489-18 Sequence 5 US-10-861-049-35 Sequence	175 6 US-11-021-874-35 Sequence 314 5 US-10-861-049-1 Sequence 314 6 US-11-021-874-1 Sequence	887 5 US-10-473-451-10 Sequence 999 4 US-10-369-493-5671 Sequence 999 4 US-10-369-493-5671 Sequence	4 US-10-369-493-5672 Sequence 5672 4 US-10-424-599-251720 Sequence 2517 3 US-09-950-9334-82 Sequence 82,	6 US-11-097-143-41457 Sequence 4145 6 US-11-097-143-26277 Sequence 2627 5 US-10-626-914-14 Sequence 14,	5 US-10-861-049-53 Sequence 53, 6 US-11-021-874-53 Sequence 53, 6 US-11-021-874-53	24/ 5 US-10-485-14 Sequence 14, 574 3 US-00-825-751A-77 Sequence 77, 574 5 US-10-851-438-77 Sequence 77,	034 3 US-09-737-149-25 Sequence 25, 034 3 US-09-737-149-30 Sequence 30,	034 4 US-10-131-409-70 Sequence 70, 034 4 US-10-139-854-70 Sequence 70, 034 4 US-10-120-801-52 Sequence 52.	034 4 US-10-150-813-70 Sequence 70,	034 4 US-10-701-283-25 Sequence 034 4 US-10-701-283-30 Sequence 426 4 US-10-473-576-14 Sequence	4 US-10-094-749-2652 Sequence 3 US-10-425-115-337171 Sequence	4 US-10-425-115-353168 Sequence 3 US-09-779-050A-46 Sequence	6 US-11-021-874-150 Sequence 6 US-11-021-874-151 Sequence 4 IS-1-0-180-703-17 Sequence	4 US-10-380-703-17 Sequence 18-10-380-703-17 Sequence 18-10-425-115-296079 Sequence 24 US-10-424-599-156199	4 US-10-424-3397-130399 Sequence 13039
.0 2675 4 US-10-028-248A-2 Sequence 2675 4 US-10-107-782-2 Sequence 418 3 US-09-866-429-2 Sequence 8 418 4 US-10-16-62-435-21 Sequence 8 418 5 US-10-860-779-21 Sequence 8 581 4 US-10-104-047-2804 Sequence 8 735 3 US-09-889-570-10 Sequence 8 445 3 US-09-889-570-12 Sequence 8 445 3 US-09-889-570-12 Sequence 8 445 3 US-09-889-570-12 Sequence 8 445 3 US-09-889-446-12 Sequence	880 4 US-10-104-047-2834 Sequence 897 4 US-10-239-663-35 Sequence 897 4 US-10-470-3904-12 Sequence 897 4 US-10-470-470-3908-12 Sequence 997 4 US-10-450-4763-3668	8 974 3 US-10-480-172-22 Sequence 8 974 3 US-09-889-570-14 Sequence 8 974 3 US-09-839-446-14 Sequence 8 974 3 US-09-839-446-14 Sequence 8 973 4 US-10-239-663-36 Sequence	8 993 4 US-10-406-073-8 Sequence (Sequence 18 993 4 US-10-406-072-15 Sequence (Sequence 18 1006 3 US-10-430-512-18 Sequence (Sequence 18 1006 3 US-09-930-512-18	8 1009 3 US-09-888-570-16 Sequence 8 1009 3 US-09-839-446-16 Sequence 8 1009 4 US-10-480-172-20 Sequence	.6 175 5 US-10-861-049-49 Sequence .6 175 6 US-11-021-874-49 Sequence .3 63 6 US-11-021-874-147 Sequence .	.3 65 4 US-10-380-703-14 Sequence .3 175 4 US-10-008-063-13 Sequence .3 175 4 US-10-380-703-9 Sequence	.3 175 4 US-10-469-420-1 Sequence .3 175 5 US-10-485-489-18 Sequence .3 175 5 US-10-861-049-35 Sequence	.3 175 6 US-11-021-874-35 Sequence .3 314 5 US-10-861-049-1 Sequence .3 314 6 US-11-021-874-1 Sequence	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	.1 999 4 US-10-369-493-5672 Sequence 5672 .9 95 4 US-10-424-599-251720 Sequence 2517 .7 99 3 US-09-950-933A-82 Sequence 82.	.7 353 6 US-11-097-143-41457 Sequence 4145 .7 798 6 US-11-097-143-26277 Sequence 26.2 6 26 US-11-056-914-14 Sequence 14.	.6 246 5 US-10-861-049-53 Sequence 53, 6 246 6 US-11-021-874-53 Sequence 53, 6 246 6 US-11-021-874-53 Sequence 53,	.6 24/5 US-10-485-489-14 Sequence 14, .4 1574 3 US-09-825-751A-77 Sequence 77, .4 1574 5 US-10-851-438-77 Sequence 77,	.4 3034 3 US-09-737-149-25 Sequence 25, 4 3034 3 US-09-737-149-30 Sequence 30,	.4 3034 4 US-10-131-409-70 Sequence 70, .4 3034 4 US-10-139-854-70 Sequence 70, .4 3034 4 US-10-120-801-52 Sequence 52.	.4 3034 4 US-10-150-813-70 Sequence 70,	.4 3034 4 US-10-701-283-25 Sequence 3 3034 4 US-10-701-283-30 Sequence 2 426 4 US-10-473-576-14 Sequence	.2 955 4 US-10-094-749-2652 Sequence 3 107 4 US-10-425-115-337171 Sequence 3	.0 142 4 US-10-425-115-353168 Sequence 3 38 3 US-09-779-050A-46 Sequence 3 3 US-09-779-050A-46	.8 71 6 US-11-021-874-150 Sequence	.8 111 4 US-10-425-175-296079 Sequence .7 8 4 US-10-425-175-296079 Sequence .7 89 4 US-10-424-598-156139	., 69 4 US-10-767-701-61450 Sequence 61450
2675 4 US-10-028-248A-2 Sequence 2675 4 US-10-107-782-2 Sequence 418 3 US-09-886-429-2 Sequence 418 4 US-10-16-435-21 Sequence 418 5 US-10-16-779-21 Sequence 581 4 US-10-104-047-2804 Sequence 735 3 US-09-898-570-12 Sequence 845 3 US-09-898-570-12 Sequence 845 3 US-09-898-570-12 Sequence	22.8 897 4 US-10-239-663-35 Sequence 22.8 897 4 US-10-239-663-35 Sequence 22.8 897 5 US-10-470-300A-12 Sequence 22.8 897 5 US-10-470-300A-12 Sequence 22.8 897 5 US-10-450-763-3668 Sequence 23.9 897 5 US-10-450-763-3668 Sequence 23.9 897 5 US-10-450-763-3668	22.8 939 4 US-10-406-172-22 Sequence 22.8 974 3 US-09-898-570-14 Sequence 22.8 974 3 US-09-839-446-14 Sequence 22.8 974 3 US-09-839-446-14 Sequence 22.8 993 4 US-10-239-663-36 Sequence	22.8 993 4 US-10-406-073-8 Sequence 22.8 993 4 US-10-406-073-15 Sequence 22.8 993 4 US-10-480-172-21 Sequence 22.8 1006 3 US-09-930-512-18 Sequence	22.8 1009 3 US-09-898-570-16 Sequence 22.8 1009 3 US-09-839-446-16 Sequence 22.8 1009 4 US-10-480-172-20 Sequence	22.6 175 5 US-10-861-049-49 Sequence 22.6 175 6 US-11-021-874-49 Sequence 22.3 63 6 US-11-021-874-147 Sequence	22.3 65 4 US-10-380-703-14 Sequence 22.3 175 4 US-10-008-063-13 Sequence 22.3 175 4 US-10-380-703-9 Sequence	22.3 175 4 US-10-469-420-1 Sequence 22.3 175 5 US-10-485-489-18 Sequence 22.3 175 5 US-10-861-049-35 Sequence	22.3 175 6 US-11-021-874-35 Sequence 22.3 314 5 US-10-861-049-1 Sequence 22.3 314 6 US-11-021-874-1 Sequence	22.1 1887 5 US-10-473-451-10 Sequence 22.1 999 4 US-10-369-493-5671 Sequence	22.1 999 4 US-10-369-493-5672 Sequence 5672 21.9 95 4 US-10-44-599-251720 Sequence 2517 21.7 99 3 US-09-950-933A-82 Sequence 82.	21.7 353 6 US-11-097-143-41457 Sequence 4145 21.7 798 6 US-11-097-143-26277 Sequence 24.2 21.6 245 5 US-10-626-914-14 Sequence 14.2	21.6 246 5 US-10-861-049-53 Sequence 53, 21.6 246 6 US-11-021-874-53 Sequence 53, 21.6 246 6 US-11-021-874-53 Sequence 53, 21.6 246 6 US-11-021-874-53	21.6 24.7 5 US-10-485-489-14 Sequence 14, 21.4 1574 3 US-09-825-751A-77 Sequence 77, 21.4 1574 5 US-10-851-438-77 Sequence 77,	21.4 3034 3 US-09-737-149-25 Sequence 25, 21.4 3034 3 US-09-737-149-30 Sequence 30,	21.4 3034 4 US-10-131-409-70 Sequence 70, 21.4 3034 4 US-10-139-854-70 Sequence 70, 21.4 3034 4 US-10-120-801-52 Sequence 52.	21.4 3034 4 US-10-150-813-70 Sequence 70, 21.4 3034 4 US-10-150-811-70 Sequence 70,	21.4 3034 4 US-10-701-283-25 Sequence 21.4 3034 4 US-10-701-283-30 Sequence 21.2 426 4 US-10-471-576-14 Semience	21.2 955 4 US-10-094-749-2652 Sequence 21.0 107 4 US-10-425-115-337171 Sequence	21.0 142 4 US-10-425-115-353168 Sequence 20.8 38 3 US-09-779-050A-46 Sequence 3 Sequence 3	20.8 71 6 US-11-021-874-150 Sequence 20.8 71 6 US-11-021-874-151 Sequence 20.8 71 6 US-11-021-874-151 Sequence 20.8 71 4 US-11-280-20-21	20.8 17 4 US-10-425-175-17 Sequence 20.8 111 4 US-10-425-115-296079 Sequence 20.7 8 4 US-10-425-13-296079 Sequence 20.7 89 4 US-10-425-13-296079 Sequence 20.7 89 4 US-10-425-13-299-15439	20.7 156 4 US-10-767-701-61450 Sequence 61450

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100.0%; Score 283; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0;
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US-10-077-438-7

Sequence 7, Application US/10077438

Publication No. US20020165156A1

GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Browning, Deffrey
APPLICANT: Schnedide, Pascal
APPLICANT: Thompson, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jefrey
APPLICANT: Aptech RED S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: AG08PCT:
CURRENT APPLICATION NUMBER: 60/149,378
FRIOR PELICATION NUMBER: 60/149,378
FRIOR APPLICATION NUMBER: 60/149,378
FRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-11
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 184
TITLE OF INVENTION: Immunoregulatory Agent FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT FILING DATE: 2002-02-18
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR PILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTER OF SEQ ID NOS: 8
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; ORGANISM: homo sapien
US-10-077-438-7
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ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                            LENGTH: 184
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Sequence 12, Appl
Sequence 13, Appl
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Sequence 21, Appli
Sequence 21, Appli
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Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 24, Appli
Sequence 27, Appli
Sequence 18, Appli
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US-11-078-507-4
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US-09-795-006A-22
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US-10-120-398-1
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US-10-120-398-1
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; Publication No. US20020165156A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Techopp, Jung
APPLICANT: Techopp, Jung
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: APPLICANT: Bodgen, Inc.
APPLICANT: Bagen, Inc.
APPLICANT: Bagen, Inc.
APPLICANT: Baff Receptor (BCMA), An
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US-10-077-438-1

US-10-077-137-1 ; Sequence 1, Application US/10077137 ; Publication No. US20020172674A1 ; GENERAL INFORMATION:

51

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Publication No. US20030059862A1

SEQUENCE INFORMATION:
GENERAL INFORMATION:
APPLICANT Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF54
CURRENT FILING DATE: 2002-05-22
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 48
SOFTMARE: Patentin version 3.0
SEQ ID NO 47
LENGTH: 184
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100.0%; Score 283; DB 4; Length 184; 100.0%; Pred. No. 2.3e-25; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           Sequence 2, Application US/10068725 Publication No. US20030012783A1 GENERAL INFORMATION:
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US-10-068-725-2
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Best Local Similarity
Matches 51; Conserva
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US-10-115-192-8
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Best Local Similarity 100.0%; Pred. No. 2.36-25;
Matches 51; Conservative 0; Mismatches 0; Indels
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; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; Publication No. US20020172674A1
; Publicantion No. US20020172674A1
; Publicanti MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Techopp, Jurg
; APPLICANT: Techopp, Jurg
; APPLICANT: Scheider, Pascal
; APPLICANT: Biogen, Inc.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Lamunoregulatory Agent
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR PILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER: OF SEQ ID NOS: 8
; SOFTWARE: FREEER OF Windows Version 4.0
; TENENT TENENT TO A
                                             APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
APPLICANT: Schoeider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT PEPLICATION NUMBER: US/10/077,137
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
                    MacKay, Fabienne
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ORGANISM: homo sapien
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ORGANISM: homo sapien
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     Length 184;
                                                    Indels
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Publication No. US20030082175A1
GENERAL INFORMATION:
APPLICANT: Apotech R & D S.A.
APPLICANT: Biogen, Inc.
TILLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
FILE REPERENCE: A083PCT
Query Match
100.0%; Score 283; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0;
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1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51

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; ORGANISM: Homo sapiens
US-10-216-074-11
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ORGANISM: Homo sapiens
    ORGANISM: Homo sapiens
                US-10-152-363A-27
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publication No. US20030092164A1

GENERAL INPORMATION:

APPLICANT: Gross, Jane A.

APPLICANT: ALOW, Wenfeng

APPLICANT: ALOW, Wenfeng

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor

FILE REFERENCE: 00-103

CURRENT APPLICATION NUMBER: US/10/008,063

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PastSEQ for Windows Version 4.0

ELENGTH: 184
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Sequence 27, Application US/10152363A

Publication No. US20030103986A1

GENERAL INFORMATION:

APPLICANT: Rixon, Mark W.

APPLICANT: Gross, Jane A.

TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERBNCE: 01-20

CURRENT FILING DATE: 2002-05-20

PRIOR PLIING DATE: 2001-05-24

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 3.0
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llarity 100.0%; Pred. No. 2.3e-25;
Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/215688
FRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/181807
PRIOR APPLICATION NUMBER: 60/157933
PRIOR PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 8: SEQ ID NOS: 12
SEQ ID NO 9: SEQ ID NO 9: 10.00
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US-10-008-063-7
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ORGANISM: homo sapiens
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nes 51; Conserve
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LENGTH: 184
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Best Local
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Mark, David H.

APPLICANT: Markowitz, Sanford David

APPLICANT: Bos Biotechnology, Inc.

APPLICANT: Case Western Reserve University

TITLE OF INVENTION: No. US20030235820Alel Methods of Screening for

TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer,

TITLE REFERENCE: 018501-0004040.

CURRENT APPLICATION NUMBER: US 60/281,149

PRIOR FILING DATE: 2001-04-17

PRIOR PILING DATE: 2001-04-17

PRIOR FILING DATE: 2001-04-17

SEQ ID NO 39

LENGTH: 184

LENGTH: 184
                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10216074

Sequence 11, Application US/10216074

Sublication No. US20030148445A1

GENERAL INFORMATION:

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT APPLICATION NUMBER: US/09/565,423

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: UNKNOWN

PRIOR PILING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 11

LENGTH: 184
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   Length 184,
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Query Match
100.0%; Score 283; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0;
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100.0%; Score 283; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0;
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; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
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Publication No. US20050070689A1
GENERAL INFORMATION:
APPLICANT: Dixit, Vishva
APPLICANT: Bridgway, John
APPLICANT: Ridgway, John
APPLICANT: Yan, Minhong
TITLE OF INVENTION: TAGIS and BR3 Polypeptides and Uses Thereof
FILE REFERENCE: 11669.175USWO
CURRENT APPLICATION NUMBER: US/10/485,489
CURRENT APPLICATION NUMBER: PCT/US02/23487
FRIOR APPLICATION NUMBER: PCT/US02/23487
PRIOR APPLICATION NUMBER: US 60/310,114
PRIOR APPLICATION NUMBER: US 60/310,114
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 6
LENGTH: 184
                                                                                             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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Publication No. US20050095243A1

GENERAL INCRNATION:

APPLICANT: Andrew Chan

APPLICANT: Qian Gong

APPLICANT: Qian Gong

APPLICANT: Qian Gong

APPLICANT: Plavius Martin

ITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

FILE REFERENCE: P2040R1US

CURRENT APPLICATION NUMBER: US/10/861,049

CURRENT APPLICATION NUMBER: US 60/476,531

PRIOR FILING DATE: 2003-06-06

PRIOR FILING DATE: 2003-06-05

PRIOR FILING DATE: 2003-06-05

NUMBER: OF SEQ ID NOS: 145

SEQ ID NOS: 145
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                     Indels
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1. Similarity 100.0%; Pred. No. 2.3e-25;
51; Conservative 0; Mismatches 0;
Local Similarity 100.0%; Pred. No. 2.3e-25; nes 51; Conservative 0; Mismatches 0;
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Pred. No. 2.3e-25;
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100.0%; Score 283; DE
Best Local Similarity 100.0%; Pred. No. 2.34
Matches 51; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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US-10-861-049-27
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Best Local Similarity
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US-10-861-049-27
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US-10-485-489-6
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Sequence 9, Application US/20040208824A1

Publication No. US20040208824A1

Publication No. US20040208824A1

APPLICANT: Parmelee, David

APPLICANT: Yeh, Ren-Hwa

APPLICANT: Hilbert, David

APPLICANT: Hilbert, David

APPLICANT: Hilbert, David

APPLICANT: Hilbert, David

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses Th

TITLE OF INVENTION: UNMBER: US/10/742,634

CURRENT FILING DATE: 2003-12-22
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       ; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member; CTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39
                                                                                                                                                                  Gaps
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Sequence 7, Application US/10626914

Publication No. US20050043516A1

GENERAL INFORMATION:

PAPLICANT: CHUNTHARAPAI, ANAN

APPLICANT: GREWAL, IQBAL,

APPLICANT: KIM, KYUNG JIN

APPLICANT: KYUNG JIN

TITLE OF INVENTION: TACI Antibodies and Uses Thereof

FILE REFERENCE: P1942R1

CURRENT FILING DATE: 2003-07-25

PRIOR APPLICATION NUMBER: US/10/626,914

CURRENT FILING DATE: 2003-07-25

PRIOR FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 17
                                                                                                                  100.0%; Score 283; DB 4; 100.0%; Pred. No. 2.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 283; DB 4; 100.0%; Pred. No. 2.3e-25;
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                                                                                                                                                                  0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/435,262 PRIOR FILING DATE: 2002-12-23 PRIOR PELING DATE: 2002-12-23 PRIOR PILING DATE: 2003-05-02 NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin version 3.1 SEQ ID NO 9
                                                                                                      Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 184
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US-10-115-192-12
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US-09-854-864-6
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US-09-855-158-6
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GARBEAL INCOMPAUTION:

APPLICANT: Growley, Craig

APPLICANT: Desauvage, Frederic J.

APPLICANT: Beans, Allen

APPLICANT: Eaton, Daniel L.

APPLICANT: Eston, Allen

APPLICANT: Eston, Andrew

APPLICANT: Solith, Victoria

TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of

TITLE OF INVENTION: Hematopoietic Origin

TITLE OF INVENTION: Hematopoietic Origin

TITLE OF INVENTION WHERE: US/10/989,826

CURRENT APPLICATION NUMBER: US 60/520,842

PRIOR APPLICATION NUMBER: US 60/532,426

PRIOR FILING DATE: 2003-11-17

PRIOR APPLICATION NUMBER: US 60/532,426

PRIOR APPLICATION NUMBER: US 60/532,426

NUMBER OF SEQ ID NOS: 75

LENGTH: 184
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APPLICANT: Qian Gong

APPLICANT: Qian Gong

APPLICANT: Qian Gong

TITLE CAPITATION: COMBINATION THERAPY FOR B CELL DISORDERS

FILE REFERENCE: P2040R1P1

CURRENT APPLICATION NUMBER: US/11/021,874

CURRENT PILING DATE: 2004-12-22

PRIOR FILING DATE: 2004-06-04

PRIOR FILING DATE: 2003-06-06

PRIOR PELICATION NUMBER: US 60/476,481

PRIOR APPLICATION NUMBER: US 60/476,481

PRIOR APPLICATION NUMBER: US 60/476,414

PRIOR APPLICATION NUMBER: US 60/476,414

PRIOR PILING DATE: 2003-06-05

PRIOR PILING DATE: 2003-06-05

NUMBER OF SEQ ID NOS: 165

SEQ ID NO 27
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ilarity 100.0%; Pred. No. 2.3e-25;
Conservative 0; Mismatcht.
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100.0%; Score 283; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0;
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Sequence 27, Application US/11021874

Publication No. US20050163775A1

GENERAL INFORMATION:
                                                                                                                                       ; Sequence 46, Application US/10989826; Publication No. US20050238650A1; GENERAL INFORMATION:
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US-11-021-874-27
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US-10-989-826-46
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Best Local Similarity
Matches 51; Conserv
                                                                                              RESULT 16
US-10-989-826-46
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1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51

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APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS EXDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/884,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
TYPE: PRI
ORGANISM: Homo sapiens
US-09-884-864-6
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Sequence 12, Application US/10115192

Sequence 12, Application US/10115192

Publication No. US20030082175A1

GENERAL INFORMATION:

APPLICANT: Balogen, Inc.

TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof

FILE REFERENCE: A083FCT

CURRENT APPLICATION NUMBER: US/10/115,192

CURRENT FILING DATE: 2002-04-02

PRIOR APPLICATION NUMBER: 60/1215688

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: BastsEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 302
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100.0%; Score 283; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.7e-25;
Matches 51; Conservative 0; Mismatches 0;
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Patent No. US20020081296A1
GENERAL INFORMATION:
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ORGANISM: homo sapiens
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Sequence 9, Application US/09855158
Publication No. US20020086018A1
GENERAL INFORMATION.
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL)
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT PELLING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATEURIN VERSION 3.1
SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                             Length 181;
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100.0%; Pred. No. 1e-23;
tive 0; Mismatches 0
                   CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR PELLING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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Patent No. US20020081296A1
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 48; Conservative
                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-09-854-864-9
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US-09-855-158-9
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Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: YU, GANG
ITILE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09854864

Sequence 5, Application US/09854864

Sequence 5, Application US/09854864

Sequence 10. US20020081296A1

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION:
ELYS/AGP-3, AND TACI

TITLE OF INVENTION:
FILE REFERENCE: A-686

CURRENT PILING DATE: 2000-09-11

PRIOR FILING DATE: 2000-05-12

PRIOR PPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATCH OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.1%; Score 269; DB 3; Length 51; Best Local Similarity 100.0%; Pred. No. 2.9e-24; Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-158-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 181
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US-09-855-158-5
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US-09-854-864-5
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US-09-855-158-21
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92.9%; Score 263; DB 4; Length 207;
Best Local Similarity 71.8%; Pred. No. 5.8e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 20;
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95.1%; Score 269; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 48; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Backay, Fabienne
APPLICANT: Backay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Tachopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION INMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FABELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10077137; Sequence 3, Application No. US20020172674A1; GENERAL INFORMATION: APPLICANT: MacKay, Fabienne; APPLICANT: Browning, Jeffrey; APPLICANT: Techopp, Jurg; APPLICANT: Techopp, Jurg; APPLICANT: Thompson, Jeffrey; APPLICANT: Thompson, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; sequence 3, Application US/10077438
; Publication No. US20020165156Al
; GENERAL INFORMATION:
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9
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ORGANISM: homo sapien
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Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GERERAL INFORMATION:
    GERERAL INFORMATION:
    APPLICANT: THEILL, LARS EYDE
    APPLICANT: THEILL, LARS EYDE
    APPLICANT: YU, GANG
    TITLE OF INVENTION: BLYS/AGP-3, AND TACI
    TITLE OF INVENTION: BLYS/AGP-3, AND TACI
    TITLE OF INVENTION: BLYS/AGP-3, AND TACI
    FILE REFERENCE: A-686B
    CURRENT FILING DATE: 2001-09-11
    FRIOR APPLICATION NUMBER: US 60/204,039
    FRIOR APPLICATION NUMBER: US 60/204,039
    FRIOR PAPLICATION NUMBER: US 60/214,591
    FROR RELING DATE: 2000-05-27
    NUMBER OF SEQ ID NOS: 31
    SEQ ID NO 21
    SEQ ID NO 21
    LENGTH: 58
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Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 44; Conservative 0; Mismatches 0;
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION UNMERE: US/10/077,137
CURRENT PILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 2000-02-11
SPRIOR PILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: homo sapien
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Matches 51; Conserv
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Sequence 13, Application US/0985158

Publication No. US20020086018A1

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLN
TITLE OF INVENTION: A. AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 81
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 81
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                         60/204,039
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; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GBNERAL INFORMATION:
PRIOR FILING DATE: 2000-06-27
PRIOR PELLING DATE: 2000-06-12
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
LENGTH: 34
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US-09-855-158-7
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Best Local Similarity
Matches 34; Conserv
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| Sequence 7.7. Application US/09854864
| Patent No. US20020081296A1
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: YU, GANG
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-686B
| CURRENT FILING DATE: 2001-09-11
| FRICR APPLICATION NUMBER: US 60/204, 039
| PRIOR PLLING DATE: 2000-05-12
| PRIOR PLLING DATE: 2000-06-27
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: Patentin version 3.1
| SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT PILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
                              BI
  APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PLENCHIN VERSION 3.1
SEQ ID NO 21
LENGTH: 58
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71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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GENERAL INFORMATION:
APPLICANT: THELLL, LARS EYDE
APPLICANT: YU, GANG
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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US-09-854-864-7
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US-09-855-158-7
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| Sequence 10, Application US/09854864 |
| Sequence 10, Application US/09854864 |
| Patent No. US20020081296A1 |
| GENERAL INPORMATION: |
| APPLICANT: THEILL, LARS EYDE |
| APPLICANT: THEILL, LARS EYDE |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLXS/AGP-3, AND TACI |
| CURRENT APPLICATION NUMBER: US 60/204,039 |
| PRIOR PELLING DATE: 2000-05-12 |
| PRIOR PELLING DATE: 2000-06-27 |
| PRIOR FILING DATE: 2000-06-27 |
| NUMBER OF SEQ ID NOS: 31 |
| SOFTWARE: Patentin version 3.1 |
| SOFTWARE: Patentin version 3.1 |
| SEG ID NO 10 |
| TENNION 10 10 |
                                                                                                                                                                                                       Sequence 17, Application US/10216074

Sequence 17, Application US/10216074

Publication No. US2030148445A1

GENERAL INFORMATION:

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 2879-72

CURRENT PAPLICATION NUMBER: US/10/216,074

CURRENT PILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US/09/565,423

PRIOR APPLICATION NUMBER: UNNOWN

PRIOR PLING DATE: 2000-05-05

PRIOR PLING DATE: 2000-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3-1

FENDING DATE: 1000-05-06

SEQ ID NOS: 17
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Pred. No. 3.6e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 181; DB 4; Length Luc
Pred, No. 2.4e-13;
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                   4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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Best Local Similarity 70.8%;
Matches 34; Conservative 4
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Best Local Similarity 70.8%;
Matches 34; Conservative
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US-09-854-864-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus
US-10-216-074-17
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Sequence 11. Application US/09855158

Publication No. US20020086018A1

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: TY, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
TITLE OF INVENTION: 3, AND TACI
FILE REPERENCE: 4.686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2000-09-11
PRIOR PILING DATE: 2000-06-27
PRIOR PLING DATE: 2000-06-12
PRIOR PLING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SECTION 0.11
SERVICH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09854864

Sequence 11, Application US/09854864

Batent No. US20020081236A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: TY, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: WETHODS AND TACI

FILE REFERENCE: A-686B

CURRENT FILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-06-12

PRIOR PLILOG DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 11

LENGTH: 185

"WENDER DELICATION NUMBER: US 60/214,591

BENOR FILING DATE: 2000-06-27

LENGTH: 185

"WENDER OF LENGTH: 185

"WENDER DATE: NOS: 31

SEQ ID NO 11

LENGTH: 185
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                                                                                                                          Length 81;
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                                                                                                                Score 201; DB 3; 1
; Pred. No. 4.7e-16;
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                                                                                                                    Query Match 71.0%; Score 201; DB Best Local Similarity 100.0%; Pred. No. 4.7 Matches 34; Conservative 0; Mismatches
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13
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ORGANISM: Murine
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Sequence 12, Application US/09855158
Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL)
TITLE OF INVENTION: 3, AND TACI
FILE REPERENCE: A-686A
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER.
FILE REFERENCE: 529452000122
CURRENT PAPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PELLING DATE: 2000-12-22
PRIOR FILING DATE: 2000-103-02
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36.7%; Score 104; DB 3;
Best Local Similarity 69.8%; Pred. No. 0.00018;
Matches 30; Conservative 1; Mismatches 2.
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                       CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SQO ID NO 12
LENGTH: 117
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CURRENT FILING DATE: 2001-09-11
FRIOR APPLICATION NUMBER: US 60/214,591
FRIOR APPLICATION NUMBER: US 60/204,039
FRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
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Publication No. US20020182586A1
GENERAL INFORMATION:
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ORGANISM: human-murine Consensus
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          FILE REFERENCE: A-686B
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US-09-855-158-12
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RESULT 37
US-09-855-158-10
US-08-854-10
US-08-864-10
US-08-8
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; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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Publication No. US20030195156A1
GENERAL INFORMATION:
APPLICANT: HIN, HOGUNG
APPLICANT: HSU, HAILING
APPLICANT: HSU, HAILING
TITHE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
FILE REPERENCE: A-743
CURRENT APPLICATION NUMBER: US/10/145,206
CURRENT PILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/290,196
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 MAGQCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG
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Best Local Similarity 100.
Matches 28; Conservative
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ORGANISM: Mus musculus
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US-10-145-206-197
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APPLICANT: Milet, Isabelle
APPLICANT: Milet, Isabelle
APPLICANT: Rothenberg, Mark
ITLE OF INVENTION: NO. US20030235882A1e1 Nucleic Acids and Polypeptides and Methods of TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
PRIOR APPLICATION NUMBER: 60/26599
PRIOR APPLICATION NUMBER: 60/26299
PRIOR PILING DATE: 2001-01-9
PRIOR PILING DATE: 2001-02-8
PRIOR PILING DATE: 2001-02-8
PRIOR PILING DATE: 2001-04-26
PRIOR PILING DATE: 2001-04-26
PRIOR PILING DATE: 2001-04-26
PRIOR PILING DATE: 2001-09-09
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 75
LENGTH: 5374
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFRENCE: 21402-2222(TO
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
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24.6%; Score 69.5; DB
Best Local Similarity 36.8%; Pred. No. 93;
Matches 14; Conservative 5; Mismatches
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Tchernev, Velizar,
Vernet, Corine,
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Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Gangolli, Esha,
Kekuda, Ramesh,
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Rothenberg, Mark,
Sciore, Paul,
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Miller, Charles,
Millet, Isabelle,
                                   Sciore, Paul
Millet, Isabelle
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
APPLICANT: Edinger, Shlomi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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; Sequence 2, Application US/10180903
; Publication No. US20030093824A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO
; FILE REFERENCE: R-720
; CURRENT PILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-24
; NUMBER: OF SEQ ID NOS: 4
; SOFTWARE: FeatSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TWOST: DATE: DATE: CONTROL OF SEQ ID NO 2
; LENGTH: 1548
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                                                                                                                                                                  Length 249;
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                                                                                                                                                                Score 71.5; DB 4; Length 2. Pred. No. 2.6; 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                          6 CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                                                                                                                                                                                                                    8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70.5; DI
Pred. No. 21;
5; Mismatches
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1647
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 43
US-10-02-248A-75
Sequence 75, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
    APPLICANT: Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taupier Jr, Raymond J
Kekuda, Ramesh
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Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
Gangolli, Esha
Miller, Charles
Boldog, Ferenc
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Best Local Similarity 34.7%;
Matches 17; Conservative !
                                                                                                                                                                  Query Match 25.3%;
Best Local Similarity 35.3%;
Matches 12; Conservative
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Zerhusen, Bryan
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Tchernev, Velizar
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                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1647
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US-10-180-903-2
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US-10-180-903-2
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Gape

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APPLICANT: Taupier, Raymond, jr.,
APPLICANT: Tchernev, Velizar,
APPLICANT: Vernet, Corine,
APPLICANT: Serhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
                                                                                                                                                                                                                                                                                                                                                                                                              3
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                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
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PRIOR APPLICATION NUMBER: 10/028,248

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/256,619

PRIOR APPLICATION NUMBER: 60/266,619

PRIOR PILING DATE: 2000-12-19

PRIOR PILING DATE: 2001-01-19

PRIOR PILING DATE: 2001-01-19

PRIOR PILING DATE: 2001-02-28

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-04-20

PRIOR PILING DATE: 2001-04-20

PRIOR PILING DATE: 2001-04-20

PRIOR PILING DATE: 2001-07-26

PRIOR PILING DATE: 2001-07-67-60

PRIOR PILING DATE: 2001-07-67-60
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308039
PRIOR PILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 74
LENGTH: 5376
TYPE: PRT
CREANISM: MUS MUSCULUS
US-10-028-248A-74
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PRIOR FILING DATE: 2001-03-28
UNUMBER OF SEQ ID NOS: 215
SOFTWARE: CuraSeqList version 0.1
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Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Rothenberg, Mark,
Sciore, Paul,
Shenoy, Suresh,
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APPLICANT: Cagman, Stacie
APPLICANT: Colman, Steve,
APPLICANT: Edinger, Shlomit,
APPLICANT: Gangolli, Esha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li, Li,
Liu, Xiaohong,
Malyankar, Uriel,
Miller, Charles,
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US-10-107-782-74
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APPLICANT: Si, Jungaheng
APPLICANT: Edinger, Shlomit
APPLICANT: Scione, David
APPLICANT: Scione, Paul
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Rochenberg, Mark
TITLE OF INVENTION: No. U320030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
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CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
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Publication No. US20030235882AI
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard
APPLICANT: Patturajan, Meera
APPLICANT: Vernet, Corine
APPLICANT: Genman, Stacie
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Sholoy, Suresh
APPLICANT: Sholoy, Suresh
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Boldoy, Ferenc
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR APPLICATION NUMBER: 60/266,619
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/205,189
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ 1D NOS: 215
SOFTWARE: CLEASEQLIST VETSION 0.1
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PRIOR FILING DATE: 2000-12-19
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APPLICATION NUMBER: 60/262959
FILING DATE: 2001-01-19
APPLICATION NUMBER: 60/272408
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APPLICATION NUMBER: 60/285189
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Best Local Similarity 36.8%;
Matches 14; Conservative
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Smithson, Glennda
Zerhusen, Bryan
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Tchernev, Velizar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ 1D NO 75;
; LENGTH: 5374
; TYPE: BRT
ORGANISM: Homo sapiens
US-10-107-782-75
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                                                                                                                               Query Match 24.6%; Score 69.5; DB 4; Length 5376; Best Local Similarity 36.8%; Pred. No. 93; Matches 14; Conservative 5; Mismatches 16; Indels 3
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24.2%; Score 68.5; DB 4; Length 332;
Best Local Similarity 27.9%; Pred. No. 7.8;
Matches 12; Conservative 10; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                    RESULT 47
US-10-152-363A-62
; Sequence 62, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT FILING DATE: 2002-05-20
; PRIOR FILING DATE: 2001-05-24
; PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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US-09-779-050A-45
Sequence 45, Application US/09779050A
Fatent No. US2002016416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
CURRENT PAPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 62
LENGTH: 332
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US-10-152-363A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                           TYPE: PRT;
CRGANISM: Homo sapiens
US-10-107-782-74
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          SEQ ID NO 74
LENGTH: 5376
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8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43

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Sequence 20, Application US/09854864

| Sequence 20, Application US/09854864
| Patent No. US20020081226A1
| GENERAL INPORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: TV, GANG
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
| TITLE OF INVENTION: METHODS AND TACI
| FILE REFERENCE: A-6868
| CURRENT APPLICATION NUMBER: US/09/854,864
| CURRENT APPLICATION NUMBER: US 60/204,039
| PRIOR APPLICATION NUMBER: US 60/204,039
| PRIOR PILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-05-13
| PRIOR PILING DATE: 2000-06-14
| PRIOR PILING DATE: 2000-06-17
| NUMBER OF SEQ ID NOS: 31
| SEQ ID NO 20
| LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09855158

Sequence 20, Application US/09855158

Publication No. US20020086018A1

GENERAL INFORMATION:
GENERAL INFORMATION:
THERIL, LARS EVDE
APPLICANT: THERIL,
APPLICANT: THELL,
APPLICANT: THERIL,
APPLICANT: WU, GANG
TITLE OF INVENTION: 3, AND TACI
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT PILING DATE: 2001-05-11
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67.5; DB
Pred. No. 1.8;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.9%; Score 67.5; Di
30.6%; Pred. No. 1.8;
tive 9; Mismatches
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US-09-854-864-15
; Sequence 15, Application US/09854864
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Best Local Similarity 30.6%;
Matches 11; Conservative
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Best Local Similarity 30.69
Matches 11; Conservative
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US-09-855-158-20
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| Sequence 6, Application US/11079418
| Publication No. US20050183148A1
| GENERAL INFORMATION:
| APPLICANT: Bram, Richard J.
| APPLICANT: Bram, Richard J.
| APPLICANT: Won Bulow, Gotz
| TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
| TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
| TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
| TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
| TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
| TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
| FILE REFERENCE: 44158/254623
| CURRENT APPLICATION NUMBER: US/10/293,816
| PRIOR PAPLICATION NUMBER: US 09/782,857
| PRIOR PLING DATE: 1999-01-12
| PRIOR PAPLICATION NUMBER: US 09/290,333
| PRIOR PAPLICATION NUMBER: US 08/810,572
| PRIOR PAPLICATION NUMBER: US 08/810,572
| PRIOR PAPLICATION NUMBER: US 08/810,572
| NUMBER OF SEQ ID NOS: 11
| SOFTWARRE: PRESEQ FOR WINDOWS VERBION 4.0
| SEQ ID NOS: 11
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23.9%; Score 67.5; DB 4; Length 166;
Best Local Similarity 30.6%; Pred. No. 5.1;
Matches 11; Conservative 9; Mismatches 15; Indels
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Sequence 18, Application US/10684149
Publication No. US20050009149A1
GENERAL INFORMATION:
APPLICANT: West, James W.
APPLICANT: Brandt, Cameron S.
APPLICANT: Brandt, Cameron S.
TITLE OF INVENTION: Production of Homotrimeric Fusion ITILE OF INVENTION: Production of Fire Reference: 02-17
FILE REFERENCE: 02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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30.6%; Pred. No. 5.1;
tive 9; Mismatches
CURRENT APPLICATION NUMBER: US/10/293,816
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR FILING DATE: 2001-02-14
PRIOR PILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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CORGANISM: Homo sapiens
US-11-079-418-6
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  US-10-293-816-6
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Matches
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US-09-055-150-15
is Sequence 15. Application US/09855158
is Publication No. USZ0020086018A1
is GENERAL INFORMATION:
is APPLICANT: THEILL, LARS EYDE
is APPLICANT: THEILL, LARS EYDE
is TITLE OF INVENTION:
is PRIOR PILLING DATE: 2001-09-11
is PRIOR FILLING DATE: 2000-06-27
is PRIOR FILLING DATE: 2000-06-12
is PRIOR FILLING DATE: 2000-05-12
is SOFTWARE: Patentin version 3.1
is SEQ ID NO 5.5
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                            APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: TUG GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFREENCE: A-666B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 15
LENGTH: 166
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Pred. No. 5.1;
9; Mismatches 15; Indels 1
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PUDICATION NO. US20030082173A1
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
FILE REPERENCE: 44158/254623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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23.9%; Score 67.5; DF
Best Local Similarity 30.6%; Pred. No. 5.1;
Matches 11; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.6%;
Matches 11; Conservative 9
                 Patent No. US20020081296A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-854-864-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-293-816-6
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US-11-V41-W/4-L56
; Sequence 36, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Glavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; TILE REFERENCE: P2040RLP1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR PILING DATE: 2004-06-04
; PRIOR PELING DATE: 2003-06-06
; PRIOR PELING DATE: 2003-06-06
; PRIOR PELING DATE: 2003-06-05
; PRIOR FILING DATE: 2003-06-05
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: AUGUS CONSTITUTION COMBINATION THERAPY FOR B CELL DISORDERS ITLLE REPERBENCE: P2040MINATION THERAPY FOR B CELL DISORDERS FILE REPERBENCE: P2040MINGS: CURRENT PELING DATE: 2004-06-04
PRIOR PELING DATE: 2003-06-06
PRIOR PELING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
23.9%; Score 67.5; DB 5; Length 265;
Best Local Similarity 30.6%; Pred. No. 8.1;
Matches 11; Conservative 9; Mismatches 15; Indels
                                                                                                                                                                                                                Length 265;
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                                                                                                                                                                                                                                                                      15;
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                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                         8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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                                                                                                                                                                                                                Score 67.5; Di
Pred. No. 8.1;
                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/10861049; Publication No. US20050095243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                     23.9%;
PRIOR FILING DATE: 2002-04-30
                                                                                                                                                                                                                                            Best Local Similarity 30.6
Matches 11; Conservative
                         NUMBER OF SEQ ID NOS: 19
SEQ ID NO 19
LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-489-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 58
US-10-861-049-36
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US-10-485-485-485

Sequence 19, Application US/10485489

Publication No. US20050070689A1

GENERAL INFORMATION:

APPLICANT: Dixit, Viehva

APPLICANT: Ridgway, John

APPLICANT: Ridgway, John

APPLICANT: Yan, Minhong

TITLE OF INVENTION: TAGES US/10/485,489

CURRENT APPLICATION NUMBER: US/10/485,489

CURRENT APPLICATION NUMBER: PCT/US02/23487

PRIOR FILING DATE: 2002-07-24

PRIOR FILING DATE: 2001-08-03

PRIOR PLICATION NUMBER: US 60/317,171
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
23.9%; Score 67.5; DB 5; Length 171;
Best Local Similarity 30.6%; Pred. No. 5.3;
Matches 11; Conservative 9; Mismatches 15; Indels
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APPLICANT: GREWAL, IOBAL

APPLICANT: GREWAL, IOBAL

APPLICANT: YAN, MINHONG

TITLE OF INVENTION: TACI Antibodies and Uses Thereof

FILE REFERENCE: P1942R1

CURRENT APPLICATION NUMBER: US/10/626,914

CURRENT FILING DATE: 2003-07-25

PRIOR APPLICATION NUMBER: US 60/398,530

PRIOR FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNA 43
  CURRENT APPLICATION NUMBER: US/10/684,149
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 60/417,801
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: RestSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 171
                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: TACI-HSBP fragment
US-10-684-149-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10626914; Publication No. US20050043516A1; GENERAL INFORMATION:
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 30.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 57
US-10-485-489-19
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US-10-626-914-17
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Sequence 14, Application US/09854864

Sequence 14, Application US/09854864

Sequence 14, Application US/09854864

Sequence 14, Application US/0081296A1

GENERAL INFORMATION:

APPLICANT: TU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLXS/AGP-3, AND TACI

FILE REFERENCE: A-6868

CURRENT FILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 14

SEQ ID NO 14

LENGTH: 293
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Sequence 14, Application US/09855158

Sequence 14, Application US/09855158

Publication No. US2020086018A1

GENERAL INFORMATION:
APPLICANT: THELL, LARS EYDE
APPLICANT: THELL, LARS EYDE
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-6866.
CURRENT APPLICATION NUMBER: US/09/855,158

CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.1

SEQ ID NO 14

LENGTH: 293
                                                                                       Length 293;
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Pred. No. 9;
                                                                                                                            9; Mismatches 15; Indels
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                                                                                                                                                                                        34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
                                                                                                                                                                 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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                                                                                           DB 3;
                                                                                       Score 67.5;
Pred. No. 9;
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                                                                                         Query Match 23.9%;
Best Local Similarity 30.6%;
Matches 11; Conservative
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Matches 11, Conservative
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US-09-854-864-14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-854-864-14
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23.9%; Score 67.5; DB 3; Length 291;
Best Local Similarity 30.6%; Pred. No. 8.9;
Matches 11; Conservative 9; Mismatches 15; Indels
                                                                                               Length 265;
                                                                                                                                  Indels
                                                                                         Query Match 23.9%; Score 67.5; DB 6; Best Local Similarity 30.6%; Pred. No. 8.1; Matches 11; Conservative 9; Mismatches 15;
                                                                                                                                                                                            8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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                                                                                                                                                                       8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 43
                                                                                                                                                                                                                                                          RESULT 60
US-09-779-050A-43
Sequence 43, Application US/09779050A
Sequence 43, Application US/09779050A
Patent No. US20020166416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HALLING
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REPRENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR PALOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFWARE: Patentin version 3.0
SEQ ID NO 43
LENGTH: 291
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
 ; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-36
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ORGANISM: Homo sapiens
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US-09-879-919-22
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Sequence 2, Application US/09302863
Publication No. US20030022233A1
GENERAL INFORMATION:
APPLICANT: GOOWIN, RAYMOND G
APPLICANT: Din, Wanwan S.
TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
FILE REFERENCE: 2519
CURRENT APPLICATION NUMBER: US/09/302,863
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO S.
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US-09-855-564-2
                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
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US-09-961-376-2
i Sequence 2, Application US/09961376
j Patent No. US20020106736A1
j GENERAL INFORMATION:
j APPLICANT: Ruben et al.
j TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
i TILE REFERENCE: PF534P1
j CURRENT APPLICATION NUMBER: US/09/961,376
j CURRENT FILING DATE: 2001-09-25
j FRIOR APPLICATION NUMBER: 60/235,991
j FRIOR FILING DATE: 2000-12-13
j FRIOR APPLICATION NUMBER: 60/235,991
j FRIOR FILING DATE: 2000-03-26
j FRIOR FILING DATE: 2000-03-26
j FRIOR APPLICATION NUMBER: 09/533,822
j FRIOR APPLICATION NUMBER: 09/533,822
j FRIOR APPLICATION NUMBER: 09/533,822
j FRIOR FILING DATE: 2000-03-24
j FRIOR FILING DATE: 2000-03-24
j FRIOR FILING DATE: 2000-03-10
j NUMBER OF SEQ IN DOS: 7
j SOFTWARE: PatentIn Ver. 2.1
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30.6%; Pred. No. 9;
tive 9; Mismatches 15; Indels
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15; Indels
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Pred. No. 9;
9; Mismatches 15;
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                                                                          GENERAL INFORMATION:
APPLICANT: BOYLE,
TITLE OF INVENTION: RECEPTOR FROM TWF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT APPLICATION NUMBER: 0201-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-779-050A-42; Sequence 42. Application US/09779050A; Sequence 42. Application US/09779050A; Partent No. US20020160416A1; GENERAL INFORMATION:
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Best Local Similarity 30.6%;
Matches 11; Conservative
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Matches 11; Conservative
  11; Conservative
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ORGANISM: Homo sapiens
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ORGANISM:
      Matches
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TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
TITLE OF INVENTION: 2519
CURRENT EPFERENCE: 2519
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/302,863
PRIOR PLING DATE: 1999-04-30
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Query Match
23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REPERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
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Pred. No. 9;
9; Mismatches 15;
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                                                                                                                                                                                                                                                            US-09-855-564-2
Sequence 2, Application US/09855564
Publication No. US20030165986A1
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G
APPLICANT: Din, Wanwan S.
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23.9%;
Best Local Similarity 30.6%;
Matches 11; Conservative 9
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 293
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RESULT 66

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Gaps

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US-10-151-882-46

US-10-151-882-46

Sequence 46, Application US/10151882

Publication No. US20030059862A1

GENERAL INFORMATION:

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

TITLE OF INVENTION NUMBER: US/10/151,882

CURRENT APPLICATION NUMBER: 60/293,100

PRIOR APPLICATION UNDER: 2001-05-24

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.0

SEQ ID NO 46

LENGTH: 293
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Publication No. US20030082173A1
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: Bram, Richard J.
TILE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CURRENT APPLICATION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
FILE REFERENCE: 44158/254633
CURRENT PELLONION: UNBER: US/10/293,816
CURRENT PILLONG DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR PILLING DATE: 2001-02-14
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastERG for Windows Version 4.0
SOFTWARE: PASEER FOR WINDOWS: 11
FENTING DATE: 1997-03-03
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                                                                                                34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
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23.9%; Score 67.5; D:
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches
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Best Local Similarity 30.6
Matches 11, Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
Best Local Similarity
Matches 11; Conserv
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APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Neutrokine-alpha Binding Proteins and Methods Based Thereon FILE REFERENCE: PFS24FCT US/10/084,971

CURRENT APPLICATION NUMBER: LAGILER APPLICATION NUMBER: US/09/533,822

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822

PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-03-26

PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-26

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NUMBER: OF SEQ ID NOS: 5

SOFTWARE: PATENTIN Ver. 2.1
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| Sequence 4, Application US/10068725 |
| Sequence 4, Application US/10068725 |
| Sequence 4, Application NO- US2003001278341 |
| Publication NO- US2003001278341 |
| APPLICANT: Kindsvogel, Wayne |
| TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI |
| FILE REFERENCE: 01-04 |
| CURRENT APPLICATION NUMBER: US/10/068,725 |
| CURRENT APPLICATION NUMBER: 60/270,274 |
| PRIOR PILING DATE: 2001-02-20 |
| PRIOR FILING DATE: 2001-04-12 |
| NUMBER OF SEQ ID NOS: 5 |
| SEQ ID NO 4 |
| LENGTH: 293
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NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1650
LENGTH: 293
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Publication No. US20020187526A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-10-087-192-1650
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LENGTH: 293
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; PRIOR PILICATION NUMBER: 10/082,260
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Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels
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Publication No. US20030092164A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Gross, Jane A.;
APPLICANT: Town Kandeng
APPLICANT: Town Kandeng
APPLICANT: Grant, Francis, J.;
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor;
FILE REFERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
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CORGANISM: Homo sapiens
US-10-152-363A-2
                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/328,401
PRIOR PILING DATE: 1997-03-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-05-25
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PRIOR PLING DATE: 2001-03-16
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PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-06-15
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1 US-08-326-110A-33 Sequence 33, 1 US-08-634-641-4 Sequence 40, 2 US-09-249-471-4 Sequence 40, 2	8.9 77 2 US-09-249-472-40 Sequence 40, 8.9 77 2 US-09-249-451-4 Sequence 40, 8.9 77 2 US-09-249-451-40 Sequence 40, 8.9	8.9 77 2 US-08-809-455-4 Sequence 4, 8.9 77 2 US-08-809-455-40 Sequence 40,	8.9 // 2 US-09-249-461-4 Sequence 40, 8.9 77 2 US-09-249-461-40 Sequence 40, 8.9 77 3 US-09-249-461-40 Sequence 40,	8.9 77 2 03-03-48-40 Sequence 40, Sequence 4	8.9 77 2 US-03-243-40 Sequence 40,	8.9 77 2 US-09-498-556-40 Sequence 40,	8.9 81 1 US-08-465-380-7 Sequence 7, 8.9 81 1 US-08-480-478-36 Sequence 36,	8.9 81 1 US-08-486-397-7 Sequence 7,	8.9 81 1 US-08-486-399-7 Sequence 7,	8.9 81 1 US-08-326-110A-36 Sequence 36,	8.9 81 1 US-08-634-641-7 Sequence 7,	8.9 81 2 US-09-249-471-7 Sequence 7,	8.9 81 2 US-09-249-451-7 Sequence 7,	8.9 81 2 US-08-809-455-7 Sequence 7,	8.9 81 2 US-09-249-461-7 Sequence 7, 8.9 81 2 US-09-249-448-7 Sequence 7.	8.9 81 2 US-09-249-473-7 Sequence 7,	8.9 81 2 US-09-498-556-7 Sequence 7, A	8.9 100 1 US-08-465-380-20 Sequence 20,	8.9 100 1 US-08-480-478-48 Sequence 48, 8 9 100 1 US-08-486-397-20 Sequence 20	8.9 100 1 US-08-486-399-20 Sequence 20,	8.9 100 1 US-08-461-965-20 Sequence 20, 8 9 100 1 HS-08-326-110A-48 Sequence 48	8.9 100 1 US-08-634-641-20 Sequence 20,	8.9 100 2 US-09-249-4712-20 Sequence 20, 8.9 100 2 US-09-249-472-20 Sequence 20,	8.9 100 2 US-09-249-451-20 Sequence 20,	8.9 100 2 US-09-249-461-20 Sequence 20,	8.9 100 2 US-09-249-448-20 Sequence 20, 8 9 100 2 HS-09-249-473-20	8.9 100 2 US-09-498-556-20 Sequence 20,	8.9 140 2 US-09-252-991A-25894 Sequence 258	8.9 192 1 US-08-468-570-81 Sequence 81	8.9 192 1 US-08-290-665A-81 Sequence 81, 8.9 192 2 US-08-466-601A-81 Sequence 81,	8.9 192 4 PCT-US95-10398-81 Sequence 81	8.7 381 2 US-09-23/-380-2 8.7 93 2 US-09-640-211A-975 Sequence 979	8.7 103 2 US-09-950-933A-52 Sequence 52, App	8.7 108 2 US-09-950-933A-61 Sequence 61, App 8 7 119 2 US-08-206-945D-129 Semience 129, Ap	8.7 153 1 US-08-050-319B-52 Sequence 52, App	8.7 153 1 US-08-465-982-52 Sequence 52,	8.7 153 2 US-08-477-347-12 Sequence 12,	8.7 153 2 US-08-476-862-3 Sequence 3,	8.7 153 2 US-09-800-909-3 Sequence 3,	8.7 153 2 US-09-800-908-12 Sequence 12,	8.7 154 2 US-08-828-683A-12 Sequence 12,	8.7 154 2 US-09-523-323-53 Seguence 53, 8.7 157 1 US-08-050-3198-50 Seguence 50,

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RESULT 3
US-09-854-864-6

J GSQUENCE 6, Application US/09854864

REGULGAUT. THILL LARS EYDE

A PAPLICANT: THILL, LARS EYDE

APPLICANT: THILL OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-6868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 51

TYPE: PRI
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US-09-949-016-11115, Application US/09949016
; Sequence 11115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    TITLE OF INVENTION: POLYMORPHIGNS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    FILE REFERENCE: CLOO1307
    CURRENT APPLICATION NUMBER: US/09/949,016
    CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/211,755
    PRIOR PELING DATE: 2000-10-20
    PRIOR PLING DATE: 2000-10-03
    PRIOR PLING DATE: 2000-10-03
    PRIOR PLING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOFTHARE: PSECSEQ for Windows Version 4.0
; SEQ ID NO 11115

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Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 51; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-05-06
              ; NUMBER OF SEQ ID NOS: 17; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 11; LENGTH: 184; TYPE: PT ; ORGANISM: Homo sapiens US-09-565-423-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human
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US-09-565-423-11
US-09-565-423-11
Squence 11, Application US/09565423
Squence 11, Application US/09565423
GGENERAL INFORMATION:
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
SPRIOR PILLING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
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Sequence 21, Application US/09854864

Sequence 21, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-666B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 58
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING AFRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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                             1 MAGOCSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.0%; Score 249; DB 2; 1
100.0%; Pred. No. 1.3e-22;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 41
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09854864
Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.04
Matches 44; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                 RESULT 6
US-09-854-864-21
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US-09-854-864-13
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| Patent No. 6774106
| Patent No. 6774106
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: THEILL, LARS EYDE
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-6868
| CURRENT APPLICATION NUMBER: US/09/854,864
| CURRENT APPLICATION NUMBER: US 60/204,039
| PRIOR FILING DATE: 2000-05-12
| PRIOR FILING DATE: 2000-06-17
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 9
| LENTH: 283
                                                                                                                                                                                                                                                                       RESULT 4

US-09-854-864-5

i Sequence 5, Application US/09854864

j Patent No. 6774106

i GENERAL INFORMATION:
    APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
    TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-6868

CURRENT FILING DATE: 2001-09-12

PRIOR PILING DATE: 2001-05-12

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR PILING DATE: 2000-05-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 5

LENGTH: 181
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95.1%; Score 269; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.1%; Score 269; DB 2; Length 283; Best Local Similarity 100.0%; Pred. No. 2.9e-24; Matches 48; Conservative 0; Mismatches 0; Indels
                                                                 95.1%; Score 269; DB 2; Length 51; 100.0%; Pred. No. 4.7e-25; ive 0; Mismatches 0; Indels
                                                                                                                                                               4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                         Best Local Similarity 100.0
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5
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; ORGANISM: Homo sapiens
US-09-854-864-9
; ORGANISM: Homo sapiens
US-09-854-864-6
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US-09-854-864-9
                                                                        Query Match
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Sequence 10, Application US/09854864

| Sequence 10, Application US/09854864
| Patent No. 6774106
| GENERAL INPORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: YU, GANG
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-6868
| CURRENT APPLICATION NUMBER: US 60/204,039
| PRIOR PILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-05-17
| NUMBER OF SEQ ID NOS: 31
| SEQ ID NO 10
| SEQ ID NO 10
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Sequence 12, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: TU, GAMP

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 64.0%; Score 181; DB 2; Length 281; Best Local Similarity 70.8%; Pred. No. 8.2e-14; Matches 34; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                    64.0%; Score 181; DB 2; Length 185; 70.8%; Pred. No. 5.2e-14; ive 4; Mismatches 8; Indels
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                                     CURRENT FILING DATE: 2001-09-11
PRICR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
LENGTH: 185
                    CURRENT APPLICATION NUMBER: US/09/854,864
                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-854-864-12
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US-09-854-864-10
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sequence 13, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REPERENCE: A-6868

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTIN VERSION 3.1

LENGTH: 81
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, GANG
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLXS/AGP-3, AND TACI
FILE REFERENCE: A-686B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09565423

| Sequence 17, Application US/09565423
| Patent No. 6475987
| GENERAL INFORMATION:
| APPLICANT Shu, Hong-Bing |
| TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND |
| TITLE OF INVENTION: METHODS OF USE THEREOF |
| TITLE OF INVENTION: METHODS OF USE THEREOF |
| TITLE OF INVENTION: METHODS OF USE THEREOF |
| TITLE OF INVENTION: METHODS OF USE THEREOF |
| TITLE OF INVENTION: METHODS OF USE THEREOF |
| TITLE OF INVENTION: METHODS: US/09/565,423 |
| CURRENT FILING DATE: 2000-05-05 |
| PRIOR APPLICATION NUMBER: GO/132,892 |
| PRIOR PELING DATE: 1999-05-06 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTWARE: PATENTIN VET. 2.1 |
| SOFTWARE: PATENTIN VET. 2.1 |
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Pred. No. 9.2e-17;
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Pred. No. 5.2e-14;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.0%; Score 201; DB Best Local Similarity 100.0%; Pred. No. 9.2% Matches 34; Conservative 0; Mismatches
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Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%;
70.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Mus musculus US-09-565-423-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Consensus
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US-09-854-864-11
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S-US-ZOU-ZOUE 6, Application US/09290333
Sequence 6, Application US/09290333
Sequence 6, Application US/09290333
Sequence 6, Application US/09290333
GENERAL INFORMATION:
APPLICANT: Bram. Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: A LYMPHOCYTE ACIDS ENCODING THE SAME AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.9%; Score 67.5; D
30.6%; Pred. No. 1.4;
Live 9; Mismatches
               APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNAY AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REPERENCY DOCKET NUMBER: 1340-1-007
TELECHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 201-487-5800
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            TELEPAX: 201-143-1684
INPORMATION POS SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 30.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-termir
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-810-572A-6
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US-09-290-333-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09854864

| Batent No. 6774106 |
| General Information US/09854864 |
| Batent No. 6774106 |
| General Information US/09854864 |
| General Information US/09664 |
| General Information US/09664 |
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI |
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI |
| FILE REFERENCE: A-686B |
| CURRENT APPLICATION NUMBER: US/09/854,864 |
| CURRENT APPLICATION NUMBER: US 60/204,039 |
| PRIOR PLING DATE: 2000-05-12 |
| PRIOR PILING DATE: 2000-05-12 |
| PRIOR FILING DATE: 2000-06-17 |
| NUMBER OF SEQ ID NOS: 31 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 20 |
| TENTY: SPECIAL OF SET OF
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Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: Bram, Richard J.
APPLICANT: OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE TITLE OF INVENTION: 11 FERSOF NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                          Score 104; DB 2; Length 117;
Pred. No. 4.5e-05;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 2 AQCEYFDSLLHAC-PC-LRCS----PPTCQ-YC--SVT-SVKG 34
                                                                                                                                                                                                                                                                                                                                     9 SONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: SIBM PC comparible
OPERATER: PSTEPM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67.5; DB 2;
Pred. No. 0.47;
9; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 43
                                                                                        ; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12
SOFTWARE: Patentin version 3.1 SEQ ID NO 12
                                                                                                                                                                                                       Query Match
Best Local Similarity 69.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 23.9%;
Best Local Similarity 30.6%;
Matches 11; Conservative
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-854-864-20
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US-08-810-572A-6
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Sequence 2, Application US/08810572A

Sequence 2, Application US/08810572A

Patent No. 5869102:

GENERAL INFORMATION:

APPLICANT: Won Bulow, Gotz

TITLE OF INVENTION: ALYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: #11 Hackensack Ave, Continental Plaza, 4th
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTONREY/AGENT INPORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET NUMBER: 1340-1-007
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
                                          8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
                 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
23.9%; Score 67.5; Di
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 9; Mismatches
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07601
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von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SUBFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
                                                                                                                                                                                                                            7;
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                                                                                                                                                                             Query Match

23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
WIEDLING TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             34 CPEEQYWDPLLGICMSCKTICNHQS-QRTCAAFCRS 68
                                                                                                                                                                                                                                                                     8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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CIGASILIANG DATE: 14-Feb-2001
CIASSIPETCATION: cURKNOWN:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: cURKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNDER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                      ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09782857A Patent No. 6500428 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THEREOF
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N.terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.9
Best Local Similarity 30.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
US-09-782-857A-6
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APPLICANT: Bram, Richard J.
APPLICANT: Bram, Gotz
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                <u>:</u>
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <university control of the control of 
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23.9%; Score 67.5; Dl
Best Local Similarity 30.6%; Pred. No. 2.6;
Matches 11; Conservative 9; Mismatches
   1 Similarity 30.6%; Pred. No. 2.6; 11; Conservative 9; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09782857A Patent No. 6500428 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09879919
Patent No. 6541224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-879-919-22
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US-09-782-857A-2
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APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADAVIG A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 26,742
REPERBUCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 201-487-5800
TELEPAR: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.9%; Score 67.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ); SEQUENCE DESCRIPTION; SEQ ID NO: US-09-290-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09290333; Patent No. 6316222; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          23.9%;
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 293 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                α...
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                     N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.9°
Best Local Similarity 30.6°
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             US-08-810-572A-2
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US-09-290-333-2
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APPLICANT: THEILL, LARS EVDE
APPLICANT: THEILL, LARS EVDE
APPLICANT: THEILL, LARS EVDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/984,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIIN VERSION 3.1
SQPTWARE: PATCHIIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
23.9%; Score 67.5; DB 2; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.6;
Matches 11; Conservative 9; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67.5; DB Pred. No. 3.5; 9; Mismatches
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18-09-854-864-16
Sequence 16, Application US/09854864
Patent No. 6774106
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Best Local Similarity 30.6'
Matches 11; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-854-864-18
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APPLICANT: Baker, Kevin
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
TITLE OF INVENTION: Thereon
FILE REFERENCE: FF527
CURRENT APPLICATION NUMBER: US/09/848,295
CURRENT APPLICATION NUMBER: 60/202,193
PRIOR PILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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JAMERAL INFORMATION: Human Tumor Necrosis Factor Delta and Epsilon TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon FILE SERERENCE: PE253P1
CURRENT PELING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 1990-03-12
PRIOR PILING DATE: 1997-03-12
PRIOR PILING DATE: 1997-03-12
PRIOR PILING DATE: 1997-03-12
PRIOR PILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver: 2.1
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Pred. No. 2.6;
9; Mismatches 15;
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Patent No. 6623941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local S
Matches 11
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Sequence 9626, Application US/09949016

Sequence 9626, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 05/241, 755

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NOS: 207012
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32.6%; Pred. No. 36;
...ve 6; Mismatches 21; Indels
                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       898 KCSPSEYWDEDAPGCKPCHVKCFHCMGPAEDQ--CQTCPMNSL 938
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                                                                                                                                                                    635 QCSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 673
                                                                                                                  ---RCSSNT 32
       30.8%; Pred. No. 19; tive 5; Mismatches
                                                                                                                      7 OCSONEYFDSLLHACIPCOL-
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, ORGANISM: Arabidopsis thaliana
US-09-950-933A-82
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Best Local Similarity 32.6
Matches 14; Conservative
                                             12; Conservative
       Best Local Similarity
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US-09-949-016-9626
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                                                 Matches
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Patent No. 6943241

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 20044
LENGTH: 581
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Patent No. 6943241

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE:

PRIOR FILING DATE:

PRIOR FILING DATE:
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Best Local Similarity 30.8*; Pred. No. 12;
Matches 12; Conservative 5; Mismatches
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
LENGTH: 67
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2834
LENGTH: 880
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ORGANISM: Homo sapiens
US-10-104-047-2834
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US-10-104-047-2804
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-854-864-16
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US-10-104-047-2834
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US-10-104-047-2804
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; Sequence 82, Application US/09950933A
; Sequence 82, Application US/09950933A
; Patent No. 6875907
; GANEAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of ITLE OF INVENTION: Use
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; RIOR PILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 99
Score 63; DB 2; Length 1106;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
21.7%; Score 61.5; DB 2; Length 99;
Best Local Similarity 35.6%; Pred. No. 4.2;
Matches 16; Conservative 7; Mismatches 17; Indels
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20.5%; Score 58; DB 2; Length 1800;
Best Local Similarity 21.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16;
                                                                                                                                                   Query Match
20.7%; Score 58.5; DB 2; Length 670;
Best Local Similarity 42.9%; Pred. No. 72;
Matches 15; Conservative 3; Mismatches 14; Indels
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20.5%; Score 58; DB 2; Length 1792;
Best Local Similarity 21.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 1
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| Patent No. 663807
| GENERAL INFORMATION:
| APPLICANT: Kortesmaa, Jarrko
| APPLICANT: Tryggvason, Karl
| TITLE OF INVERTION: Laminin 8 and Methods For Its Use
| FILE REFERENCE: 99,274-D
| CURRENT APPLICATION NUMBER: US/09/561,818A
| CURRENT PILING DATE: 2000-04-28
| CURRENT PILING DATE: 2000-04-28
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09561818A

Sequence 10. 6638907

GENERAL INFORMATION:

APPLICANT: Kortesmaa, Jarrko

APPLICANT: Tryggvason, Karl

TITLE OF INVENTION: Laminin 8 and Methods For Its Use

FILE REPERENCE: 99,274-D

CURRENT APPLICATION NUMBER: US/09/561,818A

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                       6 GOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORY
                                                   FEATURE:
COTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56253
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TYPE: PRT
ORGANISM: Drosophila melanogaster
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ORGANISM: Homo sapiens
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99 RG 100
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Sequence 18110, Application US/09252991A

Sequence 18110, Application US/09252991A

Sequence 18110, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PELING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18110
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.8%; Score 59; DB 2; Length 556; Best Local Similarity 40.0%; Pred. No. 51; Matches 14; Conservative 6; Mismatches 11; Indels
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Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18110
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LENGTH: 670
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Thu Dec 22 14:13:27 2005

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; ORGANISM: Drosophila melanogaster
US-09-270-767-46867
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20.1%;
Best Local Similarity 31.1%;
Matches 14; Conservative
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US-09-270-767-31650
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US-09-270-767-46867
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40 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDGSGYCVHCQRNTTGEHCEKCLDGYIGDSI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 20.5%; Score 58; DB 2; Length 1824;
1 Similarity 21.0%; Pred. No. 2.4e+02;
13; Conservative 13; Mismatches 20; Indels 16; Gaps
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Squence 2, Application US/09561818A

Patent No. 653807

GENERAL INFORMATION:

APPLICANT: Korteeman, Jarrko

APPLICANT: Arrygovason, Karl

TITLE OF INVENTION: Laminin 8 and Methods For Its Use

FILE REFERENCE: 99,274-D

CURRENT APPLICATION NUMBER: US/09/561,818A

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 1816
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Patent No. 6638907

GENERAL INFORMATION;

APPLICANT: Kryegvason, Karl

TITLE OF INVENTION: Laminin 8 and Methods For Its Use

FITE REFERENCE: 99,274-D

CURRENT APPLICATION NUMBER: US/09/561,818A

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 2; I Pred. No. 2.4e+02;
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Best Local Similarity 21.0%; Prec. No.
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LENGTH: 1824
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-561-818A-2
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Best Local Similarity
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123 RG 124
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99 RG 100
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                                      50 KG 51
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US-09-561-818A-6
                                                                                                                                    RESULT 35
US-09-561-818A-2
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US-09-848-295-2
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; Sequence 2, Application US/09848295;
Patent No. 6623941
; GENERAL INFORMATION:
APPLICANT: Baker, Kevin
; APPLICANT: Baker, Kevin
; TITLE OF INVENTION: Thereon
; TITLE OF INVENTION: Thereon
; TITLE OF INVENTION: Thereon
; FILE REFERENCE: PFS27
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT PILING DATE: 2001-05-04
; PRIOR PILING DATE: 2001-05-04
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NOS: 4
; SEQ ID NOS: 4
; SEQ ID NOS: 4
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Sequence 46867, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 46867

LENGTH: 201
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31650
LENGTH: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 2; Length 201;
Pred. No. 30;
4; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 KCQENSSF----ACPKTNCSLECESGYQMDSNGCPTCECRNYCN 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , TYPE: PRT
, ORGANISM: Drosophila melanogaster
US-09-270-767-31650
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Gaps

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4
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION UMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CSQNEYFDSLLHACIP-CQ---LRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                               Query Match
19.8%; Score 56; DB 1; I
Best Local Similarity 31.6%; Pred. No. 5.7e+02;
Matches 12; Conservative 8; Mismatches 14;
                                                        UTSD:418\KIT
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PRIOR FILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR APPLICATION NUMBER: 60/292,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
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APPLICATION NUMBER: 60/303,231
             NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10037417
Patent No. 6903201
GENERAL INFORMATION:
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Miller, Charles E
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APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
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Vernet, Corine A.M.
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Gorman, Linda
Bedinger, Shlomit R
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Spytek, Kimberly A
                                                                                                                     TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
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Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malyankar, Uriel
Rothenberg, Mark
Stone, David J
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-276-967-2
                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guo, Xiaojia
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Patent No. 581817
GENERAL INFORMATION:
APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Sperm
TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 2; Length 201;
Pred. No. 30;
4; Mismatches 13; Indels
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                                                                                                      7 QCSQNEYFDSLLHAC--IPCQLRC----SSNTPPLTCQRYCN 42
                                                                                                                                             33 KCQENSSF----ACPKTNCSLECESGYQMDSNGCPTCECRNYCN 72
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ZIP: 77210-4433
ZIP: 77210-4433
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          US-09-289-8928-11

Sequence 11, Application US/09589892B

Patent No. 6689583

GENERAL INFORMATION:
APPLICANT: Laible, Gotz

APPLICANT: Laible, Gotz

APPLICANT: Donal
APPLICANT: Donal
APPLICANT: Donal
APPLICANT: Donal
APPLICANT: Bisenhaber, Frank
APPLICANT: Rea, Stephen
TITLE OF INVENTION: Chromatin-Regulator Genes
FILE REFERENCE: 0652.167001
CURRENT APPLICATION NUMBER: US/09/589,892B
CURRENT FILING DATE: 2000-06-09
FRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1996-05-02
PRIOR APPLICATION NUMBER: DE 195 16 776.7
PRIOR FILING DATE: 1995-05-10

NUMBER OF SEQ ID NOS: 21
SEQ ID NO 11
LENGTH: 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-589-892B-11
                   Query Match
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Houstor STATE: Texas
                                                                                                                                                                                                            RESULT 40
US-09-589-892B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-276-967-2
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us-10-077-137-1_copy_1_51.rai

Page 14

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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10932
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
19.8%; Score 56; DB 2; Length 3597;
Best Local Similarity 27.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 5; Mismatches 20; Indels 18; Gaps
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APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tauduser Jr, Araymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT APPLICATION NUMBER: 00/260,018
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR PILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-02-28
PRIOR PLING DATE: 2001-02-28
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-02
PRIOR FILING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR PILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 3597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Lepley, Denise M
APPLICANT: Vernet, Cotine E
APPLICANT: Vernet, Cotine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10037417; Patent No. 6903201; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ellerman, Karen
Malyankar, Uriel M
Rothenberg, Mark
Stone, David J
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Gorman, Linda
Edinger, Shlomit R
Sciore, Paul
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Guo, Xiaojia
Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-10-037-417-6
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SERVERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE REFERENCE: CL001307

CURRENT PAPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 66/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

LENGTH: 3647
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                                                                                                                                                                                                                                                                                                                                                                                                                                             7 QCSQNEYFD---SLLHACIPCQ-------LRCSSNTPPLTCQRYCNASVTNS 48
                                                                                                                                                                                                                                                                                                                                                                                                           -----CSSNTPPLTCQRYCNASVTNS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.6%; Score 55.5; DB 2; Length 3647;
Best Local Similarity 26.7%; Pred. No. 9.9e+02;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                        20; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                Query Match
19.8%; Score 56; DB 2; Length 3600;
Best Local Similarity 27.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MORIKAWA, MINORU
APPLICANT: HARADA, NAOKI
ATILIE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH STREET: PO BOX 747
CITY: FALLS CHURCH STATE: VA COUNTRY: USA COUNTRY: USA ZIP: 22040-0747
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-10932
; Sequence 10932, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                              7 QCSQNEYFD---SLLHACIPCQLR--
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION WUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9, Application US/08718388
; Patent No. 6271362
                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-10-037-417-2
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Gaps

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Sequence 11984, Application US/09902540
; Sequence 11984, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Roger C.
; APPLICANT: Blater, Steven C.
; APPLICANT: Magand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: 120/9902,540
; FILE REFERENCE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; RUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11984
; LENGTH: 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 AERCDAG-FFRTLSGECAPCDCNGNSHECLDGSGFCLHCQRNTTGEHCEKCLDGYIGDSI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AGGCSQNEYPDSLLHACIPCQ-----LRCSSNTPPLTCQRYCNASVTNSV
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Best Local Similarity 22.6%; Pred. No. 5.3e+02;
Matches 14; Conservative 10; Mismatches 22; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 OVVSACAEDPE-DTALRGCVERPVRAIINTPPTGCSIQAPLPDAVVNAGVPLTLTG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 OMAGGCSQNEYFDSLLHACIPCOLRCSSNTPPLTC-----ORYCNASVTNSVKG 51
                                                                                                                                                                                                        Length 991;
                                                                   Score 55; DB 2; Length 392;
Pred. No. 1.1e+02;
                                                                                                                                                                   4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQR--YCNASVTNSV
                                                                                                                     20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kortesman, Jarrko
TITLE OF INVENTION: Laminin 8 and Methods For Its Use
FILE REPREBRENCE: 99,274-D
CURRENT APPLICATION MUMBER: US/09/561,818A
CURRENT APPLICATION MUMBER: US/09/561,818A
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LINGTH: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.4%; Score 55; DB 2; Best Local Similarity 26.8%; Pred. No. 2.8e+02; Matches 15; Conservative 9; Mismatches 24
                                                                                                                     8; Mismatches
  ORGANISM: Drosophila melanogaster
                                                                      Query Match
Best Local Similarity 29.2%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Myxococcus xanthus US-09-902-540-11984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|
RG 100
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             US-09-270-767-41714
                                                                                                                                                                                                                                                                                                                             US-09-902-540-11984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DAFE: 1999-03-17
CURRENT FILING DAFE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogașter
TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogașter
TITLE OF INVENTION: NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
CURRENT FILING DATE: 1999-03-17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41714
LENGTH: 392
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 VATYCPTGDYYDDSLGYCVSRQVA----TPVAGCNRCQYATSTFVNAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.2%; Pred. No. 36;
Matches 14; Conservative 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55.5; DB 2; Length 5 Pred, No. 1.5e+03; 6; Mismatches 13; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT ASYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
FLING DATE:
TLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY UR, GERALD M
REGISTRICE/DOCKET NUMBER: 0230-111
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1070S-8050
INFORMATION FROM SEQ ID NO: 9:
SEQUENCE CARARCTERISTICS:
LENGTH: 5405 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2732 ECPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 QCSQNEYFDSLLHACI-PCQLRCSSNTPPLTCQRYC 41
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; Sequence 41714, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-718-388-9
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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CORRESPONDENCE ADDRESS:
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TELEFAX: (2
                                                                                                    20005
                                                CITY: WA
STATE: D
COUNTRY:
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TYPE: PRT
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US-08-824-996-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6703491
GENERAL INFORMATION:
FALENCE S2231, Application US/09270767
FACENCE S2231, Application US/09270767
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32231
LENGTH: 145
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                Query Match 19.4%; Score 55; DB 2; Length 1816; Best Local Similarity 22.6%; Pred. No. 5.4e+02; Matches 14; Conservative 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                           Sequence 10, Application US/09561818A
Patent No. 6638907
GENERAL INFORMATION:
GENERAL INFORMATION
TITLE OF INVENTION: Laminin 8 and Methods For Its Use
FILE REFERENCE: 99,274-D
CURRENT APPLICATION NUMBER: US/09/561,818A
CURRENT APPLICATION NUMBER: US/09/561,818A
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 54.5; DB
; Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-32231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 RG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 51
US-09-270-767-32231
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                                                  US-09-561-818A-10
                                                                                                                                                                                                                                                           SEQ ID NO 10
LENGTH: 1816
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US-08-999-811-4
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Sequence 2, Application US/08824996B

Patent No. 593620

GENERAL INFORMATION:
APPLICANT: Hu, Jing-Shan
TITLE OF INVENTION:
PILE REFERENCE: PF112D1
CURRENT APPLICATION:
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1994-03-27
EARLIER PELICATION NUMBER: 08/207,550

NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 OCGANREFDENTCOCV-CKRTCPRNOPLNPGKCACECTES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
RAPLICATION DATA:
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS
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GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                       PULICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REBERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
ADDRESSEE: STERNE, KESSLER, C
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv;
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TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 6300 Seare Tower, 233 South Wacker Drive
CITY: Chicago
STREET: 6100 Seare Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION: 312/474-6300
TELEPRATION: 312/474-6300
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CONTRESSED OF SEAR TOWER, 233 South Wacker Drive STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
CITY: Chicago
STATE: 1111nois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.3%; Score 54.5; DB 2;
35.0%; Pred. No. 1.1e+02;
tive 2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-510-133A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08585895; Patent No. 6245530; GENERAL INFORMATION: APPLICANT: Alitalo, Kari; TITLE OF INVENTION: RECEPTOR INFORMER OF SEQUENCES: 35; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/585,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVID A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 35.03
Matches 14; Conservative
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                                                                                                                                                   Sequence 4, Application US/09042105
; Batent No. 6040157
; GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION:
NUMBER OF SEQUENCE: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.3%; Score 54.5; DB 2; Length 350; Best Local Similarity 35.0%; Pred. No. 1.1e+02; Matches 14; Conservative 2; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HERBWITH
CLASSIFICATION NUMBER: US 08/207,550
FLING DATE: B-MAR-1994
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
                                              258 OCGANREFDENTCOCV-CKRTCPRNOPLNPGKCACECTES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 44
QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %5.06-510-133A-33

%Sequence 33, Application US/08510133A

; Patent No. 6221839

; GENERAL INFORMATION:

APPLICANT: Alitalo, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HJ, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
                                           258 OCGANREFDENTCOCV-CKRTCPRNOPINPGKCACECTES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 OCGANREFDENTCOCV-CKRTCPRNOPLNPGKCACECTES 365
    7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 OCSONEYFDSLIHACIPCOLRCSSNTP--PLTCQRYCNAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
                                                                                                                                                               Sequence 2, Application US/08999811
Patent No. 5932540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: WARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 419 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005
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US-09-042-105-2
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US-08-999-811-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10084488
Patent No. 6734285
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTE...
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: TO-DOS/MS-DOS
OPERATING SYSTEM: TO-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      Query Match
19.3%; Score 54.5; DB 2; Length 3
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
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19.3%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 43,975
REFERENCE/DOCKET NUMBER: PF112PCT3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301)309-8504
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/623,725
FILING DATE: 07-56P-2000
APPLICATION NUMBER: US 09/042,105
FILING DATE: 13-MAR-1998
APPLICATION NUMBER: US 09/107,997
FILING DATE: 30-JUN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/084,488
FILING DATE: 28-Feb-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 28113/33072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CRARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MICHELE M. WALES
                                                                                                                                                                                                                                / MOLECULE TYPE: protein
US-08-585-895-33
                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 57
US-10-084-488-4
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/795,430
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/27
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
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Pred. No. 1.3e+02;
2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1488.1000003/EKS
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION OBTA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 1468.1000003
REFERENCE/DOCKET NUMBER: 1468.1000003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFACK: (202)371-2500
INFORMATION SEQUENCE:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                        FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
US/09/042,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 35.0%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-042-105-18
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 61
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Sequence 18, Application US/09042105

Sequence 18, Application US/09042105

Pareint No. 6040101

GENERAL INFORMATION:

APPLICANT: ROSEN, CRAIG A.

APPLICANT: CAO, LIANG

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

NUMBER OF SEQUENCES: 35

CORRESPONDENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERME, KESSLER, GOLDSTEIN & FOX

STREET: 1100 NEW YORK AVENUE

CITY: WASHINGTON

STREET: USA

ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.3%; Score 54.5; DB 2; Length 419; Best Local Similarity 35.0%; Pred. No. 1.38+02; Matches 14; Conservative 2; Mismatches 21; Indels 3
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                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IND PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
CLASSIFICATION NUMBER: US 08/207,550
FILING DATE: 06-JUN-1994
CLASSIFICATION OF AMAR-1994
CLASSIFICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION: NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION: NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION: NUMBER: 36,689
REFERENCE/DOCKET NUMBER: 1408.1000003/EKS
TELECOMMUNICATION NUMBER: 136,689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 OCSONEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 44
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   : 1100 NEW YORK AVENUE WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-09-042-105-2
                                                                                                             USA
                                                                                                             COUNTRY:
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Gaps

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44

Length 419;

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APPLICANT: Ludwig Institute for Cancer Research
Helsinki University Licensing
Alitalo, Kari(U.S. only)
Joukov, Vladmir (U.S. only)
TITLE OF INVENTION: Ascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUNTRY: United States of America
CUNTRY: United States of America
ZIP: 6060-6402
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BIM PC compatible
COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUTER: BAFF COMPUT
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                              327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                               7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS
                                                                                                                                                     Score 54.5; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
TELEPRAX: 312/474-6448
                                                                                                                                 19.3%; bcc. No. 1... 35.0%; Pred. No. 1... 2; Mismatches
                       MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-08-510-133A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-355-700-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09355700 Patent No. 6361946 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEO ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 59
                                                                                                                                 Query Match
Best Local Similarity 35.0%
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-355-700-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 63
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ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: VUNKNOWN>
ATTORNEY/AGRIT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELEPHONE: 312/44-6300
TELEPHONE: 312/44-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54.5; DB 2;
Pred. No. 1.3e+02;
      APFLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
FILING DATE: 01-AUG-1995
FILING DATE: 01-AUG-1995
FILING DATE: 14-NOV-1994
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVIG A.
REGISTRATION NUMBER: 38,153
REGISTRATION NUMBER: 28967/33691
TELEPHONE: 312/474-6300
TELEPAX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LEMETHY: 419 amino acide
LYPE: amino acide
TYPE: amino acide
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19.3%; Score 54.5; Di
Best Local Similarity 35.0%; Pred. No. 1.3e
Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alitalo, Kari
Joukov, Vladomir
TITLE OF INVENTION: Receptor Ligand
WUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 62
US-08-51-133A-35
Sequence 35, Application US/08510133A
Patent No. 6221839
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-795-430-8
APPLICATION NUMBER:
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                                                                      Length 419;
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                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 OCGANREPDENTCOCV-CKRTCPRNOPLNPGKCACECTES 365
                                                                                                                                                                                                   327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 11linois COUNTY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/601,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
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                                                                                                                                                                        7 OCSQNEYFDSLLHACIPCOLRCSSNTP--PLTCQRYCNAS
                                                                      Query Match 19.3%; Score 54.5; DB 2; 1
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.3%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lee, James

Wood, William I.

TITLE OF INVENTION: VEGF-Related Protein
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-355-700-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28113/33118
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: JOUKOV, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08706054A, Patent No. 6451764
                                                                                                                                                                                                                                                                                                                    US-08-601-132-33
; Sequence 33, Application US/08601132
; Patent No. 6403088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2811:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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amino acid
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-601-132-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-706-054A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                   RESULT 65
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US-09-355-700-58
Sequence 58, Application US/09355700
Sequence 58, Application US/09355700
Parent No. 6351946
Helsinki University Licensing
Helsinki University Licensing
Hallinki University Licensing
Hallinki University Licensing
Hallinki University Licensing
Hallinki University Licensing
Alitalo, Kari(U.S. only)
Joukov, Vladimir (U.S. only)
HITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
Frotein and Gene, Mutants Thereof, and Uses Thereof
                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 156
OTHER INFORMATION: /note= "codon 156 can be anything other than cysteine, or can be nothing"
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & Borun STRET: 6000 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                  3
                                   Length 419;
                                                                                21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                               327 OCGANREFDENTCOCV-CKRICPRNOPLNPGKCACECTES 365
                                                                                                                                  44
                                                                                                                                  7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATHORNEL/MARE: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKT NUMBER: 28967/34140
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
TELEFAX: 312/474-640
TELEFAX: 312/474-640
TELEFAX: 25-386
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 aming acids
                              19.3%; Score 54.5; DB 2; 35.0%; Pred. No. 1.3e+02; tive 2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION OFF
FILING DATE: 05-NO. 6361946-1999
CLASSIFICATION ADATA:
APPLICATION NUMBER: 08-1999
FILING DATE: 06-FEB-1997
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: PCT/F196/00427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-AUG-1996
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/58,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 11-ANG-1995
APPLICATION NUMBER: 08/30,011
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FEATURE:
                         Query Match
Best Local Similarity 35.0'
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Gape
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Sequence 33, Application US/08671573B
Sequence 33, Application US/08671573B
Setent No. General
GENERAL INFORMATION:
APPLICANT: Joukov, Vladimir
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 58
SOURBESSEE: MAISHAB11, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
FILE REFERENCE: PF112P1
CURRENT APPLICATION NUMBER: US/08/465,968E
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: PATENTIN VER. 2.0
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Indels
                                      327 QCGANREPDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Saars Tower, 233 South Wacker Drive CITY: Chicago Saars Tower, 233 South Wacker Drive CITY: Chicago Saars Tower, 233 South Wacker Drive STATE: Illinois COUNTRY: United States of America 21P: 60606-6402 COMPUTER READABLE FORM:
MEDIUM TYPE: Elloppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OF PROPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/671,573B FLING DATE: 28-40N-1996 CLASSIFICATION DATA: APPLICATION NUMBER: 08/601,132 FLING DATE: 14-FEB-1996 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/510,133 FLING APPLICATION DATA: APPLICATION NUMBER: 101-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: Gass David A. REGISTRATION NUMBER: 38,153 REFERENCE/DOCKET NUMBER: 28967/33348 REFERENCE/DOCKET NUMBER: 28967/33348
  44
7 OCSONEYFDSLLHACIPCOLRCSSNTP--PLTCORYCNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 OCSONEYFDSLLHACIPCOLRCSSNTP--PLTCQRYCNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.3%; Score 54.5; DB 2; 35.0%; Pred. No. 1.3e+02; tive 2; Mismatches 21;
                                                                                                                                                                ; Sequence 2, Application US/08465968E; Patent No. 6608182; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 35.0 nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-08-465-968-2
                                                                                                                       RESULT 68
US-08-465-968-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44
                                                                  COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS
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19.3%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21;
                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,054A
FILING DATE: 30-Aug-1996
CLASSIFICATION - UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/003491
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 67
US-09-313-299-3
Sequence 3, Application US/09313299B
Fatent No. 657660B
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Mood, William I.
TITLE OF INVENTION: VEGF-RELATED PROTEIN
FILE REFERENCE: P0953RJD1
CURRENT APPLICATION NUMBER: US/09/313,299B
CURRENT APPLICATION NUMBER: US 08/706,054
EARLIER APPLICATION NUMBER: US 08/706,054
EARLIER FILING DATE: 1996-08-30
EARLIER FILING DATE: 1995-09-08
NUMBER OF SEQ ID NOS: 12
TENDIAMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0963R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1-419
OTHER INFORMATION: Sequence source: VRP
Patent No. 6576608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.3
Best Local Similarity 35.0
Matches 14; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-706-054A-3
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Gaps

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Length 419; Indels

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US-10-084-488-2

Sequence 2, Application US/10084488

Patent No. 6734285

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPEATING SYSTEM: PC-DOS/MS-DOS
ODFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 OCGANREPDENTCOCV-CKRTCPRNOPLNPGKCACECTES 365
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19.3%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/623,725
FILING DATE: 07-Sep-2000
APPLICATION NUMBER: US 09/042,105
FILING DATE: 13-MAR-1998
APPLICATION NUMBER: US 09/107,997
FILING DATE: 30-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF112PCT3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,488
FLING DATE: 28-Feb-2002
CLASSIFICATION: <UNKNOWN>
CURRENT APPLICATION NUMBER: US/09/631,092B
CURRENT FILING DATE: 2000-08-02
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                           CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 08/671,573
PRIOR FLING DATE: 1996-06-18
PRIOR APPLICATION NUMBER: 08/601,132
PRIOR PILING DATE: 1996-02-14
PRIOR PELING DATE: 1996-01-12
PRIOR APPLICATION NUMBER: 08/510,133
PRIOR FILING DATE: 1996-01-12
PRIOR FILING DATE: 1996-01-12
PRIOR FILING DATE: 1995-08-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 419
TYPE: PRT
CREANISM: Homo sapiens
US-09-631-0928-33
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TYPE: amino acid
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                  21; Indels
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APPLICANT: LEE, MATKO
APPLICANT: UUTELA, MATKO
APPLICANT: UUTELA, MATKO
APPLICANT: UUTELA, MATKO
APPLICANT: UUTELA, MATKO
APPLICANT: OESTWAN, Arne
APPLICANT: HELDIN, CARL-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, D
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR
TITLE OF INVENTION: TELKESON et al. 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT FILING DATE: 1999-11-10
EARLIER PILING DATE: 1999-11-10
EARLIER PILING DATE: 1999-12-28
EARLIER PILING DATE: 1999-10-04
EARLIER PILING DATE: 1999-10-04
EARLIER PILING DATE: 1999-10-05
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19.3%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 1.38+02;
Matches 14; Conservative 2; Mismatches 21;
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Sequence 33, Application US/09631092B

Patent No. 6730658

Patent INFORMATION:

APPLICANT: Alitalo et al.

TITLE OF INVENTION: RECEPTOR LIGAND VEGF-C

FILE REPERENCE: 28967/33348A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09438046
Patent No. 6706687
GENERAL INPORMATION:
APPLICANT: ERIKSSON, ULF
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
            TELEPHONE: 312/474-6300
TELERAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-671-573B-33
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CORGANISM: Homo sapiens
US-09-438-046-14
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                          TOPOLOGY:
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us-10-077-137-1_copy_1_51.rai

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21; Indels

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APPLICANT: Alitalo, Kari
APPLICANT: Finegold, David N.
APPLICANT: Finegold, David N.
APPLICANT: Finegold, David N.
APPLICANT: Finegold, David N.
APPLICANT: Karkannen, Marika
TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
FILE REPERBENCE: 28967/35255A
CURRENT APPLICATION NUMBER: US(99/375,248
CURRENT FILING DATE: 1999-08-16
EARLIER APPLICATION NUMBER: PCT/US99/06133
EARLIER APPLICATION NUMBER: PCT/US99/06133
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: PATENT A19
TYPE: PRT
ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 OCGANREFDENTCOCV-CKRTCPRNOPLNPGKCACECTES 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54.5; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.0%;
Matches 14; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-468-647A-108
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                                                                                                                                                2;
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                                                                                                                                                Gaps
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Patent No. 6734285

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: HUMAN GENOME SCIENCES, INC.
ADDRESSE: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                      Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTER READBLE FORM:

ZIP: 20850
COMPUTER READBLE FORM:

COMPUTER: 1D9Py disk
COMPUTER: 1D8M PC compatible
COMPUTER: 1BM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18/10/084,488
FILING DATE: 28 FEb-2002
CLASSIFICATION: <a href="https://doi.org/10/10/10/10/10/10/">UNKNOWN></a>
                                                      ch 19.3%; Score 54.5; DB 2; Length 4 1 Similarity 35.0%; Pred. No. 1.3e+02; 14; Conservative 2; Mismatches 21; Indels
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                                                                                                                                                                                                                                      7 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS
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19.3%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21;
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APPLICATION NUMBER: US/09/623,725
FILING DATE: 07-56p-2000
APPLICATION NUMBER: US 09/042,105
FILING DATE: 13-MAR-1998
APPLICATION NUMBER: US 09/107,997
FILING DATE: 30-JUN-1998
ATTORNEY/AGENT INFORMATION:
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-084-488-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 419 amino acids TYPE: amino acid
                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 73
US-10-084-488-18
                                                                                                                                                Matches
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US-U9-468-647A-108
Sequence 108, Application US/09468647A
Sequence 108, Application US/09468647A
Setent No. 6783953
GENERAL INFORMATION:
APPLICANT: Gordon, Robert D
APPLICANT: Sprengel, Jorg J
APPLICANT: Parameter Sequence 108, APPLICANT: Gordon, Anna
APPLICANT: Dijkmans, Anna
APPLICANT: Dhanaraj, Sridevi N
APPLICANT: Us, Jean
APPLICANT: Honaraj, Sridevi N
APPLICANT: Us, Jean
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
FILE REFERENCE: B0192.70011US00
CURRENT APPLICATION NUMBER: US 60/124,967
PRIOR APPLICATION NUMBER: US 60/124,967
PRIOR PILING DATE: 1999-12-21
PRIOR PLING DATE: 1999-13-18
PRIOR PLING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.2
SEQ ID NO 108
SEQ ID NO 108
TENNET A.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.3%; Score 54.5; DB 2; Sest Local Similarity 35.0%; Pred. No. 1.3e+02; Matches 14; Conservative 2; Mismatches 21;
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Sequence 4, Application US/09375248; Patent No. 6764820; GENERAL INFORMATION: APPLICANT: Ferrell, Robert E.

RESULT 74 US-09-375-248-4